

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Harold Kleanthous et al.
- (ii) TITLE OF THE INVENTION: Identification of Polynucleotides
Encoding Novel Helicobacter Polypeptides in the Helicobacter
Genome
- (iii) NUMBER OF SEQUENCES: 370
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Clark & Elbing LLP
 - (B) STREET: 176 Federal Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/833,457
 - (B) FILING DATE: 01-APR-97
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clark, Paul T.
 - (B) REGISTRATION NUMBER: 30,162
 - (C) REFERENCE/DOCKET NUMBER: 06132/041001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-428-0200
 - (B) TELEFAX: 617-428-7045
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 51...212
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTTTTTAGTT TGTTTTGGAG TATAATCCTA CGAAAATTTT AAGGAACGGC ATG GAG      56
                                     Met Glu
                                     1

TTT TTG GGA CTG ATT TTA AGT CTG GCC GCT ATT TTG ATA GCG TTT AAA      104
Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala Phe Lys
      5                      10                      15

AAG CCT GAA AAA GAA AAT TGG GCG TTT GGG ATT TTG ATG GTG GTG TGG      152
Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val Val Trp
      20                      25                      30

TTA GTG GAG CTT ATT ATT TTT ATA GCC CAC AGC TCT AGC GTT TTG CCT      200
Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val Leu Pro
      35                      40                      45                      50

AAC ATG AAT CTA TAAGGGGGAT GCATGGATAA AGAAACCCGA TTTTACAACC TTTT      257
Asn Met Asn Leu

TCTTTGGC      265

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala
  1                      5                      10                      15
Phe Lys Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val
      20                      25                      30
Val Trp Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val
      35                      40                      45
Leu Pro Asn Met Asn Leu
      50

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...617
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCATAGACG ACAAATCAA GCGGTTTTAT CAAAACCAAA AAACTTTAGA ATG AAA	56
Met Lys	
1	
AAA ATT GCT TTC ATT TTG GCT TTA TGG GTG GGC TTG TTA GGG GCG TTT	104
Lys Ile Ala Phe Ile Leu Ala Leu Trp Val Gly Leu Leu Gly Ala Phe	
5 10 15	
GAG CCT AAA AAA AGT CAT ATT TAT TTT GGG GCT ATG GTG GGT TTA GCT	152
Glu Pro Lys Lys Ser His Ile Tyr Phe Gly Ala Met Val Gly Leu Ala	
20 25 30	
CCT ATT AAA ATA ACC CCA AAA CCG GCT AGT GAT TCT TCT TAT ACG GCT	200
Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr Thr Ala	
35 40 45 50	
TTT TTA TGG GGG GCT AAA GGA GGG TAT CAA TTC GCT TTT TTT AAA GCT	248
Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe Lys Ala	
55 60 65	
CTA GCG TTA AGG GGT GAA TTT TCC TAC CTT ATG GCA ATC AAA CCC ACC	296
Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys Pro Thr	
70 75 80	
GCA CTG CAC ACG ATT AAC ACT TCT TTA TTG AGC TTA AAT ATT GAT GTG	344
Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile Asp Val	
85 90 95	
TTA AGC GAT TTT TAC ACT TAC AAA AAA TAC AGC TTT GGG GTG TAT GGG	392
Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val Tyr Gly	
100 105 110	
GGG CTT GGG ATA GGG TAT TTT TAT CAA AGC AAC CAT TTA GGC ATG AAA	440
Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly Met Lys	
115 120 125 130	
AAT AGT TCG TTT ATG GGT TAT AAC GGC TTG TTT AAT GTG GGG CTT GGC	488
Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly Leu Gly	
135 140 145	
AGC ACG ATC GAT CGC CAC CAC CGC ATA GAG CTT GGG GCT AAA ATC CCT	536
Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys Ile Pro	
150 155 160	
TTT TCA AAG ACT AGA AAT TCT TTT AAA AAT CCT TAT TTT TTA GAG AGC	584
Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu Glu Ser	
165 170 175	
GTT TTT ATC CAT GCG ACT TAT AGC TAT ATG TTT TAAGAGAGAA TAGCCTATTA	637
Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe	
180 185	

GTGGTCGTTA TCAATAAGAT AAGATCCTTA ATG

670

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Lys	Ile	Ala	Phe	Ile	Leu	Ala	Leu	Trp	Val	Gly	Leu	Leu	Gly
1				5				10					15		
Ala	Phe	Glu	Pro	Lys	Lys	Ser	His	Ile	Tyr	Phe	Gly	Ala	Met	Val	Gly
		20					25					30			
Leu	Ala	Pro	Ile	Lys	Ile	Thr	Pro	Lys	Pro	Ala	Ser	Asp	Ser	Ser	Tyr
		35				40					45				
Thr	Ala	Phe	Leu	Trp	Gly	Ala	Lys	Gly	Gly	Tyr	Gln	Phe	Ala	Phe	Phe
	50				55					60					
Lys	Ala	Leu	Ala	Leu	Arg	Gly	Glu	Phe	Ser	Tyr	Leu	Met	Ala	Ile	Lys
65				70					75				80		
Pro	Thr	Ala	Leu	His	Thr	Ile	Asn	Thr	Ser	Leu	Leu	Ser	Leu	Asn	Ile
			85					90					95		
Asp	Val	Leu	Ser	Asp	Phe	Tyr	Thr	Tyr	Lys	Lys	Tyr	Ser	Phe	Gly	Val
		100					105					110			
Tyr	Gly	Gly	Leu	Gly	Ile	Gly	Tyr	Phe	Tyr	Gln	Ser	Asn	His	Leu	Gly
	115				120							125			
Met	Lys	Asn	Ser	Ser	Phe	Met	Gly	Tyr	Asn	Gly	Leu	Phe	Asn	Val	Gly
130					135					140					
Leu	Gly	Ser	Thr	Ile	Asp	Arg	His	His	Arg	Ile	Glu	Leu	Gly	Ala	Lys
145				150					155					160	
Ile	Pro	Phe	Ser	Lys	Thr	Arg	Asn	Ser	Phe	Lys	Asn	Pro	Tyr	Phe	Leu
			165				170						175		
Glu	Ser	Val	Phe	Ile	His	Ala	Thr	Tyr	Ser	Tyr	Met	Phe			
		180					185								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...380
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCGTGAAAA AAATTGAGTT GAATCAAAAC CTGCATTAAG GATTAAAAGA ATG CTC 56
Met Leu
1

AAA AAA AGT TTG TTA TTG CTT GTT TTT TTA GTC TTA CAG CTT AGC GGC 104
Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu Ser Gly
5 10 15

GCT GAA GAA AAC AAT CAA GCC CCA AAA AAC ACG CCC CCT GAA TTA AAC 152
Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu Leu Asn
20 25 30

CCC GCT AAC GCT AAG GGC GCG CCA AAC TCT AAC ACC CAG ATC ACC CCT 200
Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile Thr Pro
35 40 45 50

AAA AAC GAT AAC TCT AAC CTG TTA GAC AAA TTA GGT TCG CCT GAA AAC 248
Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro Glu Asn
55 60 65

GCT CAA ACC GAG CTT TCT GCC GGT ATT GAT TTG GCT AAA AAG GGC GAT 296
Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys Gly Asp
70 75 80

TAT CAA GGG GCT TTC AAG CTT TTT TCC CAA TCG TGC GAT AAT GGT AAT 344
Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn Gly Asn
85 90 95

GCG GCC GGG TGT TTT GCA AGT GGG GGC GAT GTA TGC TAATGGGGTA GGGATC 396
Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys
100 105 110

CAAACCAACA GATTAAAAGC CGCTCGCTAT TATGAATG 434

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu
1 5 10 15
Ser Gly Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu
20 25 30
Leu Asn Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile
35 40 45
Thr Pro Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro
50 55 60
Glu Asn Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys
65 70 75 80
Gly Asp Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn

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(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(A) NAME/KEY: Coding Sequence

- (B) LOCATION: 73...522

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

6

130 135 140

CCT GGA TAC TTC CCT TAC GCT TTT TAT TGATTGAGTG GCTTTAGAAA GCGTGGT 549
 Pro Gly Tyr Phe Pro Tyr Ala Phe Tyr
 145 150

GGTGTTGGTG TTTTACTCA AACACG 575

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	His	Gln	Asn	Asn	Lys	Thr	Phe	Leu	Pro	Ser	Gln	Ser	Ala	His	Leu
1				5					10					15	
Ser	Lys	Ile	Ile	Leu	Phe	Leu	Asn	Thr	Gly	Phe	Leu	Ala	Tyr	Leu	Leu
		20						25					30		
Ser	Ala	Cys	Gly	Ala	Asn	Val	Pro	Ile	Glu	Glu	Val	Leu	Val	Lys	Asp
		35					40					45			
Pro	Lys	Glu	Thr	Lys	Ala	Gln	Glu	Val	Ala	Arg	Glu	Glu	Lys	Ala	Ile
		50				55					60				
Gln	Gln	Glu	Asn	Ala	Thr	Ile	Asp	Ala	Arg	Thr	Thr	Pro	Leu	Ile	Asn
					70					75				80	
Arg	Phe	Thr	Asn	Tyr	Ser	Ala	Tyr	Gly	Ser	Leu	Asn	Gly	Phe	Tyr	Asn
			85						90					95	
Ser	Val	Asp	Asn	Leu	Asn	Ser	Pro	Met	Gln	Asn	Gly	Met	Tyr	Gly	Gly
			100					105					110		
Tyr	Tyr	Met	Pro	Tyr	Tyr	Tyr	Met	Pro	Tyr	Gly	Phe	Met	Pro	Tyr	Gly
		115					120					125			
Ser	Gly	Leu	Met	Pro	Tyr	Gly	Pro	Tyr	Gly	Tyr	Gly	Ala	Pro	Gly	Tyr
		130				135					140				
Phe	Pro	Tyr	Ala	Phe	Tyr										
145					150										

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...860
- (D) OTHER INFORMATION:

[illegible]

[REDACTED]

GAT CCG GCG ATT TTC CAG TTC CTT TTT AAT TTA GGG ATC CGC ACC CAT 728
 Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg Thr His
 215 220 225

ATT GGC CGG CAT CAA GAA TTT GAC TTT GGC GTG AAG ATT CCC ACT ATC 776
 Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro Thr Ile
 230 235 240

AAT GTT TAT TAT TTT AAC CAT GGG AAT TTG AGC TTC ACT TAC CGC CGT 824
 Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr Arg Arg
 245 250 255

CAA TAC AGC CTT TAT GTG GGG TAT CGT TAC AAT TTC TGATTTAAAA CGCTTG 876
 Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe
 260 265 270

TTTTTCTCTA ATTGAATTTT CAATTAGAGT TTTC 910

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu
 1 5 10 15
 Gly Asn Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln
 20 25 30
 Leu Glu Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala
 35 40 45
 Trp Tyr Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val
 50 55 60
 Lys Asn Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val
 65 70 75 80
 Gly Lys Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val
 85 90 95
 Gly Tyr Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr
 100 105 110
 Tyr Gly Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu
 115 120 125
 Thr Ser Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr
 130 135 140
 Lys Val Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val
 145 150 155 160
 Gly Ile Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe
 165 170 175
 Gly Phe Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr
 180 185 190
 Thr Gly Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr
 195 200 205
 Ser Leu Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg

210 215 220
 Thr His Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro
 225 230 235 240
 Thr Ile Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr
 245 250 255
 Arg Arg Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe
 260 265 270

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...1305
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCAATTAAA AGGAATTTTA ACTAAAATAT TGAGTTTAAA TCCACGATGA GTTTTTA ATG 60
 Met
 1

CAA TAT AAG AAA AAT AAG AAA AGA TAT TAT TAT TTA GCG TTA GGG ATC 108
 Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly Ile
 5 10 15

TTT TTT TTA AAT GGT CTG TCT TTG AAA GCT TTA GAA ATC GCC GTC AAA 156
 Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val Lys
 20 25 30

CCT TTT GGC TAT CTG GGG CTA TTA TAT AAT CAA GGG GCG CAA AAA AAC 204
 Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys Asn
 35 40 45

CCT CAC AGC TAT GTG GGG GCT TTA GCG CGT CTT GGG GTG GAT TTT TCT 252
 Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe Ser
 50 55 60 65

TAT AGC AAC GGG TGG TCC TTT GGT ATT GGA GCG ATT GGG GCT TGG AAT 300
 Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp Asn
 70 75 80

ATT TAT AAC AAA CAG CGT TTG GCT AAC CTT TAT ATC AGT CTA GGG AAT 348
 Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly Asn
 85 90 95

TTT TTT GGT AGT TCT AAA AAT GTT AAA CCT TAT TTG AGC GCT GGC GAT 396
 Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly Asp
 100 105 110

GTT TCT GAT GCG TAT GTT CAA TAC ACT AAC CAG CGT TTT AAA ATC GCT	444
Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile Ala	
115 120 125	
TTA GGG CGT TTC AAT ACC GAT TTT GTG GAT TTT GAT TGG ATA GGG GGC	492
Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly Gly	
130 135 140 145	
AAT ATT CAA GGG GTT TCT GTA GCT TTT AAG CAA AAT TCC ATG CGT TAT	540
Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg Tyr	
150 155 160	
TTT GGG ATT TTT ATG GAT AGC ATG CTT TAT AAT GGG CAT CAA ATC AAC	588
Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile Asn	
165 170 175	
AAA GAG CAA GGG AAT CGG ATC GCT ACT TCC CTA AAC GCT CTA GCG TCT	636
Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala Ser	
180 185 190	
TAT GAC CCT GTG TCT AAA CGC TTG TAT GTG GGG GGG GAA GTG TTT GTT	684
Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe Val	
195 200 205	
TTA GGT GCA GAA TAC AGG CAT GAA AAT CTT AAA GTG GTG CCT TTT ATT	732
Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe Ile	
210 215 220 225	
TTA ACG GAC ACC CGC TTG CCT TTA TCC ACC CAA AAT GTT TTA GTG CAA	780
Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val Gln	
230 235 240	
GTG GGG GGT AAG TTG GAG TAT GAC GCT TCT TTA GCT AAG GGT TTC ACT	828
Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe Thr	
245 250 255	
TCG CAC ACT CTA GTG CAT GGC ATG TAT CAA TAC GGC AAC ACT GAT GCG	876
Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp Ala	
260 265 270	
GCT ACA AGC GTT AAA AAT GCC GGC TTG TTT TTG ATC GAT CAA ACT TTT	924
Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr Phe	
275 280 285	
AAA TAC AAA ATT TTT AAT TTT GGA ACG GGT TTT TAT ATC GTT CCG GCA	972
Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro Ala	
290 295 300 305	
AGA AAC AAT AAG GGC TAT CTA TGG ACT TTT AAT GAC AGG ACT AAA TTC	1020
Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys Phe	
310 315 320	
TAT GGC CGT GGG ATC AAT GCG CCC GGC GTG CCA GCG ATT TAT TTT GCA	1068
Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe Ala	
325 330 335	
AAC TCT AGC ATT TCA GGC TAT GTT TTT TTA GGG CTT AAG ACT AAA AGG	1116
Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys Arg	

	195		200		205
Val	Leu Gly Ala Glu Tyr	Arg His Glu Asn Leu	Lys Val Val Pro Phe		
	210	215	220		
Ile	Leu Thr Asp Thr Arg	Leu Pro Leu Ser Thr	Gln Asn Val Leu Val		
225		230	235		240
Gln	Val Gly Gly Lys Leu	Glu Tyr Asp Ala Ser	Leu Ala Lys Gly Phe		
	245	250	255		
Thr	Ser His Thr Leu Val	His Gly Met Tyr Gln	Tyr Gly Asn Thr Asp		
	260	265	270		
Ala	Ala Thr Ser Val Lys	Asn Ala Gly Leu Phe	Leu Ile Asp Gln Thr		
	275	280	285		
Phe	Lys Tyr Lys Ile Phe	Asn Phe Gly Thr Gly	Phe Tyr Ile Val Pro		
	290	295	300		
Ala	Arg Asn Asn Lys Gly	Tyr Leu Trp Thr Phe	Asn Asp Arg Thr Lys		
305		310	315		320
Phe	Tyr Gly Arg Gly Ile	Asn Ala Pro Gly Val	Pro Ala Ile Tyr Phe		
	325	330	335		
Ala	Asn Ser Ser Ile Ser	Gly Tyr Val Phe Leu	Gly Leu Lys Thr Lys		
	340	345	350		
Arg	Val Arg Leu Asp Ala	Met Val Ala Phe Gly	Asp Tyr Gln Glu Tyr		
	355	360	365		
Ser	Leu Met Ser Ser Phe	Arg Val Trp Thr Tyr	Arg Ser Leu Ser Phe		
	370	375	380		
Asp	Met Gly Gly Gly Tyr	Val Tyr Ala Tyr Asn	Ser Lys Ala Thr Arg		
385		390	395		400
Lys	Ser Leu Gly Asn Ser	Ser Phe Val Phe Phe	Gly Lys Phe Leu Phe		
	405	410	415		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...1509
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTATGCTTCT TTGTTTTTAG ATCAGTTAAG AATTGTAGTC TTTAAGATGT ATTGGCTATT	60
AAAAGGAAAA AA ATG AAA AAT AGC ACG CCT TTA AAG AAT CAA GTT TTT TGT	111
Met Lys Asn Ser Thr Pro Leu Lys Asn Gln Val Phe Cys	
1 5 10	
GGG TTA TAT GTT TTA AGT TTG AGC GCT TCT TTG CAA GCG TTT GAT TAT	159
Gly Leu Tyr Val Leu Ser Leu Ser Ala Ser Leu Gln Ala Phe Asp Tyr	
15 20 25	
AAA ATT GAA GTT TCA GCG GAG TCC TTT TCT AAA GTT GGC TTT AAT AAA	207
Lys Ile Glu Val Ser Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys	

30				35				40				45				
AAA Lys	AAG Lys	ATT Ile	GAT Asp	ATA Ile 50	GCT Ala	AGG Arg	GGG Gly	ATT Ile 55	TAT Tyr	CCT Pro	ACA Thr	GAG Glu	ACT Thr	TTT Phe 60	GTA Val	255
ACC Thr	GCT Ala	GTA Val	GGG Gly 65	CAG Gln	GGC Gly	AAT Asn	ATC Ile	TAT Tyr 70	GCG Ala	GAT Asp	TTT Phe	TTA Leu	CCC Pro 75	AAA Lys	GGC Gly	303
CTT Leu	AAA Lys	GAT Asp 80	CAA Gln	GGG Gly	CAT His	GTT Val	TTA Leu 85	GAG Glu	GGA Gly	AAA Lys	ATC Ile	GGT Gly 90	GGC Gly	ACG Thr	CTA Leu	351
GGA Gly	GGG Gly 95	GTC Val	GCT Ala	TAT Tyr	GAT Asp	AGC Ser 100	ACG Thr	AAA Lys	TTC Phe	AAT Asn	CAA Gln 105	GGC Gly	GGA Gly	TCG Ser	GTT Val	399
ATT Ile 110	TAT Tyr	AAC Asn	TAC Tyr	ATC Ile	GGT Gly 115	TAT Tyr	TGG Trp	GAT Asp	GGC Gly 120	TAT Tyr	TTA Leu	GGG Gly	GGT Gly	AAA Lys	AGA Arg 125	447
GCC Ala	TTG Leu	CTT Leu	GAT Asp	GGC Gly 130	ACG Thr	AGT Ser	ATC Ile	CAT His	GAG Glu 135	TGC Cys	GCG Ala	CTT Leu	GGA Gly	TCT Ser 140	GAT Asp	495
GGC Gly	AAG Lys	GTG Val	ATT Ile 145	GAT Asp	TCT Ser	ATA Ile	GCG Ala	TGC Cys 150	GGG Gly	AAC Asn	GCT Ala	AGG Arg	GCC Ala 155	AAT Asn	AAA Lys	543
ATC Ile	CGC Arg	CGT Arg 160	AAT Asn	TAC Tyr	TTG Leu	ATG Met	AAT Asn 165	AAC Asn	GCT Ala	TTT Phe	TTA Leu	GAA Glu 170	TAC Tyr	CGC Arg	TAT Tyr	591
AAA Lys	GAT Asp 175	ATT Ile	TTT Phe	TTA Leu	GCT Ala	AAG Lys 180	GGA Gly	GGG Gly	CGT Arg	TAT Tyr	CAA Gln 185	TCC Ser	AAT Asn	GCT Ala	CCT Pro	639
TAT Tyr 190	ATG Met	AGC Ser	GGT Gly	TAC Tyr	ACG Thr 195	CAA Gln	GGC Gly	TTT Phe	GAA Glu 200	ATC Ile	AGC Ser	GCT Ala	AAA Lys	GTC Val	AAG Lys 205	687
GAT Asp	AAA Lys	AAT Asn	GAA Glu	GGA Gly 210	ATC Ile	CAC His	AAA Lys	TTA Leu	TGG Trp 215	TGG Trp	TTT Phe	AGC Ser	TCA Ser	TGG Trp 220	GGT Gly	735
AGG Arg	GCG Ala	TTC Phe	GCT Ala 225	TAT Tyr	GGG Gly	GAG Glu	TGG Trp	ATT Ile 230	TAT Tyr	GAT Asp	TTT Phe	TAT Tyr	TCT Ser 235	CCA Pro	AGA Arg	783
ACC Thr	GTG Val	GTT Val 240	AAA Lys	AAC Asn	GGG Gly	CGC Arg	ACT Thr 245	TTG Leu	AAT Asn	TAT Tyr	GGT Gly	ATC Ile 250	CAT His	TTA Leu	GTG Val	831
AAT Asn	TAT Tyr 255	ACT Thr	TAT Tyr	GAA Glu	AGA Arg	AAA Lys 260	GGG Gly	GTT Val	AGC Ser	GTT Val 265	AGC Ser	CCT Pro	TTT Phe	TTC Phe	CAA Gln	879

TTT Phe 270	TCG Ser	CCT Pro	GGG Gly	ACT Thr	TAT Tyr 275	TAT Tyr	AGC Ser	CCT Pro	GGG Gly	GTG Val 280	GTT Val	GTA Val	GGC Gly	TAT Tyr	GAT Asp 285	927	
AGT Ser	AAC Asn	CCT Pro	AAT Asn	TTT Phe 290	AAC Asn	GGC Gly	GTT Val	GGC Gly	TTT Phe 295	AGA Arg	TCC Ser	GAA Glu	ACA Thr	AAA Lys 300	GCT Ala	975	
TAT Tyr	ATT Ile	TTG Leu	CTC Leu 305	CCT Pro	GTC Val	CAT His	GAC Asp	CCC Pro 310	TTA Leu	AGA Arg	AGG Arg	GAT Asp 315	ACT Thr	TAT Tyr	CGT Arg	1023	
TAC Tyr	GCT Ala	ATA Ile 320	AAG Lys	GCT Ala	GGC Gly	ACT Thr	GCC Ala 325	GGG Gly	CAA Gln	AGC Ser	TTG Leu	CTC Leu 330	ATT Ile	AGG Arg	CAA Gln	1071	
CGA Arg	TTT Phe 335	GAT Asp	TAC Tyr	AAT Asn	GAA Glu	TTT Phe 340	AAT Asn	TTT Phe	GGG Gly	GGA Gly	GCG Ala 345	TTT Phe	TAT Tyr	AAA Lys	GTA Val	1119	
TGG Trp 350	AAA Lys	AAC Asn	GCA Ala	AAC Asn	GCT Ala 355	TAC Tyr	ATC Ile	GGC Gly	ACG Thr	ACA Thr 360	GGA Gly	AAC Asn	CCT Pro	TTA Leu	GGC Gly 365	1167	
ATT Ile	GAT Asp	TTT Phe	TGG Trp 370	ACC Thr	AAT Asn	AGC Ser	GTT Val	TAT Tyr	GAT Asp 375	ATA Ile	GGG Gly	CAA Gln	GCT Ala	TTA Leu 380	AGC Ser	1215	
CAT His	GTG Val	GTA Val	ACC Thr 385	GCT Ala	GAT Asp	GCC Ala	GTC Val	TCT Ser 390	GGT Gly	TGG Trp	GTT Val	TTT Phe	GGT Gly 395	GGG Gly	GGC Gly	1263	
GTG Val	CAT His	AAA Lys 400	AAG Lys	TGG Trp	CTG Leu	TGG Trp	GGG Gly 405	ACT Thr	TTA Leu	TGG Trp	CGT Arg	TGG Trp 410	ACT Thr	AGC Ser	GGC Gly	1311	
ACT Thr	TTA Leu 415	GCC Ala	AAT Asn	GAA Glu	GCG Ala	AGT Ser 420	GCG Ala	GCT Ala	GTT Val	AAT Asn	GTG Val 425	GGC Gly	TAT Tyr	AAG Lys	ATC Ile	1359	
AGT Ser 430	AAG Lys	AGT Ser	TTG Leu	ACA Thr	GCG Ala 435	AGC Ser	GTG Val	AAA Lys	TTA Leu	GAA Glu 440	TAT Tyr	TTG Leu	GGC Gly	GTG Val	ATG Met 445	1407	
ACG Thr	CAT His	GCA Ala	GGC Gly	TTT Phe 450	ACG Thr	GTA Val	GGG Gly	AGT Ser	TAC Tyr 455	AGG Arg	CCC Pro	ACG Thr	CCC Pro	GGC Gly 460	TCT Ser	1455	
AAA Lys	GCG Ala	CTT Leu	TAT Tyr 465	TCA Ser	GAC Asp	AGG Arg	AGT Ser	CAT His 470	TTG Leu	ATG Met	ACA Thr	ACT Thr	CTT Leu 475	AGC Ser	GCT Ala	1503	
AAA Lys	TTC Phe	TAACCAATCG			CTTTAAGCTG			TTTATTAAAG			CGTTAAAAAT			CCCTTAATAA		AA	1561

A

1562

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Asn	Ser	Thr	Pro	Leu	Lys	Asn	Gln	Val	Phe	Cys	Gly	Leu	Tyr
1				5					10					15	
Val	Leu	Ser	Leu	Ser	Ala	Ser	Leu	Gln	Ala	Phe	Asp	Tyr	Lys	Ile	Glu
			20					25					30		
Val	Ser	Ala	Glu	Ser	Phe	Ser	Lys	Val	Gly	Phe	Asn	Lys	Lys	Lys	Ile
		35					40					45			
Asp	Ile	Ala	Arg	Gly	Ile	Tyr	Pro	Thr	Glu	Thr	Phe	Val	Thr	Ala	Val
	50					55					60				
Gly	Gln	Gly	Asn	Ile	Tyr	Ala	Asp	Phe	Leu	Pro	Lys	Gly	Leu	Lys	Asp
65					70				75					80	
Gln	Gly	His	Val	Leu	Glu	Gly	Lys	Ile	Gly	Gly	Thr	Leu	Gly	Gly	Val
			85						90					95	
Ala	Tyr	Asp	Ser	Thr	Lys	Phe	Asn	Gln	Gly	Gly	Ser	Val	Ile	Tyr	Asn
			100					105					110		
Tyr	Ile	Gly	Tyr	Trp	Asp	Gly	Tyr	Leu	Gly	Gly	Lys	Arg	Ala	Leu	Leu
		115					120					125			
Asp	Gly	Thr	Ser	Ile	His	Glu	Cys	Ala	Leu	Gly	Ser	Asp	Gly	Lys	Val
	130					135					140				
Ile	Asp	Ser	Ile	Ala	Cys	Gly	Asn	Ala	Arg	Ala	Asn	Lys	Ile	Arg	Arg
145					150				155					160	
Asn	Tyr	Leu	Met	Asn	Asn	Ala	Phe	Leu	Glu	Tyr	Arg	Tyr	Lys	Asp	Ile
			165						170					175	
Phe	Leu	Ala	Lys	Gly	Gly	Arg	Tyr	Gln	Ser	Asn	Ala	Pro	Tyr	Met	Ser
			180					185					190		
Gly	Tyr	Thr	Gln	Gly	Phe	Glu	Ile	Ser	Ala	Lys	Val	Lys	Asp	Lys	Asn
		195					200					205			
Glu	Gly	Ile	His	Lys	Leu	Trp	Trp	Phe	Ser	Ser	Trp	Gly	Arg	Ala	Phe
	210					215					220				
Ala	Tyr	Gly	Glu	Trp	Ile	Tyr	Asp	Phe	Tyr	Ser	Pro	Arg	Thr	Val	Val
225					230				235					240	
Lys	Asn	Gly	Arg	Thr	Leu	Asn	Tyr	Gly	Ile	His	Leu	Val	Asn	Tyr	Thr
			245						250					255	
Tyr	Glu	Arg	Lys	Gly	Val	Ser	Val	Ser	Pro	Phe	Phe	Gln	Phe	Ser	Pro
			260					265					270		
Gly	Thr	Tyr	Tyr	Ser	Pro	Gly	Val	Val	Val	Gly	Tyr	Asp	Ser	Asn	Pro
		275					280					285			
Asn	Phe	Asn	Gly	Val	Gly	Phe	Arg	Ser	Glu	Thr	Lys	Ala	Tyr	Ile	Leu
	290					295					300				
Leu	Pro	Val	His	Asp	Pro	Leu	Arg	Arg	Asp	Thr	Tyr	Arg	Tyr	Ala	Ile
305					310					315				320	
Lys	Ala	Gly	Thr	Ala	Gly	Gln	Ser	Leu	Leu	Ile	Arg	Gln	Arg	Phe	Asp
			325						330					335	
Tyr	Asn	Glu	Phe	Asn	Phe	Gly	Gly	Ala	Phe	Tyr	Lys	Val	Trp	Lys	Asn
		340						345				350			
Ala	Asn	Ala	Tyr	Ile	Gly	Thr	Thr	Gly	Asn	Pro	Leu	Gly	Ile	Asp	Phe

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(A) NAME/KEY: Coding Sequence

- (B) LOCATION: 98...757

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:15:

17



[illegible]

[REDACTED]

(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTATCTTTA	AAAGTATTTG	CATTTATCAA	TCTCATTTTA	GGAGGCATGC	ATG AAA		56
					Met Lys		
					1		
AAG GCA AGT CAG GTT TTA TTC TTT GGG GCA TTT TTA AGC TCT TCT TTG							104
Lys Ala Ser Gln Val Leu Phe Phe Gly Ala Phe Leu Ser Ser Ser Leu							
		5				10	
CAA GGT TTT GAA GCT AAG CTC AAC GGC TTT GTG GAT CAA TCC AGC ACT							152
Gln Gly Phe Glu Ala Lys Leu Asn Gly Phe Val Asp Gln Ser Ser Thr							
	20				25		
ATC GGT TTT AAC CAG CAT AAA ATC AAT AAA GAA AGA GGT ATC TAC CCT							200
Ile Gly Phe Asn Gln His Lys Ile Asn Lys Glu Arg Gly Ile Tyr Pro							
35				40		45	50

ATG CAG CAA TTC GCA ACG ATT GCG GGC TAT TTA GGG CTT GGT TTT AGC	248
Met Gln Gln Phe Ala Thr Ile Ala Gly Tyr Leu Gly Leu Gly Phe Ser	
55 60 65	
CTG TTA CCC AAA AAG GTT TCA GAC CAT GTT CTA AAA GGC AAA ATA GGA	296
Leu Leu Pro Lys Lys Val Ser Asp His Val Leu Lys Gly Lys Ile Gly	
70 75 80	
GGC ATG GTG GGA TCT ATT TTC TAT GAT GGC ACG AAG AAG TTT GAA GAC	344
Gly Met Val Gly Ser Ile Phe Tyr Asp Gly Thr Lys Lys Phe Glu Asp	
85 90 95	
AGC TCT GTA GCT TAC AAC CTC TTT GGT TAT TAT GAT GGG TTC ATG GGG	392
Ser Ser Val Ala Tyr Asn Leu Phe Gly Tyr Tyr Asp Gly Phe Met Gly	
100 105 110	
GGT TAT ACA AAC ATC TTA CAA AGC GAT GAT TTA GCG ACA CAA AAC ATG	440
Gly Tyr Thr Asn Ile Leu Gln Ser Asp Asp Leu Ala Thr Gln Asn Met	
115 120 125 130	
AAA TAC AAT AAA AAT GTC CGC AAC TAT GTC TTT AGC GAC GCG TAT TTA	488
Lys Tyr Asn Lys Asn Val Arg Asn Tyr Val Phe Ser Asp Ala Tyr Leu	
135 140 145	
GAA TAC GCT TAT AAG AAT TAT TTT GAA ATA AAA GCC GGG CGC TAT TTA	536
Glu Tyr Ala Tyr Lys Asn Tyr Phe Glu Ile Lys Ala Gly Arg Tyr Leu	
150 155 160	
TCC ACT ATG CCT TAT AAA AGC GGT CAA ACG CAA GGC TTT CAA ATT TCT	584
Ser Thr Met Pro Tyr Lys Ser Gly Gln Thr Gln Gly Phe Gln Ile Ser	
165 170 175	
GGG CAA TAC AAG AAA GCG CGC TTG ACT TGG TTT AGC TCT TTT GGG AGG	632
Gly Gln Tyr Lys Lys Ala Arg Leu Thr Trp Phe Ser Ser Phe Gly Arg	
180 185 190	
GCG TTC GCT TAC GGC TCG TTT TTG ATG GAT TGG TTT GCC GCT AGG ACC	680
Ala Phe Ala Tyr Gly Ser Phe Leu Met Asp Trp Phe Ala Ala Arg Thr	
195 200 205 210	
ACT TAT AGC GGA GGT TTT ACC AAA AAC GAT AAG GGA GGT TAT GAT AGC	728
Thr Tyr Ser Gly Gly Phe Thr Lys Asn Asp Lys Gly Gly Tyr Asp Ser	
215 220 225	
CAT GGG CGA AAG GTG CTT TAT GGC ACG CAT GCG GTG CAA CTC ACC TAT	776
His Gly Arg Lys Val Leu Tyr Gly Thr His Ala Val Gln Leu Thr Tyr	
230 235 240	
AAA CCT CAT CGT TTC CTC ATA GAA GGC TTT TAT TAC CTT TCG CCT CAA	824
Lys Pro His Arg Phe Leu Ile Glu Gly Phe Tyr Tyr Leu Ser Pro Gln	
245 250 255	
ATC TTT AAC GCT CCG GGC GTT AAG ATT GGT TGG GAT TCT AAC CCT AAT	872
Ile Phe Asn Ala Pro Gly Val Lys Ile Gly Trp Asp Ser Asn Pro Asn	
260 265 270	
TTT AGC GGC ACA GGC TTT CGC TCT GAT ACA GCT ATC ATA GGG TTT TTC	920
Phe Ser Gly Thr Gly Phe Arg Ser Asp Thr Ala Ile Ile Gly Phe Phe	

275	280	285	290	
CCC ATT TAC TAC CCT TGG ATG ATC GTT AAA TCC AAT GGA AGC CCG GTC	Pro Ile Tyr Tyr Pro Trp Met Ile Val Lys Ser Asn Gly Ser Pro Val	968		
	295 300 305			
TAT AAA TAC GAC ACG CCT GCC ACT CAA AAT GGG CAA AAC CTC ATT ATC	Tyr Lys Tyr Asp Thr Pro Ala Thr Gln Asn Gly Gln Asn Leu Ile Ile	1016		
	310 315 320			
CTC CAA CGC TTT GAC ATC AAC AAT TAC AAT GTT TCC ATC GCT TTT TAT	Leu Gln Arg Phe Asp Ile Asn Asn Tyr Asn Val Ser Ile Ala Phe Tyr	1064		
	325 330 335			
AAA GTC TTT CAA AAC GCT AAT GGT TGG ATA GGC AAC ATG GGG AAT CCA	Lys Val Phe Gln Asn Ala Asn Gly Trp Ile Gly Asn Met Gly Asn Pro	1112		
	340 345 350			
AGC GGT GTG ATC ATG GGG AGT AAC AGC GTC TAT GCG GGT TTT ACA GGC	Ser Gly Val Ile Met Gly Ser Asn Ser Val Tyr Ala Gly Phe Thr Gly	1160		
	355 360 365 370			
ACA GCC CTT AAA AGA GAT GCC GCT ACC ATT TTC CTT TCT TGT GGC GGC	Thr Ala Leu Lys Arg Asp Ala Ala Thr Ile Phe Leu Ser Cys Gly Gly	1208		
	375 380 385			
ACT CAT TTT GCC AAA AAA TTC ACA TGG AAA TTC GCC ACG CAA TAC TCC	Thr His Phe Ala Lys Lys Phe Thr Trp Lys Phe Ala Thr Gln Tyr Ser	1256		
	390 395 400			
AAT TCA GTG GTT TCT TGG GAA GCG AGA GCG ATG ATC TCT TTA GGT TAT	Asn Ser Val Val Ser Trp Glu Ala Arg Ala Met Ile Ser Leu Gly Tyr	1304		
	405 410 415			
AAA TTC ACT GAA TAC TTG AGC GGT AGC GTG GAT CTT GCA TAT TAT GGC	Lys Phe Thr Glu Tyr Leu Ser Gly Ser Val Asp Leu Ala Tyr Tyr Gly	1352		
	420 425 430			
GTG TAT ACT AAC AAA GGA TTT AAA CCG GGT GAA AAC GGG CCT GTG CCT	Val Tyr Thr Asn Lys Gly Phe Lys Pro Gly Glu Asn Gly Pro Val Pro	1400		
	435 440 445 450			
AAA GAC TTC CCC GCC CTT TAT TCT GAC AGG AGC GCG TTA TAC ACG GCT	Lys Asp Phe Pro Ala Leu Tyr Ser Asp Arg Ser Ala Leu Tyr Thr Ala	1448		
	455 460 465			
CTA GTA GCA TCT TTT TGATGCTACC CTATGATTAT GGTGGGCGTC TTTTGATGCT G	Leu Val Ala Ser Phe	1504		
	470			
TTTCTCTAGT CT		1516		

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

[illegible]

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(v) FRAGMENT TYPE: internal
```

Met 1	Lys	Lys	Ala	Ser 5	Gln	Val	Leu	Phe	Phe 10	Gly	Ala	Phe	Leu	Ser 15	Ser
Ser	Leu	Gln	Gly 20	Phe	Glu	Ala	Lys	Leu 25	Asn	Gly	Phe	Val	Asp 30	Gln	Ser
Ser	Thr	Ile 35	Gly	Phe	Asn	Gln	His 40	Lys	Ile	Asn	Lys	Glu 45	Arg	Gly	Ile
Tyr	Pro 50	Met	Gln	Gln	Phe	Ala 55	Thr	Ile	Ala	Gly	Tyr 60	Leu	Gly	Leu	Gly
Phe 65	Ser	Leu	Leu	Pro	Lys 70	Lys	Val	Ser	Asp	His 75	Val	Leu	Lys	Gly	Lys 80
Ile	Gly	Gly	Met	Val 85	Gly	Ser	Ile	Phe	Tyr 90	Asp	Gly	Thr	Lys	Lys 95	Phe
Glu	Asp	Ser	Ser 100	Val	Ala	Tyr	Asn	Leu 105	Phe	Gly	Tyr	Tyr	Asp 110	Gly	Phe
Met	Gly	Gly 115	Tyr	Thr	Asn	Ile	Leu 120	Gln	Ser	Asp	Asp	Leu 125	Ala	Thr	Gln
Asn	Met 130	Lys	Tyr	Asn	Lys	Asn 135	Val	Arg	Asn	Tyr	Val 140	Phe	Ser	Asp	Ala
Tyr 145	Leu	Glu	Tyr	Ala	Tyr 150	Lys	Asn	Tyr	Phe	Glu 155	Ile	Lys	Ala	Gly	Arg
Tyr	Leu	Ser	Thr	Met 165	Pro	Tyr	Lys	Ser	Gly 170	Gln	Thr	Gln	Gly	Phe 175	Gln
Ile	Ser	Gly	Gln 180	Tyr	Lys	Lys	Ala	Arg 185	Leu	Thr	Trp	Phe	Ser 190	Ser	Phe
Gly	Arg	Ala 195	Phe	Ala	Tyr	Gly	Ser 200	Phe	Leu	Met	Asp	Trp 205	Phe	Ala	Ala
Arg	Thr 210	Thr	Tyr	Ser	Gly	Gly 215	Phe	Thr	Lys	Asn	Asp 220	Lys	Gly	Gly	Tyr
Asp 225	Ser	His	Gly	Arg	Lys 230	Val	Leu	Tyr	Gly	Thr 235	His	Ala	Val	Gln	Leu 240
Thr	Tyr	Lys	Pro	His 245	Arg	Phe	Leu	Ile	Glu 250	Gly	Phe	Tyr	Tyr	Leu 255	Ser
Pro	Gln	Ile	Phe 260	Asn	Ala	Pro	Gly	Val 265	Lys	Ile	Gly	Trp	Asp 270	Ser	Asn
Pro	Asn 275	Phe	Ser	Gly	Thr	Gly	Phe 280	Arg	Ser	Asp	Thr	Ala 285	Ile	Ile	Gly
Phe	Phe 290	Pro	Ile	Tyr	Tyr	Pro 295	Trp	Met	Ile	Val	Lys 300	Ser	Asn	Gly	Ser
Pro 305	Val	Tyr	Lys	Tyr	Asp 310	Thr	Pro	Ala	Thr	Gln 315	Asn	Gly	Gln	Asn	Leu 320
Ile	Ile	Leu	Gln	Arg 325	Phe	Asp	Ile	Asn	Asn 330	Tyr	Asn	Val	Ser	Ile 335	Ala
Phe	Tyr	Lys	Val 340	Phe	Gln	Asn	Ala	Asn 345	Gly	Trp	Ile	Gly	Asn 350	Met	Gly
Asn	Pro	Ser 355	Gly	Val	Ile	Met	Gly 360	Ser	Asn	Ser	Val	Tyr 365	Ala	Gly	Phe
Thr	Gly 370	Thr	Ala	Leu	Lys	Arg 375	Asp	Ala	Ala	Thr	Ile	Phe	Leu	Ser	Cys
Gly 385	Gly	Thr	His	Phe	Ala 390	Lys	Lys	Phe	Thr	Trp 395	Lys	Phe	Ala	Thr	Gln 400
Tyr	Ser	Asn	Ser	Val	Val	Ser	Trp	Glu	Ala	Arg	Ala	Met	Ile	Ser	Leu

$$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$$

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 87...323
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAATTTTATGT	TATAATTAAA	CGCATTGTAA	ATAAATTCTC	ATTTTGATAC	ATTTTTACAA		60
TAAACATTA	CTTTAAGGAA	CATCTT	ATG	AAA	AAA	ACG	113
		Met	Lys	Lys	Thr	Lys	
		1				5	
CTT	TCT	CTA	ACT	CTC	GCG	GCG	
Leu	Ser	Leu	Thr	Leu	Ala	Ala	
10				15		20	
GTT	TTT	TTA	AGC	GTG	GGT	TAT	
Val	Phe	Leu	Ser	Val	Gly	Tyr	
			30			35	
AAA	AAC	GCC	GAC	AAG	GTG	CAA	
Lys	Asn	Ala	Asp	Lys	Val	Gln	
		45				50	
AGC	CGG	CTT	TTA	ACC	AAC	GAT	
Ser	Arg	Leu	Leu	Thr	Asn	Asp	
	60				65		
CAA	NAT	CAA	CCA	AGC	GGT	TAATAATTTG	
Gln	Xaa	Gln	Pro	Ser	Gly		
	75						
GGACAACCAA	TTCCCC						

(2) INFORMATION FOR SEQ ID NO:20:

$$\frac{1}{\Gamma(\alpha)} \int_0^t (t-s)^{\alpha-1} f(s) ds = \frac{1}{\Gamma(\alpha)} \int_0^t (t-s)^{\alpha-1} f(s) ds + \frac{1}{\Gamma(\alpha)} \int_t^\infty (t-s)^{\alpha-1} f(s) ds$$

- ```
(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal
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|           |     |           |           |          |           |           |           |           |           |           |           |           |           |           |     |
|-----------|-----|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----|
| Met<br>1  | Lys | Lys       | Thr       | Lys<br>5 | Lys       | Thr       | Ile       | Leu       | Leu<br>10 | Ser       | Leu       | Thr       | Leu       | Ala<br>15 | Ala |
| Ser       | Leu | Leu       | His<br>20 | Ala      | Glu       | Asp       | Asn       | Gly<br>25 | Val       | Phe       | Leu       | Ser       | Val<br>30 | Gly       | Tyr |
| Gln       | Ile | Gly<br>35 | Glu       | Ala      | Val       | Gln       | Lys<br>40 | Val       | Lys       | Asn       | Ala       | Asp<br>45 | Lys       | Val       | Gln |
| Lys       | Leu | Ser       | Asp       | Thr      | Tyr       | Glu<br>50 | Gln       | Leu       | Ser       | Arg       | Leu<br>55 | Leu       | Thr       | Asn       | Asp |
| Asn<br>60 | Gly | Thr       | Asn       | Ser      | Lys<br>65 | Thr       | Ser       | Ala       | Gln       | Xaa<br>70 | Gln       | Pro       | Ser       | Gly       |     |

(A) LENGTH: 2169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 60...2039  
(D) OTHER INFORMATION:

|                                                                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CCCTATCATA GGGCGTGGCA TGAAGAAAAA AGCAAAAGTC TTTTGGTATT GTTTTAATC |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 59  |
| ATG                                                              | ATT | TAT | TGG | TTG | TAT | TTG | GCG | GTC | TTT | TTT | TTG | TTG | AGC | GCA | TTA | 107 |
| Met                                                              | Ile | Tyr | Trp | Leu | Tyr | Leu | Ala | Val | Phe | Phe | Leu | Leu | Ser | Ala | Leu |     |
| 1                                                                |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GAC                                                              | GCT | AAA | GAA | ATC | GCT | ATG | CAA | CGA | TTT | GAC | AAA | CAA | AAC | CAT | AAG | 155 |
| Asp                                                              | Ala | Lys | Glu | Ile | Ala | Met | Gln | Arg | Phe | Asp | Lys | Gln | Asn | His | Lys |     |
|                                                                  |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| ATT                                                              | TTT | GAA | ATC | CTT | GCG | GAT | AAA | GTG | AGC | GCT | AAA | GAC | AAT | GTG | ATA | 203 |
| Ile                                                              | Phe | Glu | Ile | Leu | Ala | Asp | Lys | Val | Ser | Ala | Lys | Asp | Asn | Val | Ile |     |
|                                                                  |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| ACC                                                              | GCA | TCA | GGG | AAT | GCG | ATC | TTA | TTG | AAT | TAT | GAT | GTG | TAT | ATT | CTA | 251 |
| Thr                                                              | Ala | Ser | Gly | Asn | Ala | Ile | Leu | Leu | Asn | Tyr | Asp | Val | Tyr | Ile | Leu |     |
|                                                                  | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GCG | GAC | AAG | GTG | CGT | TAT | GAC | ACT | AAA | ACC | AAA | GAA | GCG | TTA | TTA | GAG | 299 |
| Ala | Asp | Lys | Val | Arg | Tyr | Asp | Thr | Lys | Thr | Lys | Glu | Ala | Leu | Leu | Glu |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| GGG | AAT | ATC | AAG | GTT | TAT | AGG | GGC | GAG | GGT | TTG | CTC | GTT | AAA | ACC | GAT | 347 |
| Gly | Asn | Ile | Lys | Val | Tyr | Arg | Gly | Glu | Gly | Leu | Leu | Val | Lys | Thr | Asp |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TAC | GTG | AAA | TTG | AGT | TTG | AAT | GAA | AAA | TAT | GAA | ATC | ATT | TTC | CCC | TTT | 395 |
| Tyr | Val | Lys | Leu | Ser | Leu | Asn | Glu | Lys | Tyr | Glu | Ile | Ile | Phe | Pro | Phe |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| TAT | GTC | CAA | GAC | AGC | GTG | AGC | GGG | ATT | TGG | GTG | AGC | GCG | GAT | ATT | GCC | 443 |
| Tyr | Val | Gln | Asp | Ser | Val | Ser | Gly | Ile | Trp | Val | Ser | Ala | Asp | Ile | Ala |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| AGC | GGA | AAG | GAT | CAA | AAA | TAT | AAG | GTT | AAA | AAC | ATG | AGC | ACT | TCA | GGG | 491 |
| Ser | Gly | Lys | Asp | Gln | Lys | Tyr | Lys | Val | Lys | Asn | Met | Ser | Thr | Ser | Gly |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| TGC | AGC | ATT | GAT | AAC | CCC | ATT | TGG | CAT | GTC | AAT | GCG | ACT | TCA | GGC | TCA | 539 |
| Cys | Ser | Ile | Asp | Asn | Pro | Ile | Trp | His | Val | Asn | Ala | Thr | Ser | Gly | Ser |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| TTC | AAC | ATG | CAA | AAA | TCG | CAT | TTG | TCT | ATG | TGG | AAT | CCT | AAG | ATC | TAT | 587 |
| Phe | Asn | Met | Gln | Lys | Ser | His | Leu | Ser | Met | Trp | Asn | Pro | Lys | Ile | Tyr |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| GTC | GGT | GAT | ATT | CCT | GTA | TTG | TAT | TTG | CCC | TAT | ATT | TTC | ATG | TCC | ACG | 635 |
| Val | Gly | Asp | Ile | Pro | Val | Leu | Tyr | Leu | Pro | Tyr | Ile | Phe | Met | Ser | Thr |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| AGC | AAT | AAA | AGA | ACT | ACT | GGG | TTT | TTA | TAC | CCT | GAG | TTT | GGC | ACT | TCC | 683 |
| Ser | Asn | Lys | Arg | Thr | Thr | Gly | Phe | Leu | Tyr | Pro | Glu | Phe | Gly | Thr | Ser |     |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| AAC | TTA | GAC | GGC | TTT | ATT | TAT | TTG | CAA | CCC | TTT | TAT | TTA | GCC | CCC | AAA | 731 |
| Asn | Leu | Asp | Gly | Phe | Ile | Tyr | Leu | Gln | Pro | Phe | Tyr | Leu | Ala | Pro | Lys |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| AAC | TCA | TGG | GAT | ATG | ACC | TTT | ACC | CCA | CAA | ATC | CGC | TAT | AAA | AGG | GGT | 779 |
| Asn | Ser | Trp | Asp | Met | Thr | Phe | Thr | Pro | Gln | Ile | Arg | Tyr | Lys | Arg | Gly |     |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| TTT | GGC | TTG | AAT | TTT | GAA | GCG | CGC | TAC | ATT | AAC | TCT | AAA | AAC | GAC | AGG | 827 |
| Phe | Gly | Leu | Asn | Phe | Glu | Ala | Arg | Tyr | Ile | Asn | Ser | Lys | Asn | Asp | Arg |     |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |     |
| TTT | TTA | TTC | AAC | GCG | CGC | TAT | TTT | AGG | AAT | TAC | ACC | CAA | TAT | GTC | AAA | 875 |
| Phe | Leu | Phe | Asn | Ala | Arg | Tyr | Phe | Arg | Asn | Tyr | Thr | Gln | Tyr | Val | Lys |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| CGC | TAC | GAT | TTG | AGG | AAT | CAA | AAT | ATC | TAC | GGG | TTT | GAA | TTT | TTA | AGC | 923 |
| Arg | Tyr | Asp | Leu | Arg | Asn | Gln | Asn | Ile | Tyr | Gly | Phe | Glu | Phe | Leu | Ser |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| TCT | AGC | AGG | GAC | ACT | TTA | CAA | AAA | TAC | TTC | CAC | CTT | AAG | TCT | AAT | ATT | 971 |
| Ser | Ser | Arg | Asp | Thr | Leu | Gln | Lys | Tyr | Phe | His | Leu | Lys | Ser | Asn | Ile |     |

| 290               |                   | 295               |                   | 300               |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                          |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------------|------|
| GAC<br>Asp<br>305 | AAC<br>Asn<br>Gly | GGG<br>His<br>Tyr | CAT<br>Tyr<br>Ile | TAC<br>Ile<br>Asp | ATT<br>310 | GAC<br>Asp<br>Phe | TTT<br>Leu<br>Tyr | TTA<br>Leu<br>Tyr | TAC<br>Met<br>315 | AAC<br>Asn<br>Asp | GAT<br>Leu<br>Asp | TTG<br>Leu<br>Asp | GAC<br>Tyr<br>320 | TAT<br>Tyr<br>320 | 1019                     |      |
| GTG<br>Val        | CGT<br>Arg        | TTT<br>Phe        | GAA<br>Glu        | AAG<br>Lys        | GTT<br>325 | AAT<br>Val        | AAG<br>Asn        | CGT<br>Lys        | ATC<br>Arg        | ACA<br>Ile        | GAC<br>Thr        | GCC<br>Ala        | ACG<br>Thr        | CAC<br>His        | ATG<br>Met               | 1067 |
| TCT<br>Ser        | AGG<br>Arg        | GCG<br>Ala        | AAT<br>Asn        | TAC<br>Tyr        | TAT<br>340 | TTG<br>Tyr        | CAA<br>Leu        | ACA<br>Gln        | GAA<br>Thr        | AAC<br>Glu        | AAT<br>Asn        | TAT<br>Asn        | TAC<br>Tyr        | GGC<br>Gly        | TTG<br>Leu               | 1115 |
| AAT<br>Asn        | ATC<br>Ile        | AAG<br>Lys        | TAT<br>Tyr        | TTT<br>Phe        | TTA<br>Leu | AAC<br>Asn        | CTG<br>Leu        | AAT<br>Asn        | AAA<br>Lys        | ATC<br>Ile        | AAC<br>Asn        | AAT<br>Asn        | AAC<br>Asn        | CGC<br>Arg        | ACT<br>Thr               | 1163 |
| TTC<br>Phe        | CAA<br>Gln        | TCT<br>Ser        | GTC<br>Val        | CCT<br>Pro        | AAT<br>Asn | TTG<br>Leu        | CAA<br>Gln        | TAC<br>Tyr        | CAT<br>His        | AAA<br>Lys        | TAT<br>Tyr        | TTA<br>Leu        | AAT<br>Asn        | TCT<br>Ser        | TTG<br>Leu               | 1211 |
| TAT<br>Tyr<br>385 | TTT<br>Phe        | AGA<br>Arg        | AAT<br>Asn        | TTG<br>Leu        | TTG<br>390 | TAT<br>Tyr        | TCG<br>Ser        | GTG<br>Val        | GAT<br>Asp        | TAT<br>Tyr        | CAG<br>Gln        | TTT<br>Phe        | AGA<br>Arg        | AAC<br>Asn        | ACC<br>Thr<br>400        | 1259 |
| GCA<br>Ala        | AGA<br>Arg        | GAG<br>Glu        | ATT<br>Ile        | GGT<br>Gly        | TAT<br>405 | GGC<br>Tyr        | TAT<br>Gly        | GTG<br>Tyr        | CAA<br>Val        | AAC<br>Gln        | GCT<br>Ala        | TTG<br>Leu        | AAT<br>Asn        | GTG<br>Val        | CCG<br>Pro               | 1307 |
| GTG<br>Val        | GGC<br>Gly        | TTG<br>Leu        | CAA<br>Gln        | TTT<br>Phe        | TCT<br>420 | TTG<br>Ser        | TTT<br>Leu        | AAA<br>Phe        | AAG<br>Lys        | TAT<br>Lys        | TTG<br>Tyr        | TCT<br>Leu        | TTA<br>Ser        | GGG<br>Leu        | CTT<br>Gly<br>Leu        | 1355 |
| TGG<br>Trp        | AAT<br>Asn        | GAT<br>Asp        | CTC<br>Leu        | CAA<br>Gln        | CTA<br>Leu | TCT<br>Ser        | AAT<br>Asn        | GTG<br>Val        | GCT<br>Ala        | TTA<br>Leu        | ATG<br>Met        | CAA<br>Gln        | TCT<br>Ser        | AAA<br>Lys        | AAT<br>Asn               | 1403 |
| TCC<br>Ser        | TTC<br>Phe        | GTG<br>Val        | CCT<br>Pro        | ACG<br>Thr        | ATC<br>Ile | CCT<br>Pro        | AAT<br>Asn        | GAA<br>Glu        | TCA<br>Ser        | AGG<br>Arg        | GAA<br>Glu        | TTT<br>Phe        | GGG<br>Gly        | AAT<br>Asn        | TTT<br>Phe               | 1451 |
| GTG<br>Val<br>465 | TCT<br>Ser        | TCA<br>Ser        | AAT<br>Asn        | TTT<br>Phe        | TCC<br>470 | ATG<br>Met        | TAT<br>Tyr        | GTC<br>Val        | AAT<br>Asn        | ACG<br>Thr        | GAT<br>Asp        | TTG<br>Leu        | GCT<br>Ala        | AGA<br>Arg        | GAA<br>Glu<br>480        | 1499 |
| TAC<br>Tyr        | AAC<br>Asn        | AAG<br>Lys        | CTT<br>Leu        | TTC<br>Phe        | CAC<br>485 | ACG<br>His        | ATC<br>Thr        | CAA<br>Ile        | CTA<br>Gln        | GAA<br>Leu        | GCG<br>Glu        | ATT<br>Ala        | TTC<br>Ile        | AAC<br>Phe        | ATC<br>Asn<br>Ile<br>495 | 1547 |
| CCT<br>Pro        | TAT<br>Tyr        | TAC<br>Tyr        | ACC<br>Thr        | TTT<br>Phe        | AAA<br>500 | AAC<br>Lys        | GGC<br>Asn        | TTA<br>Gly        | TTT<br>Leu        | TCT<br>Phe        | CAA<br>Ser        | AAC<br>Gln        | ATG<br>Met        | TAT<br>Tyr        | GCT<br>Ala               | 1595 |
| TTA<br>Leu        | AGC<br>Ser        | GCG<br>Ala        | CAA<br>Gln        | GCC<br>Ala        | TTA<br>Leu | AAC<br>Asn        | AGC<br>Ser        | TAC<br>Tyr        | ACT<br>Thr        | TCG<br>Ser        | CCT<br>Pro        | TTA<br>Leu        | TTG<br>Leu        | AGA<br>Arg        | GAT<br>Asp               | 1643 |



TAT GAT TAT CAA GGG CGT TTG TAT GAC TCG GTG TGG AAT CCT AGC AGT 1691  
Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser  
530 535 540

ATT TTA CCT AGC AAT GCG AGC AAC AAG ACG GTG GAT TTA ACC CTA ACG 1739  
Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr  
545 550 555 560

CAA TAC CTT TAT GGC TTA GGG GGG CAA GAG TTA TTG TAT TTT AAA ATA 1787  
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile  
565 570 575

TCG CAA CTC ATC AAT CTT GAC GAT AAA GTT TCG CCC TTT AGA ATG CCA 1835  
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro  
580 585 590

CTA GAG AGC AAG ATC GGG TTT TCG CCC TTA ACG GGA TTG AAC ATC TTT 1883  
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe  
595 600 605

GGG AAT GTC TTT TAT TCG TTT TAT CAA AAC CGC TTA GAA GAA ATC TCT 1931  
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser  
610 615 620

GTG AAC GCC AAT TAC CAA CGC AAG TTT TTA AGC TTT AAC CTC TCT TAT 1979  
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr  
625 630 635 640

TTT TTA AAA AAC AAT TTT AGC AGT GGG ATT AAT AGC ATT GTA GAA AAT 2027  
Phe Leu Lys Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn  
645 650 655

CTG CGG ATT ATT TAAAGGCGGG TTTTAGCAAC GACTTTGGCT ATTTTTCAT GAGCGC 2085  
Leu Arg Ile Ile  
660

GGATGTGGGT TATGATATTA GAAACAATGT GGTTTAAAT TGGAATGTGG GGATTATATAA 2145  
AAAAATCCGT TGTTTGGGA TTGG 2169

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu  
1 5 10 15  
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys  
20 25 30  
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile  
35 40 45

Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu  
 50 55 60  
 Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu  
 65 70 75 80  
 Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp  
 85 90 95  
 Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe  
 100 105 110  
 Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala  
 115 120 125  
 Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly  
 130 135 140  
 Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser  
 145 150 155 160  
 Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr  
 165 170 175  
 Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr  
 180 185 190  
 Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser  
 195 200 205  
 Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys  
 210 215 220  
 Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly  
 225 230 235 240  
 Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg  
 245 250 255  
 Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys  
 260 265 270  
 Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser  
 275 280 285  
 Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile  
 290 295 300  
 Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr  
 305 310 315 320  
 Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met  
 325 330 335  
 Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu  
 340 345 350  
 Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr  
 355 360 365  
 Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu  
 370 375 380  
 Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr  
 385 390 395 400  
 Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro  
 405 410 415  
 Val Gly Leu Gln Phe Ser Leu Phe Lys Tyr Leu Ser Leu Gly Leu  
 420 425 430  
 Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn  
 435 440 445  
 Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe  
 450 455 460  
 Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu  
 465 470 475 480  
 Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile  
 485 490 495  
 Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala  
 500 505 510

Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp  
 515 520 525  
 Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser  
 530 535 540  
 Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr  
 545 550 555 560  
 Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile  
 565 570 575  
 Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro  
 580 585 590  
 Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe  
 595 600 605  
 Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser  
 610 615 620  
 Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr  
 625 630 635 640  
 Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn  
 645 650 655  
 Leu Arg Ile Ile  
 660

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...401
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TCAAGGTGTG CCAAACATGC CTTGAAACTC AATTTTTTGAA TCTCAATTTT ATG AAA | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| GGA TTT GTT ATG AGT GGA TTA AAA GCA TTT AGT TGT GTA GTG GTT TTA | 104 |
| Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val Val Leu |     |
| 5 10 15                                                         |     |
| TGC GGT GCA ATG GCT AAT ACG GCT ATA GCT GGT CCT AAA ATA GAA GCA | 152 |
| Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile Glu Ala |     |
| 20 25 30                                                        |     |
| AGG GGT GAG TTT GGC AGA TTT TGG GGG GGA GCT GTT GGT GGT GCA ATT | 200 |
| Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly Ala Ile |     |
| 35 40 45 50                                                     |     |
| GGG GGT GGT GTT GGT GGT GCA GTG GGG GGA GCT GTT GGT GGT CCT GCG | 248 |
| Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly Pro Ala |     |

k

| 55                                                                | 60  | 65  |     |
|-------------------------------------------------------------------|-----|-----|-----|
| GGT GGT TGG GCT GGC AGA TTA GTT GGT GGT TCT GTG GGG AGA GAG TTT   |     |     | 296 |
| Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg Glu Phe   |     |     |     |
| 70                                                                | 75  | 80  |     |
| GGT CGG GAA ATA GGC GAT AGG GTA GAA GAT TAC ATC CGT GGC GTT GAT   |     |     | 344 |
| Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly Val Asp   |     |     |     |
| 85                                                                | 90  | 95  |     |
| AGA GAG CCA CAA GCC CCA AGA GAA CCC ACC TAT GAT CGT CAT TTC GTG   |     |     | 392 |
| Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His Phe Val   |     |     |     |
| 100                                                               | 105 | 110 |     |
| TAT GAC AGG TAGCTTTGGG CGAGAAAGGA GAGAGCATGA ATGTCAAAAA TCGTTTGAG |     |     | 450 |
| Tyr Asp Arg                                                       |     |     |     |
| 115                                                               |     |     |     |
| CGAT                                                              |     |     | 454 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val |  |
| 1 5 10 15                                                       |  |
| Val Leu Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile |  |
| 20 25 30                                                        |  |
| Glu Ala Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly |  |
| 35 40 45                                                        |  |
| Ala Ile Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly |  |
| 50 55 60                                                        |  |
| Pro Ala Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg |  |
| 65 70 75 80                                                     |  |
| Glu Phe Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly |  |
| 85 90 95                                                        |  |
| Val Asp Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His |  |
| 100 105 110                                                     |  |
| Phe Val Tyr Asp Arg                                             |  |
| 115                                                             |  |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 59...802  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|                                                                                                                                    |     |
|------------------------------------------------------------------------------------------------------------------------------------|-----|
| GCCATTTTAA GCTAATATAA TATAGAGCGA TTATCAAAAA ATAAAGGGAA AAGACTGA                                                                    | 58  |
| ATG TTG AAA AGA ATG ATA TTA TTA GGG GCT TTG GGT GTT TTA GCG AGC<br>Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser | 106 |
| 1 5 10 15                                                                                                                          |     |
| GCT GAA GAG AGT GCG GCT TTT GTG GGA GTC AAT TAC CAG GTG AGC ATG<br>Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met | 154 |
| 20 25 30                                                                                                                           |     |
| ATA CAA AAT CAG ACT AAA ATG GTG AAT GAC AAC GGC TTG CAA AAG CCT<br>Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro | 202 |
| 35 40 45                                                                                                                           |     |
| TTG ATA AAG TTT CCG CCT TAC GCA GGA GCG GGT TTT GAA GTG GGC TAT<br>Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr | 250 |
| 50 55 60                                                                                                                           |     |
| AAG CAA TTT TTT GGT AAG AAA AAA TGG TTT GGC ATG CGT TAT TAT GGG<br>Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly | 298 |
| 65 70 75 80                                                                                                                        |     |
| TTT TTT GAC TAC GCG CAC AAC CGC TTT GGC GTG ATG AAA AAG GGC ATT<br>Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile | 346 |
| 85 90 95                                                                                                                           |     |
| CCG GTG GGC GAT AGT GGG TTT ATT TAC AAT AGT TTT AGT TTT GGA GGG<br>Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly | 394 |
| 100 105 110                                                                                                                        |     |
| AAC ACT TTA ACG GAA AGG GAT TCC TAT CAG GGG CAA TAC TAT GTC AAT<br>Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn | 442 |
| 115 120 125                                                                                                                        |     |
| TTA TTC ACT TAT GGC GTG GGG TTA GAT ACG CTG TGG AAT TTT GTG AAT<br>Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn | 490 |
| 130 135 140                                                                                                                        |     |
| AAA GAA AAC ATG GTT TTT GGT TTT GTG GTG GGG ATC CAA TTA GCG GGG<br>Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly | 538 |
| 145 150 155 160                                                                                                                    |     |
| GAT AGT TGG GCA ACG AGC ATC AGT AAA GAA ATC GCT CAT TAT GCA AAA<br>Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys | 586 |
| 165 170 175                                                                                                                        |     |
| CAC CAC AGC AAT TCC AGT TAT AGC CCG GCC AAT TTC CAG TTT TTA TGG                                                                    | 634 |

His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp  
 180 185 190  
 AAG TTT GGG GTC CGC ACC CAT ATC GCT AAA CAC AAT AGC CTA GAA TTA 682  
 Lys Phe Gly Val Arg Thr His Ile Ala Lys His Asn Ser Leu Glu Leu  
 195 200 205  
 GGG ATT AAA GTG CCT ACG ATC ACA CAC CAG CTT TTC TCT CTT ACC AAC 730  
 Gly Ile Lys Val Pro Thr Ile Thr His Gln Leu Phe Ser Leu Thr Asn  
 210 215 220  
 GAA AAG GGA TAC ACC TTA CAG GCT GAT GTG CGT AGA GTT TAT GCG TTT 778  
 Glu Lys Gly Tyr Thr Leu Gln Ala Asp Val Arg Arg Val Tyr Ala Phe  
 225 230 235 240  
 CAA ATC AGT TAC TTG AGG GAT TTT TAACCCCTTT TTAGATACAA TCACGCCTGA AA 834  
 Gln Ile Ser Tyr Leu Arg Asp Phe  
 245  
 CTATCCATTT AAAGGTGTGA AA 856

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser  
 1 5 10 15  
 Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met  
 20 25 30  
 Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro  
 35 40 45  
 Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr  
 50 55 60  
 Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly  
 65 70 75 80  
 Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile  
 85 90 95  
 Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly  
 100 105 110  
 Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn  
 115 120 125  
 Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn  
 130 135 140  
 Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly  
 145 150 155 160  
 Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys  
 165 170 175  
 His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 69...2699  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

33



|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAC ACC GTG ATC GAT CCT AAC ATG ATT AAA GAA GTG GAA GTG ATC AAG | 446  |
| Asn Thr Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys |      |
| 115 120 125                                                     |      |
| GGG GCG GCG AAC GCT TCA GCA GGC CCA GGT GCG GTG GCG GGT AAA TTG | 494  |
| Gly Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu |      |
| 130 135 140                                                     |      |
| TCT TTC ACC ACG ATT GAC GCT AAC GAC TTC TTA AGA AAG AAT CAA ACT | 542  |
| Ser Phe Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr |      |
| 145 150 155                                                     |      |
| TAT GGC GCT AAA GCG GAA GCG GCC TTT TAT ACC AAC TTC GGG TAT CGC | 590  |
| Tyr Gly Ala Lys Ala Glu Ala Phe Tyr Thr Asn Phe Gly Tyr Arg     |      |
| 160 165 170                                                     |      |
| ATG AAC GCC ACT GCG GCT TAC CGG GGG AAA AAC TGG GAC ATC CTA GCC | 638  |
| Met Asn Ala Thr Ala Ala Tyr Arg Gly Lys Asn Trp Asp Ile Leu Ala |      |
| 175 180 185 190                                                 |      |
| TAT TAC AAC CAT CAA AAT ATT TTT TAC TAC AGA GAC GGG AAC AAC GCT | 686  |
| Tyr Tyr Asn His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly Asn Asn Ala |      |
| 195 200 205                                                     |      |
| TTT AGG AAT GTC TTC CAC CCT AAC TAC GAT TTA CAA GAT CCA AGC AAT | 734  |
| Phe Arg Asn Val Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn |      |
| 210 215 220                                                     |      |
| AGC GAT ATG AGC GTA GGG ACT CCC AGT GAA GTC AAT AGC GTT TTA GCT | 782  |
| Ser Asp Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala |      |
| 225 230 235                                                     |      |
| AAA ATT AAT GGC TAT ATC AAC GAA ACA GAC AGC ATT AGC GTG AGC TAC | 830  |
| Lys Ile Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr |      |
| 240 245 250                                                     |      |
| AAC CTC ACA CGA GAC AAT TCT ACA AGG CTT TTA CGC CCT AAC ACC ACT | 878  |
| Asn Leu Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr |      |
| 255 260 265 270                                                 |      |
| TCA GCC CTC TCT AAA GCC AAT GAC CCA GGA AGC CAG CCA GCC CCC TTT | 926  |
| Ser Ala Leu Ser Lys Ala Asn Asp Pro Gly Ser Gln Pro Ala Pro Phe |      |
| 275 280 285                                                     |      |
| GTG ATT GAC TTT GGG AAA GAA TTA GCC CAT ACG ATC AAC TTC AAC CAC | 974  |
| Val Ile Asp Phe Gly Lys Glu Leu Ala His Thr Ile Asn Phe Asn His |      |
| 290 295 300                                                     |      |
| AAT TTG AGC TTG AAA TAC AAG CAT GAA GGC GGC CCT AAT TTT AAC CAG | 1022 |
| Asn Leu Ser Leu Lys Tyr Lys His Glu Gly Gly Pro Asn Phe Asn Gln |      |
| 305 310 315                                                     |      |
| CCG CGC GTT GAA TCC ACC GCC TTT TTA GGG GTA AGG GGG GGC AAT TAT | 1070 |
| Pro Arg Val Glu Ser Thr Ala Phe Leu Gly Val Arg Gly Gly Asn Tyr |      |
| 320 325 330                                                     |      |
| AAC CCT GTG GTG AAT CCT TTC GCT TAC AAT TCT AAC GAG CCG GCT AAC | 1118 |
| Asn Pro Val Val Asn Pro Phe Ala Tyr Asn Ser Asn Glu Pro Ala Asn |      |



1

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GTG GGT GCG GGA ACT CGT TAT GAT ATT TAC ACC TTG CTA GAC AAA AAC | 1838 |
| Val Gly Ala Gly Thr Arg Tyr Asp Ile Tyr Thr Leu Leu Asp Lys Asn |      |
| 575 580 585 590                                                 |      |
| GGC CGC ACG CAT GTA ACT TCT GGT TTC TCG CCT TCT GCA ACC GTG CTT | 1886 |
| Gly Arg Thr His Val Thr Ser Gly Phe Ser Pro Ser Ala Thr Val Leu |      |
| 595 600 605                                                     |      |
| TAT AAC CCC ATT GAA AGC ATT GGC TTG AAA GTG AGT TAT GCG TAT GTA | 1934 |
| Tyr Asn Pro Ile Glu Ser Ile Gly Leu Lys Val Ser Tyr Ala Tyr Val |      |
| 610 615 620                                                     |      |
| ACT AAG GGG GCT TTG CCT GGC GAT GGC GTT TTG ATG CGC GAT CCT ACG | 1982 |
| Thr Lys Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr |      |
| 625 630 635                                                     |      |
| GTG ATT TAT CAA AGG AAT TTG CGC CCT GCG ATC GGT CAA AAT GTG GAA | 2030 |
| Val Ile Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu |      |
| 640 645 650                                                     |      |
| TTT AAT GTG GAT TTC AAC AGC AAG TAT TTC AAT GTG CGC GGG GCA GCG | 2078 |
| Phe Asn Val Asp Phe Asn Ser Lys Tyr Phe Asn Val Arg Gly Ala Ala |      |
| 655 660 665 670                                                 |      |
| TTC TAT CAA GTC ATC AAT AAT TTC ATC AAC AGC TAC GGG CAA GAC ACT | 2126 |
| Phe Tyr Gln Val Ile Asn Asn Phe Ile Asn Ser Tyr Gly Gln Asp Thr |      |
| 675 680 685                                                     |      |
| TCT AAA AAT GGA GGG GGT AAC GCA ACC GCA AAA AAC ATG TCA GGG AAT | 2174 |
| Ser Lys Asn Gly Gly Asn Ala Thr Ala Lys Asn Met Ser Gly Asn     |      |
| 690 695 700                                                     |      |
| TTA CCC GAA ACC ATT AAC ATT TAT GGT TAT GAA GTT TCA GGG AAT GTG | 2222 |
| Leu Pro Glu Thr Ile Asn Ile Tyr Gly Tyr Glu Val Ser Gly Asn Val |      |
| 705 710 715                                                     |      |
| AGG TAT AAG AAT TTC TTA GGG ACT TTC TCA GTG GCT CGC TCT TGG CCA | 2270 |
| Arg Tyr Lys Asn Phe Leu Gly Thr Phe Ser Val Ala Arg Ser Trp Pro |      |
| 720 725 730                                                     |      |
| ACG GCT AGG GGG CAT TTA TTA GCG GAC ACT TAC GCT CTA GCT GCA ACG | 2318 |
| Thr Ala Arg Gly His Leu Leu Ala Asp Thr Tyr Ala Leu Ala Thr     |      |
| 735 740 745 750                                                 |      |
| ACT GGG AAT GTG TTT ATT TTA AAA GCC GAT TAT GAT GTT CGC AGG TGG | 2366 |
| Thr Gly Asn Val Phe Ile Leu Lys Ala Asp Tyr Asp Val Arg Arg Trp |      |
| 755 760 765                                                     |      |
| GGG CTT ACT TTA ACC TGG CTC TCG CGC TTT GTA ACT AAC ATG TAT TAT | 2414 |
| Gly Leu Thr Leu Thr Trp Leu Ser Arg Phe Val Thr Asn Met Tyr Tyr |      |
| 770 775 780                                                     |      |
| GAG GGC TAT TCT ATC TAT TAC CCG CAA TAC GGC TTG ATC AAA ATC CAT | 2462 |
| Glu Gly Tyr Ser Ile Tyr Tyr Pro Gln Tyr Gly Leu Ile Lys Ile His |      |
| 785 790 795                                                     |      |
| AAA CCC GGG TAT GGC GTG CAT AAT GTC TTT ATC AAC TGG ACT CCG CCT | 2510 |
| Lys Pro Gly Tyr Gly Val His Asn Val Phe Ile Asn Trp Thr Pro Pro |      |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

- ```
(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEO ID NO:28:

37



Asn	Val	195	Phe	His	Pro	Asn	Tyr	200	Asp	Leu	Gln	Asp	Pro	205	Ser	Asn	Ser	Asp
Met	Ser	210	Val	Gly	Thr	Pro	Ser	215	Glu	Val	Asn	Ser	220	Val	Leu	Ala	Lys	Ile
225	Asn	Gly	Tyr	Ile	Asn	Glu	Thr	230	Asp	Ser	Ile	Ser	235	Val	Ser	Tyr	Asn	Leu
				245							250					255		
Thr	Arg	Asp	Asn	Ser	Thr	Arg	Leu	260	Leu	Arg	Pro	Asn	Thr	270	Thr	Ser	Ala	
Leu	Ser	Lys	275	Ala	Asn	Asp	Pro	280	Gly	Ser	Gln	Pro	Ala	285	Pro	Phe	Val	Ile
Asp	Phe	Gly	Lys	Glu	Leu	Ala	His	295	Thr	Ile	Asn	Phe	Asn	300	His	Asn	Leu	
Ser	Leu	Lys	Tyr	Lys	His	Glu	Gly	310	Gly	Gly	Pro	Asn	Phe	315	Asn	Gln	Pro	Arg
305	Val	Glu	Ser	Thr	Ala	Phe	Leu	325	Gly	Val	Arg	Gly	Gly	330	Asn	Tyr	Asn	Pro
																335		
Val	Val	Asn	Pro	Phe	Ala	Tyr	Asn	340	Ser	Asn	Glu	Pro	Ala	345	Asn	Pro	Asp	
Tyr	Ile	Pro	Glu	Val	Lys	Glu	Trp	355	Cys	Asn	Asn	Pro	Asp	360	Asn	Ile	Ser	
Gln	Cys	Thr	Gln	Gly	Ala	Ile	Arg	370	Pro	Ser	Asn	Gly	Gly	375	Tyr	Gln	Ile	
Gly	Tyr	Gly	Thr	Pro	Asn	Ser	Ile	385	Asn	Trp	Gln	Gly	Thr	390	Ser	Asp	Ser	
385	Ser	Gly	Gly	Ala	Gln	Ala	Gly	395	Tyr	Gly	Gln	Leu	Asn	400	Ala	Ile	Ser	Thr
				405														
Ser	Ala	Asn	Val	Tyr	His	Gly	Leu	410	Val	Pro	Lys	Asn	Pro	415	Asp	Tyr	Asp	
				420														
Met	Thr	Pro	Pro	Asn	Ala	Gln	Asn	425	Pro	Ser	Ala	Asn	Asp	430	Trp	Thr	Leu	
Gly	Asn	Ala	Asp	Ala	Glu	Gly	Thr	435	Leu	Ala	Arg	Arg	Ile	440	Phe	Leu	Ile	
Asn	Ser	Gly	Val	Asn	Phe	Lys	Val	445	Thr	His	Pro	Ile	Ser	450	Glu	Asp	Tyr	
465	Gly	Asn	Val	Phe	Glu	Tyr	Gly	455	Met	Ile	Tyr	Gln	Asn	460	Leu	Ser	Val	Phe
Ser	Gly	Leu	Asp	Lys	Gly	Lys	Asn	470	Gly	Tyr	Tyr	Lys	Asn	475	Asn	Ile	Asp	
Pro	Asn	Asp	Pro	Asn	Gly	Pro	Gly	485	Leu	Pro	Tyr	Arg	His	490	Tyr	Tyr	Thr	
Asp	Gln	Ser	Ser	Gln	Tyr	Pro	Gln	500	Asn	Leu	Asn	Thr	Pro	505	Asn	Pro	Leu	
Tyr	Arg	Asn	Met	Pro	Gln	Asn	Ser	515	His	Ala	Ile	Gly	Asn	520	Ile	Ile	Gly	
545	Gly	Phe	Met	Gln	Ala	Asn	Tyr	525	Asn	Ile	Leu	Ser	Asn	530	Val	Ile	Val	Gly
Ala	Gly	Thr	Arg	Tyr	Asp	Ile	Tyr	535	Thr	Leu	Leu	Asp	Lys	540	Asn	Gly	Arg	
Thr	His	Val	Thr	Ser	Gly	Phe	Ser	550	Pro	Ser	Ala	Thr	Val	555	Leu	Tyr	Asn	
Pro	Ile	Glu	Ser	Ile	Gly	Leu	Lys	565	Val	Ser	Tyr	Ala	Tyr	570	Val	Thr	Lys	
Gly	Ala	Leu	Pro	Gly	Asp	Gly	Val	580	Leu	Met	Arg	Asp	Pro	585	Thr	Val	Ile	
625	Tyr	Gln	Arg	Asn	Leu	Arg	Pro	590	Ala	Ile	Gly	Gln	Asn	595	Val	Glu	Phe	Asn
Val	Asp	Phe	Asn	Ser	Lys	Tyr	Phe	600	Asn	Val	Arg	Gly	Ala	605	Ala	Phe	Tyr	

Gln Val	Ile	Asn	Asn	Phe	Ile	Asn	Ser	Tyr	Gly	Gln	Asp	Thr	Ser	Lys
	675					680				685				
Asn Gly	Gly	Gly	Asn	Ala	Thr	Ala	Lys	Asn	Met	Ser	Gly	Asn	Leu	Pro
	690				695					700				
Glu Thr	Ile	Asn	Ile	Tyr	Gly	Tyr	Glu	Val	Ser	Gly	Asn	Val	Arg	Tyr
705				710					715					720
Lys Asn	Phe	Leu	Gly	Thr	Phe	Ser	Val	Ala	Arg	Ser	Trp	Pro	Thr	Ala
			725						730					735
Arg Gly	His	Leu	Leu	Ala	Asp	Thr	Tyr	Ala	Leu	Ala	Ala	Thr	Thr	Gly
	740						745					750		
Asn Val	Phe	Ile	Leu	Lys	Ala	Asp	Tyr	Asp	Val	Arg	Arg	Trp	Gly	Leu
	755					760					765			
Thr Leu	Thr	Trp	Leu	Ser	Arg	Phe	Val	Thr	Asn	Met	Tyr	Tyr	Glu	Gly
	770				775					780				
Tyr Ser	Ile	Tyr	Tyr	Pro	Gln	Tyr	Gly	Leu	Ile	Lys	Ile	His	Lys	Pro
785				790					795					800
Gly Tyr	Gly	Val	His	Asn	Val	Phe	Ile	Asn	Trp	Thr	Pro	Pro	Ser	Lys
			805					810					815	
Lys Trp	Gln	Gly	Leu	Arg	Ile	Ser	Ala	Val	Phe	Asn	Asn	Ile	Leu	Asn
			820				825					830		
Lys Gln	Tyr	Val	Asp	Gln	Thr	Ser	Val	Phe	Gln	Ala	Ser	Ala	Asp	Ala
	835					840					845			
Pro Ala	Ser	Asp	Met	Ile	Pro	Lys	Gly	Lys	Arg	Met	Ala	Leu	Pro	Ala
	850				855					860				
Pro Gly	Phe	Asn	Ala	Arg	Phe	Glu	Val	Ser	Tyr	Gln	Phe			
865				870					875					

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...317
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTAAATCA CCCGTTACAG CATCACTGAA ATCACTAATA GGGGTGATTG ATG CGT	56
Met Arg	
1	
AAG GTT TTA TAC GCT CTT GTG GGC TTT TTG TTG GCT TTT AGC GCT TTA	104
Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser Ala Leu	
5 10 15	
AAA GCC GAT GAT TTT TTA GAA GAA GCG AAC GAA ACA GCC CCG GCG CAT	152
Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro Ala His	
20 25 30	

TTA AAC CAC CCT ATG CAG GAT TTA AAC GCC ATT CAA GGG AGC TTT TTT 200
 Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser Phe Phe
 35 40 45 50

GAC AAA AAC CGC TCA AAA ATG TCC AAC ACT TTG AAC ATT GAT TAC TTT 248
 Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp Tyr Phe
 55 60 65

CAA GGG CAA ACT TAT AAA ATC CCG CTT GCG TTA TGC GAT GGC GMC CTT 296
 Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly Xaa Leu
 70 75 80

ATT GTT TTT TTC AAA ACC CAT TAGCGATTTT GTTTTAGGGG ATAAGGTGGG TTTT 351
 Ile Val Phe Phe Lys Thr His
 85

GATGCGAAAA TTTTAGAAA 370

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Arg Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser
 1 5 10 15
 Ala Leu Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro
 20 25 30
 Ala His Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser
 35 40 45
 Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp
 50 55 60
 Tyr Phe Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly
 65 70 75 80
 Xaa Leu Ile Val Phe Phe Lys Thr His
 85

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...305
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCAATAAA AAAAGAAATT CTTAGGATTT CTCACATTAA GGAGTTTAA ATG AAA 56
Met Lys
1

AAG GTT TTT TTA GGT ATG GCA TTA GCC TTT AGT GTG TCC ATG GCA GAA 104
Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met Ala Glu
5 10 15

AAA AGT GGC GCG TTT TTA GGA GGG GGG TTT CAA TAT TCT AAT TTA GAA 152
Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn Leu Glu
20 25 30

AAC CAA AAC ACC ACC CGC ACC CCA GGC GCT AAC AAT AAC ACC CCG ATA 200
Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr Pro Ile
35 40 45 50

GAC ACT TCA ATG TTT GGC AGC AAC AAA ACA GCT CCA GCC CAA GAA ACG 248
Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln Glu Thr
55 60 65

CAA AGC GCT TCC AAA CCG GAC ACT AAA GTC AAT CCA AGC GCA AGT TGG 296
Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala Ser Trp
70 75 80

ATG AAA AAA TAAGAAGGAA GTTATGAAAA AGTCATTCAA AAAATTAGGC TTTGTCTCT 354
Met Lys Lys
85

TTA 357

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Lys Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met
1 5 10 15
Ala Glu Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn
20 25 30
Leu Glu Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Thr
35 40 45
Pro Ile Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln
50 55 60
Glu Thr Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala
65 70 75 80
Ser Trp Met Lys Lys

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATGTAGCA TTTAGAACTC AAGTAGAGAA AATGTAGAAG GAAGGAATAC ATG AAG	56
Met Lys	
1	
AAA TCT GTT ATA GTA GGT GCT ATC TCT CTA GCA ATG ACA AGC TTA TTG	104
Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser Leu Leu	
5 10 15	
TCA GCA GAG ACC CCT AAG CAA GAA AAA GCT ATT AAG ACT AGC CCT ACC	152
Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser Pro Thr	
20 25 30	
AAA AAA GGT GAA AGA AAT GCT GCT TTT ATA GGG ATT GAT TAC CAG TTG	200
Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr Gln Leu	
35 40 45 50	
GGT ATG CTC AGC ACT ACC GCT CAA AAT TGT TCC CAT GGG AAT TGC AAT	248
Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn Cys Asn	
55 60 65	
GGT AAT CAA AGT GGG GCT TAC GGC TCT AAT ACG CCT AAC ATG CCT ACA	296
Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met Pro Thr	
70 75 80	
GCG TCA AAC CCA ACA GGA GGG TTT ACT CAT GGC GCT CTA GGG ACT CGT	344
Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly Thr Arg	
85 90 95	
GGG TAT AAA GGC TTA AGC AAC CAA CAA TAC GCT ATC AAT GGT TTT GGT	392
Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly Phe Gly	
100 105 110	
TTT GTT GTA GGG TAT AAG CAT TTT TTC AAG AAA TCC CCG CAA TTT GGA	440
Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln Phe Gly	
115 120 125 130	
ATG CGT TAT TAC GGA TTC TTT GAT TTT GCA AGC TCT TAT TAT AAG TAT	488

Met	Arg	Tyr	Tyr	Gly	Phe	Phe	Asp	Phe	Ala	Ser	Ser	Tyr	Tyr	Lys	Tyr	
				135					140					145		
TAC	ACT	TAT	AAT	GAT	TAT	GGC	ATG	AGA	GAC	GCT	CGC	AAG	GGT	TCT	CAA	536
Tyr	Thr	Tyr	Asn	Asp	Tyr	Gly	Met	Arg	Asp	Ala	Arg	Lys	Gly	Ser	Gln	
			150					155					160			
AGT	TTC	ATG	TTT	GGC	TAT	GGG	GCT	GGC	ACA	GAT	GTG	TTG	TTT	AAC	CCG	584
Ser	Phe	Met	Phe	Gly	Tyr	Gly	Ala	Gly	Thr	Asp	Val	Leu	Phe	Asn	Pro	
		165					170					175				
GCT	ATT	TTC	AAT	CGT	GAG	AAC	TTG	CAT	TTT	GGG	TTT	TTC	TTG	GGC	GTT	632
Ala	Ile	Phe	Asn	Arg	Glu	Asn	Leu	His	Phe	Gly	Phe	Phe	Leu	Gly	Val	
	180					185					190					
CGC	ATC	GGT	GGC	ACC	TCT	TGG	GGT	CCA	ACA	AAC	TAT	TAT	TTT	AAG	GAC	680
Ala	Ile	Gly	Gly	Thr	Ser	Trp	Gly	Pro	Thr	Asn	Tyr	Tyr	Phe	Lys	Asp	
195					200					205					210	
TTG	GCT	GAT	GAG	TAT	AGA	GGG	AGT	TTC	CAC	CCA	TCA	AAT	TTC	CAG	GTC	728
Leu	Ala	Asp	Glu	Tyr	Arg	Gly	Ser	Phe	His	Pro	Ser	Asn	Phe	Gln	Val	
				215					220					225		
TTA	GTT	AAT	GGT	GGG	ATT	CGC	TTA	GGC	ACT	AAA	CAC	CAA	GGT	TTT	GAA	776
Leu	Val	Asn	Gly	Gly	Ile	Arg	Leu	Gly	Thr	Lys	His	Gln	Gly	Phe	Glu	
			230				235						240			
ATT	GGC	TTG	AAA	ATC	CAA	ACC	ATC	CGC	AAC	AAT	TAC	TAC	ACC	GCT	AGT	824
Ile	Gly	Leu	Lys	Ile	Gln	Thr	Ile	Arg	Asn	Asn	Tyr	Tyr	Thr	Ala	Ser	
		245					250					255				
CGC	GAT	AAT	GTG	CCT	GAA	GGG	ACT	ACT	TAT	AGA	TTC	ACT	TTC	CAC	CGC	872
Ala	Asp	Asn	Val	Pro	Glu	Gly	Thr	Thr	Tyr	Arg	Phe	Thr	Phe	His	Arg	
	260					265					270					
CCC	TAT	GCC	TTT	TAT	TGG	CGT	TAC	ATT	GTA	AGC	TTT	TAAGGTGTTT	TAGGGC			924
Pro	Tyr	Ala	Phe	Tyr	Trp	Arg	Tyr	Ile	Val	Ser	Phe					
275					280					285						
TAATCTTATG	GGGGCATAGA	AAAGGGCTTT	TGCTCTT													961

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Lys	Lys	Ser	Val	Ile	Val	Gly	Ala	Ile	Ser	Leu	Ala	Met	Thr	Ser	
1				5				10						15		
Leu	Leu	Ser	Ala	Glu	Thr	Pro	Lys	Gln	Glu	Lys	Ala	Ile	Lys	Thr	Ser	
			20					25					30			

$$\begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \end{pmatrix} \rightarrow \begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \end{pmatrix} \rightarrow \begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \end{pmatrix} \rightarrow \begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \end{pmatrix}$$

1

(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 51...236

(D) OTHER INFORMATION:

44

5 10 15

TTA ACA GCT ATT AGA GCT ACT ATA ATG GCG TTT AAA GGC GAT ACT GAT 152
 Leu Thr Ala Ile Arg Ala Thr Ile Met Ala Phe Lys Gly Asp Thr Asp
 20 25 30

GAT GAT GAA GTT GAG AGT GAT GGG TTT TTT AGT AGA ATA TGG GAT AAA 200
 Asp Asp Glu Val Glu Ser Asp Gly Phe Phe Ser Arg Ile Trp Asp Lys
 35 40 45 50

TTC GTT GAA TAT TTC GGC TAT ACT CTA GTT ACT ATA TAATGTTTTT TCCTTA 252
 Phe Val Glu Tyr Phe Gly Tyr Thr Leu Val Thr Ile
 55 60

TATAATTGGA CCAGTTATCG CTTTAATTTT TATATTT 289

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Phe Arg Asp Ile Val Asp Ile Leu Ile Ser Val Val Ile Ile Gly
 1 5 10 15
 Leu Val Leu Thr Ala Ile Arg Ala Thr Ile Met Ala Phe Lys Gly Asp
 20 25 30
 Thr Asp Asp Asp Glu Val Glu Ser Asp Gly Phe Phe Ser Arg Ile Trp
 35 40 45
 Asp Lys Phe Val Glu Tyr Phe Gly Tyr Thr Leu Val Thr Ile
 50 55 60

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1491
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACACACATT AGTTATAGTT TCTAAGAGAG TTCTCCCCCT ATCTCTTAGA T ATG CCT 57

Met	Pro
1	

TTT Phe	TGT Cys	ATT Ile 5	TTT Phe	ATT Ile	TTA Leu	ATA Ile	TCT Ser 10	TTG Leu	GGA Gly	GTT Val	AGG Arg	GTT Val 15	TTG Leu	GAA Glu	ATT Ile	105
AAG Lys	AAA Lys 20	TAT Tyr	TTT Phe	TCT Ser	TAC Tyr	TCT Ser 25	CTA Leu	TTT Phe	TTT Phe	TTG Leu	CTT Leu 30	TTT Phe	TCT Ser	AGT Ser	CTC Leu	153
TTT Phe 35	TTA Leu	TCC Ser	AAA Lys	CTT Leu	CAA Gln 40	GCT Ala	TAT Tyr	AAA Lys	TTC Phe 45	AAC Asn	ATG Met	AGC Ser	ATT Ile	GTT Val	GGA Gly 50	201
AAG Lys	GTG Val	AGC Ser	AGC Ser	TAT Tyr 55	ACC Thr	AAG Lys	TTT Phe	GGC Gly	TTT Phe 60	AAC Asn	AAC Asn	CAA Gln	AGA Arg	TAC Tyr 65	CAG Gln	249
CCT Pro	TCT Ser	AAA Lys	GAC Asp 70	ATT Ile	TAT Tyr	CCT Pro	ACA Thr	GGT Gly 75	AGC Ser	TAC Tyr	ACT Thr	TCT Ser 80	TTA Leu	CTC Leu	GGC Gly	297
GAA Glu	TTG Leu	AAT Asn 85	TTG Leu	AGC Ser	ATG Met	GGT Gly	TTA Leu 90	TAC Tyr	AAG Lys	GGT Gly	TTG Leu	AGA Arg 95	GCG Ala	GAA Glu	GTG Val	345
GGG Gly 100	GCT Ala	ATG Met	ATG Met	GCA Ala	GCG Ala	CTC Leu 105	CCC Pro	TAT Tyr	GAC Asp	TCT Ser	ACC Thr 110	GCC Ala	TAT Tyr	CAA Gln	GGC Gly	393
AAC Asn 115	AAT Asn	ATC Ile	CCT Pro	AAC Asn	GGC Gly 120	CAG Gln	CCC Pro	GGC Gly	TCT Ser	AGG Arg 125	ACC Thr	GAT Asp	CCT Pro	TTT Phe	GGG Gly 130	441
GCG Ala	GGT Gly	ATC Ile	TTT Phe	TGG Trp 135	CAA Gln	TAT Tyr	ATT Ile	GGT Gly	TGG Trp 140	TAT Tyr	GCG Ala	GGG Gly	CAT His	AGT Ser 145	GGT Gly	489
TTG Leu	CAA Gln	GTG Val	CAA Gln 150	AAA Lys	CCT Pro	CGT Arg	TTA Leu 155	GCC Ala	ATG Met	GTG Val	CAT His	AAC Asn 160	GCT Ala	TTT Phe	TTG Leu	537
AGC Ser	TAC Tyr	AAC Asn 165	TAC Tyr	AAA Lys	AAA Lys	GAC Asp 170	AAA Lys	TTC Phe	AGT Ser	TTT Phe	GGC Gly 175	GTG Val	AAA Lys	GGG Gly	GGG Gly	585
CGC Arg	TAT Tyr 180	GAC Asp	GCT Ala	GAA Glu	GAG Glu	TAT Tyr 185	GAT Asp	TGG Trp	TTC Phe	ACT Thr	TCT Ser 190	TAC Tyr	ACT Thr	CAA Gln	GGG Gly	633
GTT Val 195	GAA Glu	GGC Gly	TTT Phe	GTC Val	AAA Lys 200	TAT Tyr	AAA Lys	GAC Asp	ACC Thr	AGA Arg 205	TTC Phe	AGG Arg	GTG Val	ATG Met	TAT Tyr 210	681
TCA Ser	GAC Asp	GCT Ala	AGG Arg	GCT Ala 215	TCA Ser	GCG Ala	TCA Ser	AGC Ser	GAC Asp 220	TGG Trp	TTT Phe	TGG Trp	TAT Tyr	TTT Phe 225	GGG Gly	729

CGT TAC TAT ACA AGC GGT AAG GCT CTA ATG GTA GCT GAT TTG AAA TAT	777
Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu Lys Tyr	
230 235 240	
GAA AAA GAC AAC CTA AAA ATC AAC CCT TAT TTT TAT GCG ATC TTT CAA	825
Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile Phe Gln	
245 250 255	
AGA ATG TAT GCG CCA GGC ATT AAT ATC ACT TAT GAC ACC AAC CCT AAT	873
Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn Pro Asn	
260 265 270	
TTC AAC AAT AAG GGT TTT CGT TTT GTA GGC ACT TTC GTA GGG TTT TTC	921
Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly Phe Phe	
275 280 285 290	
CCC ATT TTT GCC ACT CCG GCT AAT CAA AAT GAT ATT ATC CTC TTC CAA	969
Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu Phe Gln	
295 300 305	
CAA GTG CCA TTA GGC AAG AGT GGG CAA ACT TAT TTC TTC CGC ACT CGT	1017
Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg Thr Arg	
310 315 320	
TTT TAC TAT AAT AAG TGG CAA TTT GGG GGC AGC GTC TAT AAA AAC ATC	1065
Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys Asn Ile	
325 330 335	
GGT AAC GCT AAT GGT GAT ATA GGT ATT TAT GGC GAC CCT TTG GGG TAT	1113
Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu Gly Tyr	
340 345 350	
AAC ATT TGG ACG AAT AGT ATT TAT GAC GCA GAA ATT AAC AAT ATT GTT	1161
Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn Ile Val	
355 360 365 370	
GGC GCT GAT GTT ATT AAC GGG TTT TTG TAT GTA GGC TCA CAA TAT AGA	1209
Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln Tyr Arg	
375 380 385	
GGG TTT AGT TGG AAA ATT TTA GGC CGT TGG ACG GAT AGC CCA AGG GCT	1257
Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro Arg Ala	
390 395 400	
GAT GAA AGG AGT CTC GCG CTC TTT TTG AGT TAT TTT TCT AAT AAG TAT	1305
Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn Lys Tyr	
405 410 415	
AAT ATT AGA ATG GAT TTA AAA CTA GAA TAT TAT GGC AAT ATC ACC AAA	1353
Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile Thr Lys	
420 425 430	
AAA GGC TAT TGT ATT GGG TAT TGT GGC ATG TAT GTT CCA GTC GAT CCT	1401
Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val Asp Pro	
435 440 445 450	
AAC GGG CCT GGG ACA CAG CCT TTA ACG CAC AAT GTG TAT TCT GAC AGG	1449
Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser Asp Arg	

455 460 465

AGC CAT ATA ATG TTT AAC ATT GCT TAC GGT TTT AGG ATT TAC TAGCATT TTT 1500
 Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr
 470 475 480

ATCCTTAATG GATATTTTTTG ATTAGCCTTT TTAAATATT GAAA 1544

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Pro	Phe	Cys	Ile	Phe	Ile	Leu	Ile	Ser	Leu	Gly	Val	Arg	Val	Leu
1				5					10					15	
Glu	Ile	Lys	Lys	Tyr	Phe	Ser	Tyr	Ser	Leu	Phe	Phe	Leu	Leu	Phe	Ser
		20						25					30		
Ser	Leu	Phe	Leu	Ser	Lys	Leu	Gln	Ala	Tyr	Lys	Phe	Asn	Met	Ser	Ile
		35					40					45			
Val	Gly	Lys	Val	Ser	Ser	Tyr	Thr	Lys	Phe	Gly	Phe	Asn	Asn	Gln	Arg
	50					55				60					
Tyr	Gln	Pro	Ser	Lys	Asp	Ile	Tyr	Pro	Thr	Gly	Ser	Tyr	Thr	Ser	Leu
65					70					75				80	
Leu	Gly	Glu	Leu	Asn	Leu	Ser	Met	Gly	Leu	Tyr	Lys	Gly	Leu	Arg	Ala
				85					90					95	
Glu	Val	Gly	Ala	Met	Met	Ala	Ala	Leu	Pro	Tyr	Asp	Ser	Thr	Ala	Tyr
			100					105					110		
Gln	Gly	Asn	Asn	Ile	Pro	Asn	Gly	Gln	Pro	Gly	Ser	Arg	Thr	Asp	Pro
		115					120					125			
Phe	Gly	Ala	Gly	Ile	Phe	Trp	Gln	Tyr	Ile	Gly	Trp	Tyr	Ala	Gly	His
	130					135				140					
Ser	Gly	Leu	Gln	Val	Gln	Lys	Pro	Arg	Leu	Ala	Met	Val	His	Asn	Ala
145					150					155				160	
Phe	Leu	Ser	Tyr	Asn	Tyr	Lys	Lys	Asp	Lys	Phe	Ser	Phe	Gly	Val	Lys
			165						170					175	
Gly	Gly	Arg	Tyr	Asp	Ala	Glu	Glu	Tyr	Asp	Trp	Phe	Thr	Ser	Tyr	Thr
		180						185					190		
Gln	Gly	Val	Glu	Gly	Phe	Val	Lys	Tyr	Lys	Asp	Thr	Arg	Phe	Arg	Val
		195					200					205			
Met	Tyr	Ser	Asp	Ala	Arg	Ala	Ser	Ala	Ser	Ser	Asp	Trp	Phe	Trp	Tyr
	210					215					220				
Phe	Gly	Arg	Tyr	Tyr	Thr	Ser	Gly	Lys	Ala	Leu	Met	Val	Ala	Asp	Leu
225					230					235				240	
Lys	Tyr	Glu	Lys	Asp	Asn	Leu	Lys	Ile	Asn	Pro	Tyr	Phe	Tyr	Ala	Ile
			245						250					255	
Phe	Gln	Arg	Met	Tyr	Ala	Pro	Gly	Ile	Asn	Ile	Thr	Tyr	Asp	Thr	Asn
		260					265					270			
Pro	Asn	Phe	Asn	Asn	Lys	Gly	Phe	Arg	Phe	Val	Gly	Thr	Phe	Val	Gly
	275					280						285			
Phe	Phe	Pro	Ile	Phe	Ala	Thr	Pro	Ala	Asn	Gln	Asn	Asp	Ile	Ile	Leu

290		295		300
Phe Gln Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg				
305		310		315
Thr Arg Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys				
	325		330	335
Asn Ile Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu				
	340		345	350
Gly Tyr Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn				
	355		360	365
Ile Val Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln				
	370		375	380
Tyr Arg Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro				
385		390		395
Arg Ala Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn				
	405		410	415
Lys Tyr Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile				
	420		425	430
Thr Lys Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val				
	435		440	445
Asp Pro Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser				
	450		455	460
Asp Arg Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr				
465		470		475
				480

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...605
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AATTTTAGGT TATTAGTTAC CATTTTATTA TTCTTAAGGA TGTGTTTATA ATG AGA	56
Met Arg	
1	
ATT AAG GCT TAT TTT TTG CGT TTT ATC GCG CTG GTT TTG ATT GTT TTG	104
Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile Val Leu	
5 10 15	
TTA GGT TTT AGT GCT TGT AAA AAT TCT CAA AAA TCT CAA GAT TCT CAA	152
Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp Ser Gln	
20 25 30	
AAC AAT ACC CCC CAA CAA GAT AGC CCT AAA ACC TAC ACC GCT ATG GAT	200
Asn Asn Thr Pro Gln Asp Ser Pro Lys Thr Tyr Thr Ala Met Asp	
35 40 45 50	

TTG AAT AAC CAA GAA TAC ACC ATC ACA GGC GAT TTA GAT TCT CTC AAT	248
Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser Leu Asn	
55 60 65	
ATC AGC CCG GAT TCC AAC ACC CCT ACC CTA TTA GTT TTA AGC GCT TTA	296
Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser Ala Leu	
70 75 80	
GAT AAT TCT TTA AAA GAT TAC GCC CCC AGC TTT AAC ATC TTA AAA AAA	344
Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu Lys Lys	
85 90 95	
ACT TTT AAA GAT CGT TTG AGG GTG CTT ATT TTA CTC AAT AAA CCC TAT	392
Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Asn Lys Pro Tyr	
100 105 110	
TCA AGC GAT GCA ATC AAA GAC TTT AGC GCG CAT TTT CAA GCT GAT TTG	440
Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala Asp Leu	
115 120 125 130	
ATG ATT TTA AAC CCT AAA GAT ACC GCT CTT TTT GAT CAT TTA AAG TAT	488
Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu Lys Tyr	
135 140 145	
GAC GCT TTA AAC CAT TCT TTT AAC ATG CTC TTA TAC CAC AAA CAC CAA	536
Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys His Gln	
150 155 160	
TTG ATC AAA ATG TAT CAA GGG ATC GTG CCA ATA GAA ATG CTC CAA TTT	584
Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu Gln Phe	
165 170 175	
GAT ATT TCC AAT TTA AAG GAT TAAAAAAAC CATGTTTAAT TTTTTCAAAA AAAT	639
Asp Ile Ser Asn Leu Lys Asp	
180 185	
TGTCAATAAA ATTAAGGGT	658

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Arg Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile	
1 5 10 15	
Val Leu Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp	
20 25 30	
Ser Gln Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala	
35 40 45	
Met Asp Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser	

50	55	60
Leu Asn Ile Ser Pro Asp	Ser Asn Thr Pro Thr	Leu Leu Val Leu Ser
65	70	80
Ala Leu Asp Asn Ser Leu	Lys Asp Tyr Ala Pro	Ser Phe Asn Ile Leu
	85	90
Lys Lys Thr Phe Lys Asp	Arg Leu Arg Val Leu	Ile Leu Leu Asn Lys
	100	105
Pro Tyr Ser Ser Asp Ala	Ile Lys Asp Phe Ser	Ala His Phe Gln Ala
	115	120
Asp Leu Met Ile Leu Asn	Pro Lys Asp Thr Ala	Leu Phe Asp His Leu
	130	135
Lys Tyr Asp Ala Leu Asn	His Ser Phe Asn Met	Leu Leu Tyr His Lys
	145	150
His Gln Leu Ile Lys Met	Tyr Gln Gly Ile Val	Pro Ile Glu Met Leu
	165	170
Gln Phe Asp Ile Ser Asn	Leu Lys Asp	
	180	185

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...407
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATCCCTTCA AAAATGATAT AATAGACTTG ATGAATCAT TTTAAGGAAA ATG CCC	56
Met Pro	
1	
ATG CGT TTG CAC ACT GCC TTT TTT GGT ATT AAT TCA TTG CTT GTT GCC	104
Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu Val Ala	
5 10 15	
TCT CTT TTG ATA AGC GGT TGC AGT CTC TTT AAA AAG CGT AAC ACT AAC	152
Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn Thr Asn	
20 25 30	
GCC CAG CTA ATC CCC CCT TCA GCT AAT GGC TTG CAA GCC CCC ATT TAT	200
Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro Ile Tyr	
35 40 45 50	
CCC CCA ACC AAT TTC ACC CCT AGA AAG AGC ATT CAG CCT CTC CCA AGC	248
Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu Pro Ser	
55 60 65	
CCT CGC CTT GAG AAT AAC GAT CAG CCC GTC ATT AGT TCT AAC CCC ACT	296

Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn Pro Thr
70 75 80

AAC GCT ATC CCT AAC ACC CCC ATT CTC ACG CCT AAT AAT GTC ATT GAA 344
Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val Ile Glu
85 90 95

TTG AAC GCA TGG GCA TGG GCG TGG CTC CAG AAT CCA CCA TTT CAC CCT 392
Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe His Pro
100 105 110

CTC AAG CCC TGG CTC TAGCCAAGCG GGCGGCTATC GTTGATGGCT ACCGCCAGTT G 448
Leu Lys Pro Trp Leu
115

GGTGAAAAAA TG 460

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Pro Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu
1 5 10 15
Val Ala Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn
20 25 30
Thr Asn Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro
35 40 45
Ile Tyr Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu
50 55 60
Pro Ser Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn
65 70 75 80
Pro Thr Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val
85 90 95
Ile Glu Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe
100 105 110
His Pro Leu Lys Pro Trp Leu
115

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

[illegible]

GTTGTGATTT TATTGTGTTT TCATATCAAT TTTCATATCA AGGAGTTTAA ATG AAA Met Lys 1															56	
GAA Glu	ACA Thr	AGA Arg 5	CTT Leu	TTA Leu	AAA Lys	TTG Leu	AGA Arg 10	GCG Ala	TTG Leu	AGC Ser	TTA Leu	GCA Ala 15	TGT Cys	TTA Leu	ATG Met	104
GGA Gly	TTA Leu 20	GGC Gly	GTG Val	AGT Ser	GGG Gly 25	TGC Cys	GCG Ala	TTT Phe	TTA Leu	GAT Asp 30	AAG Lys	CAA Gln	ATC Ile	TTA Leu	AAC Asn	152
GAC Asp 35	CAT His	TTG Leu	ACT Thr	AAA Lys 40	GCT Ala	AAA Lys	AAT Asn	AAC Asn	CCA Pro	AAA Lys 45	TAC Tyr	GAT Asp	TGC Cys	CAA Gln	AAA Lys 50	200
GAA Glu	ATG Met	TGG Trp	TCT Ser 55	TTC Phe	CCT Pro	AAA Lys	AAA Lys	TAC Tyr 60	GAT Asp	GGG Gly	ATA Ile	AAT Asn	CAG Gln 65	TGT Cys	TTA Leu	248
AAG Lys	GCT Ala	CAA Gln 70	GAA Glu	GAG Glu	CTT Leu	ATT Ile	GAA Glu 75	CCA Pro	ATC Ile	ATC Ile	ACT Thr	AAA Lys 80	AAG Lys	ATC Ile	GAT Asp	296
CAG Gln	TAT Tyr 85	CAA Gln	TGC Cys	GAT Asp	GAT Asp	TTC Phe 90	ACT Thr	AAT Asn	GAA Glu	GGC Gly	TTA Leu 95	AAA Lys	GAT Asp	AAG Lys	TGT Cys	344
TTC Phe 100	AAA Lys	AGA Arg	AAC Asn	GAT Asp	GCC Ala	TAC Tyr 105	TTA Leu	AAC Asn	ACC Thr	CTT Leu 110	TTA Leu	ACG Thr	CCC Pro	ATC Ile	ATT Ile	392
CAA Gln 115	AAA Lys	CAA Gln	GAG Glu	CGT Arg 120	CGT Arg	TTT Phe	AGC Ser	TGC Cys	TCT Ser	GAT Asp 125	TTC Phe	CAT His	AAC Asn	CCA Pro	GAG Glu 130	440
CTA Leu	AAA Lys	GAA Glu	CAA Gln 135	TGC Cys	ATG Met	GAT Asp	AAA Lys	ACT Thr 140	AAC Asn	GCT Ala	TAT Tyr	GAA Glu	AAG Lys	CAA Gln 145	AAA Lys	488
GAC Asp	CGA Arg	CAA Gln 150	AAA Lys	AGA Arg	CTA Leu	ATT Ile	AAT Asn 155	CTC Leu	GTG Val	CAA Gln	TTA Leu	GAA Glu 160	GCG Ala	TTT Phe	GAA Glu	536
AAA Lys	GAA Glu 165	TAC Tyr	GCG Ala	CAA Gln	TAT Tyr	AAA Lys 170	CCA Pro	TAC Tyr	ATT Ile	ATC Ile	CCT Pro 175	TAC Tyr	TTC Phe	ACC Thr	AAA Lys	584
GAA Glu	TGC Cys	GTT Val	AAA Lys	AAT Asn	GCG Ala	CCC Pro	CAT His	TTA Leu	GCC Ala	AAC Asn	AAG Lys	GAA Glu	AGA Arg	CTA Leu	TGC Cys	632

1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Lys	Glu	Thr	Arg	Leu	Leu	Lys	Leu	Arg	Ala	Leu	Ser	Leu	Ala	Cys
1				5					10					15	
Leu	Met	Gly	Leu	Gly	Val	Ser	Gly	Cys	Ala	Phe	Leu	Asp	Lys	Gln	Ile
			20					25					30		
Leu	Asn	Asp	His	Leu	Thr	Lys	Ala	Lys	Asn	Asn	Pro	Lys	Tyr	Asp	Cys
		35					40					45			
Gln	Lys	Glu	Met	Trp	Ser	Phe	Pro	Lys	Lys	Tyr	Asp	Gly	Ile	Asn	Gln
	50					55					60				
Cys	Leu	Lys	Ala	Gln	Glu	Glu	Leu	Ile	Glu	Pro	Ile	Ile	Thr	Lys	Lys
65					70				75						80
Ile	Asp	Gln	Tyr	Gln	Cys	Asp	Asp	Phe	Thr	Asn	Glu	Gly	Leu	Lys	Asp
				85					90					95	
Lys	Cys	Phe	Lys	Arg	Asn	Asp	Ala	Tyr	Leu	Asn	Thr	Leu	Leu	Thr	Pro
			100					105					110		
Ile	Ile	Gln	Lys	Gln	Glu	Arg	Arg	Phe	Ser	Cys	Ser	Asp	Phe	His	Asn
	115						120					125			
Pro	Glu	Leu	Lys	Glu	Gln	Cys	Met	Asp	Lys	Thr	Asn	Ala	Tyr	Glu	Lys
	130					135					140				
Gln	Lys	Asp	Arg	Gln	Lys	Arg	Leu	Ile	Asn	Leu	Val	Gln	Leu	Glu	Ala
145					150					155					160
Phe	Glu	Lys	Glu	Tyr	Ala	Gln	Tyr	Lys	Pro	Tyr	Ile	Ile	Pro	Tyr	Phe
				165					170					175	
Thr	Lys	Glu	Cys	Val	Lys	Asn	Ala	Pro	His	Leu	Ala	Asn	Lys	Glu	Arg
			180					185					190		
Leu	Cys	Gln	Lys	Glu	Val	His	Glu	Lys	Phe	Asp	Asp	Pro	Tyr	Ser	Ser
	195						200					205			
Ser	Lys	Glu	Leu	Ser	Val	Gln	Ser	Ala	Ile	Ser	Phe	Cys	Ile	Lys	Lys
	210					215					220				
Val	Asp	Ala	Lys	Leu	Glu	Lys	Ala	Ala	Leu	Met	Asn	Gly	Val	Tyr	Ile
225					230					235					240
Ser	Pro	Tyr	Lys	Lys	Ser	Thr	His	Cys	Gln	Arg	Thr	His	Leu	Glu	Asn
			245						250					255	
Lys	Ser	Leu	Lys	Glu	Ile	Ala	Leu	Asn	Met	Asn	Pro	Lys	Leu	Glu	Lys
			260					265					270		
Gln	Ser	Pro	Phe	Ile	Asp	Ala	Asp	Lys	Met	Ala	Met	Gln	Ser	Ala	Gly
	275					280						285			
Leu	Leu	Arg	Lys	Asn	Lys	Gly	Val	Leu	Ile	Ala	Phe	Ala	Thr	Asp	Ile
	290					295					300				
Cys	Met	Glu	Arg	Asn	Glu	His	Lys	Lys	Glu	Glu	Phe	Ile	Ser	Leu	Lys
305					310					315					320
Asp	Ser	Cys	Thr	Gln	Ser	Gln	Ala	Lys	Ile	Tyr	Asn	Asn	Lys	Glu	Arg
				325					330					335	
Phe	Asp	Lys	Phe	Ile	Gln	Asp	Tyr	Gln	Lys	Asp	Leu	Lys	Thr	Cys	Leu
			340					345					350		
Leu	Asp	Thr	Ser	Asn	Thr	Lys	Glu	Glu	Val	Glu	Gln	Asn	Phe	Ser	Gln
		355				360						365			
Cys	Gln	Lys	Glu	Gln	Leu	Arg	Asp	Asp	Asn	Lys	Gly	Leu	Gly	Phe	Thr

370
Leu Glu Glu Leu Val Lys Lys Tyr Ala Lys
385 390

380

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 84...704
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTGATCATTC TTATTTTCGCA CAACCCAAGC ACGCTAAAAT TAGCCACTAA GCATGTGAAA	60
TTAGAGCATG GCGGTTTGAC AGA ATG CTA AGG GTT TTA AGC GTT GGT GTT GCT	113
Met Leu Arg Val Leu Ser Val Gly Val Ala	
1 5 10	
TTT ATT TTA CTA GGG TGT CAG TTT TTC AAC AAA ACG ACG CTG CAT TTA	161
Phe Ile Leu Leu Gly Cys Gln Phe Phe Asn Lys Thr Thr Leu His Leu	
15 20 25	
AAA TAT AAA GAT TAC CCC AAA AAT AGC GCT TTA AAA ACC GCT TTC ACT	209
Lys Tyr Lys Asp Tyr Pro Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr	
30 35 40	
TTA ACC CCC CCT AAA ATC TTT TTT AAC GCC CGT TTT GTG CCG CCC TTT	257
Leu Thr Pro Pro Lys Ile Phe Phe Asn Ala Arg Phe Val Pro Pro Phe	
45 50 55	
TAC CAA AAA GAA TTT AAA AAA GCG ATC ACC CAA CAA ATC GCT TAT TTT	305
Tyr Gln Lys Glu Phe Lys Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe	
60 65 70	
TTA AAA GAT AAA AGT GCT TTT ATT CTC AAT GTT TCA GGC AAT GTT TTT	353
Leu Lys Asp Lys Ser Ala Phe Ile Leu Asn Val Ser Gly Asn Val Phe	
75 80 85 90	
TTT TCT TTT GAA GAG AAT CCT AAA GAT TTA AAA GCC ATT AAA GAA AGG	401
Phe Ser Phe Glu Glu Asn Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg	
95 100 105	
CTT AAA AAG ACG ATT GAG CCT AAC GCT GAC CCA AAA GCC GTC ATG CGT	449
Leu Lys Lys Thr Ile Glu Pro Asn Ala Asp Pro Lys Ala Val Met Arg	
110 115 120	
TTT TTA AAC CTT CAA GCG AGC TTG ATT TTA GAA TGC GTC CCG CAA ACC	497
Phe Leu Asn Leu Gln Ala Ser Leu Ile Leu Glu Cys Val Pro Gln Thr	

125	130	135	
ACT TGC CCG TTT GAC ACC CTT TTA ATC CCC ACC GCT TTC AGC GTG CCT			545
Thr Cys Pro Phe Asp Thr Leu Leu Ile Pro Thr Ala Phe Ser Val Pro			
140	145	150	
GTT TAT TAC GCT AAT CGT TTG GGC GAT AAC CCC TCT CTT TTT TCC CAA			593
Val Tyr Tyr Ala Asn Arg Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln			
155	160	165	170
GAG GAT AAA ACC TAT CAT AAC GCT TTG ATC AAA GCC CTT AAT AAG GCT			641
Glu Asp Lys Thr Tyr His Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala			
175	180	185	
TAC TAT TCT CTT ATG GAG GGT TTA GAA AAG CGT TTG AAC GCT ATA AAA			689
Tyr Tyr Ser Leu Met Glu Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys			
190	195	200	
AAT GCA GAG TGG CTT TAAGGCATGA AAAAGATTGC ATTTTTTATT TTTGTCATTT T			745
Asn Ala Glu Trp Leu			
205			
GTTCGCGTA GGGATTTATT TAATTTGGCA TGTTTTATTG GAAAAAGCCC TAGAATTGAA			805
ATTAGCAACC TCAGCTAATG ATTTGCTTTT			835

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Leu	Arg	Val	Leu	Ser	Val	Gly	Val	Ala	Phe	Ile	Leu	Leu	Gly	Cys
1				5					10					15	
Gln	Phe	Phe	Asn	Lys	Thr	Thr	Leu	His	Leu	Lys	Tyr	Lys	Asp	Tyr	Pro
			20					25					30		
Lys	Asn	Ser	Ala	Leu	Lys	Thr	Ala	Phe	Thr	Leu	Thr	Pro	Pro	Lys	Ile
			35				40					45			
Phe	Phe	Asn	Ala	Arg	Phe	Val	Pro	Pro	Phe	Tyr	Gln	Lys	Glu	Phe	Lys
			50			55					60				
Lys	Ala	Ile	Thr	Gln	Gln	Ile	Ala	Tyr	Phe	Leu	Lys	Asp	Lys	Ser	Ala
65				70					75					80	
Phe	Ile	Leu	Asn	Val	Ser	Gly	Asn	Val	Phe	Phe	Ser	Phe	Glu	Glu	Asn
			85					90					95		
Pro	Lys	Asp	Leu	Lys	Ala	Ile	Lys	Glu	Arg	Leu	Lys	Lys	Thr	Ile	Glu
			100				105						110		
Pro	Asn	Ala	Asp	Pro	Lys	Ala	Val	Met	Arg	Phe	Leu	Asn	Leu	Gln	Ala
			115			120						125			
Ser	Leu	Ile	Leu	Glu	Cys	Val	Pro	Gln	Thr	Thr	Cys	Pro	Phe	Asp	Thr
	130				135						140				
Leu	Leu	Ile	Pro	Thr	Ala	Phe	Ser	Val	Pro	Val	Tyr	Tyr	Ala	Asn	Arg
145					150					155				160	

Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln Glu Asp Lys Thr Tyr His
165 170 175
Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala Tyr Tyr Ser Leu Met Glu
180 185 190
Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys Asn Ala Glu Trp Leu
195 200 205

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...710
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAAAATAAC CATGAGTTAT TCAAAAATTT AACTTTATAA GACAGGTGGC ATG CGT	56
Met Arg	
1	
TTA AAA CAT TTT AAA ACT TTC CTT TTT ATC ACA ATG GCA ATC ATT GTA	104
Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile Ile Val	
5 10 15	
ATA GGT ACC GGT TGC GCG AAC AAA AAG AAA AAA AAA GAC GAA TAC AAC	152
Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Lys Asp Glu Tyr Asn	
20 25 30	
AAA CCG GCG ATC TTT TGG TAT CAA GGG ATT TTG AGA GAA ATC CTT TTT	200
Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile Leu Phe	
35 40 45 50	
GCT AAT TTA GAA ACA GCG GAC AAT TAC TAT TCT TCT TTA CAA AGC GAA	248
Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln Ser Glu	
55 60 65	
CAC ATC AAT TCC CCC CTT GTC CCA GAA GCG ATG CTA GCT TTA GGG CAA	296
His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu Gly Gln	
70 75 80	
GCG CAC ATG AAA AAG AAA GAG TAT GTT TTA GCG TCT TTT TAC TTT GAT	344
Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr Phe Asp	
85 90 95	
GAA TAC ATC AAG CGC TTT GGG ACT AAG GAC AAT GTG GAT TAT TTG ACT	392
Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr Leu Thr	
100 105 110	

TTT TTA AAA TTG CAA TCG CAT TAT TAC GCT TTC AAA AAC CAT TCT AAA 440
 Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys
 115 120 125 130
 GAC CAG GAA TTT ATC TCT AAT TCT ATT GTG AGT TTA GGC GAA TTT ATA 488
 Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile
 135 140 145
 GAA AAA TAC CCT AAC AGC CGT TAC CGC CCC TAT GTA GAA TAC ATG CAA 536
 Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln
 150 155 160
 ATC AAA TTC ATT TTA GGG CAA AAT GAG CTC AAT CGC GCG ATC GCG AAT 584
 Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn
 165 170 175
 GTC TAT AAA AAA CGC CAC AAG CCT GAG GGC GTG AAA CGC TAT TTA GAA 632
 Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu
 180 185 190
 AGG ATA GAT GAG ACT TTA GAA AAA GAG ACT AAA CCC AAA CCA TCG CAC 680
 Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His
 195 200 205 210
 ATG CCT TGG TAT GTG TTA ATT TTT GAT TGG TAGGATATTT CAAAACCATA CAC 733
 Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
 215 220
 ATTATAACAG AGAGATGAAA AATGACTGAA 763

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii).MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Arg Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile
 1 5 10 15
 Ile Val Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Lys Asp Glu
 20 25 30
 Tyr Asn Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile
 35 40 45
 Leu Phe Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln
 50 55 60
 Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu
 65 70 75 80
 Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr
 85 90 95
 Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr
 100 105 110
 Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His

115 120 125
 Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu
 130 135 140
 Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr
 145 150 155 160
 Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile
 165 170 175
 Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr
 180 185 190
 Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro
 195 200 205
 Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
 210 215 220

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...749
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAAAAAGGCT CTGCTTTGAT AGATAAATTT GACGCTAACC CCTATAAAAC GATTTTTTGA 60
 GAAAGGAAAT AATC ATG AGA GCT ACG GCG ATA AAA ATC TTT TCA CTC TCA 110
 Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser
 1 5 10

TCA GCA TTA GCC CTA TTG CTT CAT GGT TGC TTG AGC ATC AAT TTA AAA 158
 Ser Ala Leu Ala Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys
 15 20 25

CAA ATG CTA CCA GAG ATC AGA ACT TAC GAT TTG AAT GCG AGT TCT TTT 206
 Gln Met Leu Pro Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe
 30 35 40

GAA ATC ACG CAA TGC GCT AAA CCT TTG ACT GAA GTG AGG CTC ATT AGT 254
 Glu Ile Thr Gln Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser
 45 50 55 60

ATT TTG AGC GCG GAT TTA TTC AAC ACT AAA GAG ATC GTT TTT AAA GCC 302
 Ile Leu Ser Ala Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala
 65 70 75

AAA GAC GGG CAG ATC ACG CAT GGG AAG CAC CAA AAA TGG ATA GAC TTG 350
 Lys Asp Gly Gln Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu
 80 85 90

CCT CGC AAC ATG CTA AAA ACC ATG TTC ATG CAA GAA GCG CAA AAA GCA	398
Pro Arg Asn Met Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala	
95 100 105	
TGC TTA GGC GTG GCT TTG CCT CCT TAT GGC GCG GGT GCA CCC ACT TAT	446
Cys Leu Gly Val Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr	
110 115 120	
GCG GTT CGT TTT ACG ATT TTA TCG TTT TCT CTT TTA GAA AAA GAA AAT	494
Ala Val Arg Phe Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn	
125 130 135 140	
TCT ACC TAT AGG GCG GAA TTT GCA CTA GGC TAT GAC ATT AGC GTG AAA	542
Ser Thr Tyr Arg Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys	
145 150 155	
GGC GAT TCG CAT TCT GGG GTG ATC ATT AAG CAT GAA AAT ATT TCT AGC	590
Gly Asp Ser His Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser	
160 165 170	
TTG GAA AAT AAA ACG ACC AAA ACG AGT AAA AAT GGC AAT CAA GAT TTT	638
Leu Glu Asn Lys Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe	
175 180 185	
CAA GAA AGC GCG ATA CAA TCT CTC CAA CAT GTA AGC GTG CAA GCG ATT	686
Gln Glu Ser Ala Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile	
190 195 200	
CAA GAA GCG GTT TCT TTG ATT AAA AAA GCC ATT GAA GCG CAA AGC GTA	734
Gln Glu Ala Val Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val	
205 210 215 220	
AGC CCG TTA AAA AAA TAAAAAATAA GGAGGAATTG TTTGATTTTA CGATTGGCTG G	790
Ser Pro Leu Lys Lys	
225	
AGCAAGCGTT T	801

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser Ser Ala Leu Ala	
1 5 10 15	
Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys Gln Met Leu Pro	
20 25 30	
Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe Glu Ile Thr Gln	
35 40 45	
Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser Ile Leu Ser Ala	

50	55	60
Asp Leu Phe Asn Thr Lys	Glu Ile Val Phe Lys	Ala Lys Asp Gly Gln
65	70	75
Ile Thr His Gly Lys	His Gln Lys Trp Ile	Asp Leu Pro Arg Asn Met
85	90	95
Leu Lys Thr Met Phe Met	Gln Glu Ala Gln Lys	Ala Cys Leu Gly Val
100	105	110
Ala Leu Pro Pro Tyr Gly	Ala Gly Ala Pro Thr	Tyr Ala Val Arg Phe
115	120	125
Thr Ile Leu Ser Phe Ser	Leu Leu Glu Lys Glu	Asn Ser Thr Tyr Arg
130	135	140
Ala Glu Phe Ala Leu Gly	Tyr Asp Ile Ser Val	Lys Gly Asp Ser His
145	150	155
Ser Gly Val Ile Ile Lys	His Glu Asn Ile Ser	Ser Ser Leu Glu Asn Lys
165	170	175
Thr Thr Lys Thr Ser Lys	Asn Gly Asn Gln Asp	Phe Gln Glu Ser Ala
180	185	190
Ile Gln Ser Leu Gln His	Val Ser Val Gln Ala	Ile Gln Glu Ala Val
195	200	205
Ser Leu Ile Lys Lys Ala	Ile Glu Ala Gln Ser	Val Ser Pro Leu Lys
210	215	220
Lys		
225		

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...395
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTTATGATA AGATAGTCAA ATTATACATT GACTTAAGGA AATTTAATTG ATG AAA	56
Met Lys	
1	
TCT AAA ATC ACT CAT TTT ATC GCT ATC TCT TTT GTT TTA AGC CTG TTT	104
Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser Leu Phe	
5 10 15	
AGC GCA TGC AAA GAC GAG CCT AAA AAA TCG TCT CAA TCG CAC CAA AAC	152
Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His Gln Asn	
20 25 30	
AAC ACT AAA ATC ACT AAA AAC AAT CCA ATC AAT CAA GCG AAT AAT GAT	200
Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn Asn Asp	
35 40 45 50	

ATA AGA AAA ATT GAG CAT GAA GAA GAA GAT GAA AAA GCC ACC AAA GAA 248
 Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr Lys Glu
 55 60 65

 GTG AAC GAT TTG ATC AAT AAC GAA AAT AAA ATT GAT GAA ATC AAT AAT 296
 Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile Asn Asn
 70 75 80

 GAA GAA AAC GCT GAT CCT TCG CAA AAA AGA ACG AAC AAC GTT TTG CAA 344
 Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val Leu Gln
 85 90 95

 CGA GCC ACT AAC CAC CAA GAC AAT CTC AAT TCC CCA CTC AAC AGG AAG 392
 Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn Arg Lys
 100 105 110

 TAT TAAAGTGTGA AACTTTTTTC AAAGGATTTA TTTAAAAAAG TAACCCCTTT ATT 448
 Tyr
 115

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser
 1 5 10 15
 Leu Phe Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His
 20 25 30
 Gln Asn Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn
 35 40 45
 Asn Asp Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr
 50 55 60
 Lys Glu Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile
 65 70 75 80
 Asn Asn Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val
 85 90 95
 Leu Gln Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn
 100 105 110
 Arg Lys Tyr
 115

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 121...1065
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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CTATCAAGTC AGTATTTCCA ATATCCAATT AGCCAATGAT CTCAAAGATT CTAATATTTT      60
TATCCACCAG CGTTTAATCA TCCCCACCAA CAAAAAATTA CTCGCTACAA GGAATTTTA      120
ATG GGT TTG GCG TTG GAA AAA GTT TGT TTT TTA GGC GTT ATT TTT TTG      168
Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu
  1             5             10             15

ATT AGC GCT TGC ACG GTT AAA AAA GAG GGG GTA AAG AAT TTG TCT TAC      216
Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr
          20             25             30

AAG CAT GAA AGC TTG CGC GCT TAT GAA AAC GCT AAA GAT TAT GAT CCG      264
Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro
          35             40             45

ACA ACC AAA AAA GCC GCC TAT AAA CGC AAT TTT TTT GAA CGC CAT TTC      312
Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe
          50             55             60

AAA CGC TAC TCC GAT TCG CAA GAT AGC AAC ACA AAA GAT CAG CCA CTA      360
Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
          65             70             75             80

GAT AAC GGC ATG CGC GAT TCT AGC TCG ATC CAA AGA GCC ACC ATG CGC      408
Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
          85             90             95

CCT TAT CAA GTG GGG GGC AAG TGG TAT TAC CCC ACT AAA GTG GAT TTA      456
Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
          100            105            110

GGC GAA AAA TTT GAT GGC GTT GCG AGT TGG TAT GGC CCT AAC TTC CAT      504
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His
          115            120            125

GCC AAA AAA ACC AGT AAT GGG GAA ATT TAT AAC ATG TAT GCC CAC ACC      552
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr
          130            135            140

GCC GCG CAC AAA ACT TTA CCC ATG AAC ACC GTG GTG AAA GTC ATC AAT      600
Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn
          145            150            155            160

GTT GAT AAT AAC TTA AGC ACC ATT GTG CGC ATC AAC GAT AGA GGG CCT      648
Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro
          165            170            175

TTT GTG AGC GAT CGC ATC ATT GAT TTG TCT AAT GCG GCC GCT AGG GAT      696
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Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp	
180 185 190	
ATT GAC ATG GTT AAA AAA GGC ACA GCC AGC GTG CGT CTC ATT GTT TTG	744
Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu	
195 200 205	
GGC TTT GGT GGG GTT ATC TCC ACG CAA TAC GAA CAA TCC TTT AAC GCC	792
Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala	
210 215 220	
AGC TCT TCA AAG ATC TTG CAC AAG GAA TTT AAA GTC GGC GAG AGC GAA	840
Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu	
225 230 235 240	
AAA AGC GTG AGC GGA GGG AAA TTT TCT TTG CAA ATG GGG GCT TTT AGA	888
Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg	
245 250 255	
AAC CAA ATA GGT GCT CAA ACT TTA GCG GAT AAA TTG CAA GCA GAA AAT	936
Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn	
260 265 270	
CCA AAT TAC AGC GTC AAG GTT GCT TTT AAA GAC GAT TTG TAT AAA GTT	984
Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val	
275 280 285	
TTA GTT CAA GGG TTT CAA AGC GAA GAA GAG GCT AGG GAT TTT ATG AAA	1032
Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys	
290 295 300	
AAA TAC AAC CAG AAT GCG GTT TTA ACG AGA GAA TGATTAAGTT ATTGCTTTTA	1085
Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu	
305 310 315	
GATGTGGATG GCACGCTCAC AGACGGATCG TTGTAT	1121

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu	
1 5 10 15	
Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr	
20 25 30	
Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro	
35 40 45	
Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe	
50 55 60	

Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
 65 70 75 80
 Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
 85 90 95
 Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
 100 105 110
 Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His
 115 120 125
 Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr
 130 135 140
 Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn
 145 150 155 160
 Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro
 165 170 175
 Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp
 180 185 190
 Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu
 195 200 205
 Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala
 210 215 220
 Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu
 225 230 235 240
 Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg
 245 250 255
 Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn
 260 265 270
 Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val
 275 280 285
 Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys
 290 295 300
 Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu
 305 310 315

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...761
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TATAATAAGG AAATTCTAAA CGAAAATTAA ACTGAATGAA AGGAGTTTGA ATG AAA 56
 Met Lys
 1
 AAA ATC GTT TTA GTA GCG ATA GCC TTA TTG ATG AGC GCT TGC GCG AGC 104
 Lys Ile Val Leu Val Ala Ile Ala Leu Leu Met Ser Ala Cys Ala Ser

5					10					15						
TAT	AAG	ATC	ACG	CCT	GAA	CAT	GTT	ACT	TCC	TAT	AAT	AAT	GGG	ATT	CAA	152
Tyr	Lys	Ile	Thr	Pro	Glu	His	Val	Thr	Ser	Tyr	Asn	Asn	Gly	Ile	Gln	
20						25					30					
GTG	ATG	ACT	TCC	ACG	CAA	GCC	AAA	TCT	AAA	GTC	CAG	CTA	GAA	ATC	GCT	200
Val	Met	Thr	Ser	Thr	Gln	Ala	Lys	Ser	Lys	Val	Gln	Leu	Glu	Ile	Ala	
35					40					45					50	
CAA	AGC	AAG	TTG	AAA	GGC	TTG	AAC	GAG	TCC	CCC	TTA	GTG	CTG	TAT	GTA	248
Gln	Ser	Lys	Leu	Lys	Gly	Leu	Asn	Glu	Ser	Pro	Leu	Val	Leu	Tyr	Val	
				55					60					65		
GCG	GCG	CAA	GTT	ATA	GAG	GGA	AGT	CCT	GTG	GTG	TTT	AGC	CGT	AAA	GCC	296
Ala	Ala	Gln	Val	Ile	Glu	Gly	Ser	Pro	Val	Val	Phe	Ser	Arg	Lys	Ala	
			70					75					80			
ATT	TCA	GTG	TCT	ATC	AAC	CAA	ACG	AAT	TTA	CCG	GTC	TTA	AGC	CTG	AGA	344
Ile	Ser	Val	Ser	Ile	Asn	Gln	Thr	Asn	Leu	Pro	Val	Leu	Ser	Leu	Arg	
		85					90					95				
CAG	GTG	ATG	AAA	TCC	AGT	TTT	GAT	TTT	GAG	GGT	ATT	TTA	CAA	AGT	TTT	392
Gln	Val	Met	Lys	Ser	Ser	Phe	Asp	Phe	Glu	Gly	Ile	Leu	Gln	Ser	Phe	
	100					105					110					
AAT	ATC	GCC	GTG	CCG	ACC	ACC	CCT	ATT	GAT	AAT	GTC	AAT	ATG	ATC	ACC	440
Asn	Ile	Ala	Val	Pro	Thr	Thr	Pro	Ile	Asp	Asn	Val	Asn	Met	Ile	Thr	
115					120					125					130	
CCG	CCT	ATG	TTT	TAT	TAC	GGG	CAA	GGG	GGA	TTT	TTA	GCT	TAT	AAC	GGC	488
Pro	Pro	Met	Phe	Tyr	Tyr	Gly	Gln	Gly	Gly	Phe	Leu	Ala	Tyr	Asn	Gly	
				135					140					145		
ATG	ATG	TAT	GGG	GGA	ATG	GGC	ATG	TAT	GGG	CCA	GGC	TTT	GGC	ATG	ATG	536
Met	Met	Tyr	Gly	Gly	Met	Gly	Met	Tyr	Gly	Pro	Gly	Phe	Gly	Met	Met	
			150					155					160			
ATG	ATG	GAT	GAT	GTA	GAA	GAG	CAA	GAA	GTC	ATG	CAA	GAA	AGC	CGC	CAA	584
Met	Met	Asp	Asp	Val	Glu	Glu	Gln	Glu	Val	Met	Gln	Glu	Ser	Arg	Gln	
		165					170					175				
GCT	TTA	AAA	ATC	CTA	GCG	ATC	AAT	TAC	CTT	AAA	AAC	AAC	ACC	CTT	AAT	632
Ala	Leu	Lys	Ile	Leu	Ala	Ile	Asn	Tyr	Leu	Lys	Asn	Asn	Thr	Leu	Asn	
	180					185					190					
GTT	GAG	AGT	AAG	GCT	AAG	GGA	GGG	TTT	GTG	GTG	GTG	GAT	ACC	AAA	AAC	680
Val	Glu	Ser	Lys	Ala	Lys	Gly	Gly	Phe	Val	Val	Val	Asp	Thr	Lys	Asn	
195					200					205				210		
CTT	AAA	ACC	CCG	GGT	GTG	GTG	GTG	GTT	AAA	GTC	TTT	TTA	GAA	GAT	GAA	728
Leu	Lys	Thr	Pro	Gly	Val	Val	Val	Val	Lys	Val	Phe	Leu	Glu	Asp	Glu	
				215					220					225		
ATC	CAC	ACC	TTT	AAA	ATT	GAT	ATT	TCT	AAG	ATG	TAATCGCCCC	CTTTAATAAAA				781
Ile	His	Thr	Phe	Lys	Ile	Asp	Ile	Ser	Lys	Met						
			230					235								

AGCCTTTGGG CCATCCACCT AAAGGTTTTT

811

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Lys	Lys	Ile	Val	Leu	Val	Ala	Ile	Ala	Leu	Leu	Met	Ser	Ala	Cys
1				5					10					15	
Ala	Ser	Tyr	Lys	Ile	Thr	Pro	Glu	His	Val	Thr	Ser	Tyr	Asn	Asn	Gly
			20					25					30		
Ile	Gln	Val	Met	Thr	Ser	Thr	Gln	Ala	Lys	Ser	Lys	Val	Gln	Leu	Glu
		35					40					45			
Ile	Ala	Gln	Ser	Lys	Leu	Lys	Gly	Leu	Asn	Glu	Ser	Pro	Leu	Val	Leu
	50					55				60					
Tyr	Val	Ala	Ala	Gln	Val	Ile	Glu	Gly	Ser	Pro	Val	Val	Phe	Ser	Arg
65					70					75				80	
Lys	Ala	Ile	Ser	Val	Ser	Ile	Asn	Gln	Thr	Asn	Leu	Pro	Val	Leu	Ser
			85					90					95		
Leu	Arg	Gln	Val	Met	Lys	Ser	Ser	Phe	Asp	Phe	Glu	Gly	Ile	Leu	Gln
		100						105					110		
Ser	Phe	Asn	Ile	Ala	Val	Pro	Thr	Thr	Pro	Ile	Asp	Asn	Val	Asn	Met
		115					120					125			
Ile	Thr	Pro	Pro	Met	Phe	Tyr	Tyr	Gly	Gln	Gly	Gly	Phe	Leu	Ala	Tyr
	130					135					140				
Asn	Gly	Met	Met	Tyr	Gly	Gly	Met	Gly	Met	Tyr	Gly	Pro	Gly	Phe	Gly
145					150					155				160	
Met	Met	Met	Met	Asp	Val	Glu	Glu	Gln	Glu	Val	Met	Gln	Glu	Ser	
			165					170				175			
Arg	Gln	Ala	Leu	Lys	Ile	Leu	Ala	Ile	Asn	Tyr	Leu	Lys	Asn	Asn	Thr
		180					185					190			
Leu	Asn	Val	Glu	Ser	Lys	Ala	Lys	Gly	Gly	Phe	Val	Val	Val	Asp	Thr
		195					200					205			
Lys	Asn	Leu	Lys	Thr	Pro	Gly	Val	Val	Val	Val	Lys	Val	Phe	Leu	Glu
	210					215					220				
Asp	Glu	Ile	His	Thr	Phe	Lys	Ile	Asp	Ile	Ser	Lys	Met			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 97...1371
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TAAAAAAAAC	TACCCTTAAA	AAAATCAATC	TAAAATTCTT	AAATTAAAAAT	ATAGCTATAA	60
TACACTAAAA	CAATCTCAAG	GTTTCAAAAT	TTAGCC	ATG CGT CTT CTT CTG TTC		114
			Met	Arg Leu Leu Leu Phe		
			1	5		
AAT CAA AAC GCT TTT TTA TTA GCG TGC ATG TTT GTT TCA AGC GTG TAT						162
Asn Gln Asn Ala Phe Leu Leu Ala Cys Met Phe Val Ser Ser Val Tyr						
	10		15		20	
GTG AAC GCT GTC TTA GAC GCT TAT GCA ATT GAA AAC CCC TAT ATT TCT						210
Val Asn Ala Val Leu Asp Ala Tyr Ala Ile Glu Asn Pro Tyr Ile Ser						
	25		30		35	
ATC ACA CTC ACA AGC CTA TTA GCC CCT TTA AGC ATG CTA GCG TTT TTA						258
Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu Ser Met Leu Ala Phe Leu						
	40		45		50	
AAA ACC CCT AGA AAT AGT GCT TTT GCT TTG GGG TTT TTT GTG GGG GCG						306
Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly Phe Phe Val Gly Ala						
	55		60		65	70
TTA TTG TTT TAT TGG TGC GCT TTA AGC TTT CGC TAC TCG GAT TTC ACT						354
Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe Arg Tyr Ser Asp Phe Thr						
	75		80		85	
TAT TTA TTG CCC TTA ATC ATT GTT TTA ATA GCG TTA GTT TAT GGG GTT						402
Tyr Leu Leu Pro Leu Ile Ile Val Leu Ile Ala Leu Val Tyr Gly Val						
	90		95		100	
TTA TTT TAT TTG TTG CTC TAT TTT GAA AAC CCC TAT TTC AGG CTT TTG						450
Leu Phe Tyr Leu Leu Leu Tyr Phe Glu Asn Pro Tyr Phe Arg Leu Leu						
	105		110		115	
AGT TTT TTA GGC TCT AGT TTT ATC CAC CCC TTT GGA TTT GAT TGG TTA						498
Ser Phe Leu Gly Ser Ser Phe Ile His Pro Phe Gly Phe Asp Trp Leu						
	120		125		130	
GTC CCA GAT AGC TTT TTT TCT TAT AGC GTG TTT AGA GTG GAT AAA TTA						546
Val Pro Asp Ser Phe Phe Ser Tyr Ser Val Phe Arg Val Asp Lys Leu						
	135		140		145	150
TCG CTA GGG CTT GTT TTT TTG GCT TGC ATT TTT TTG AGC ACT AAA CCA						594
Ser Leu Gly Leu Val Phe Leu Ala Cys Ile Phe Leu Ser Thr Lys Pro						
	155		160		165	
TTG AAA AAA TAT AGG ATC ATA GGG GTT TTA TTG TTA CTT GGC GCG TTG						642
Leu Lys Lys Tyr Arg Ile Ile Gly Val Leu Leu Leu Leu Gly Ala Leu						
	170		175		180	
GAT TTT AAT GGT TTC AAA ACA AGC GAT TTA AAA AAG GTT GGA AAT ATT						690
Asp Phe Asn Gly Phe Lys Thr Ser Asp Leu Lys Lys Val Gly Asn Ile						

185					190					195									
GAA	TTA	GTC	TCT	ACA	AAA	ACG	CCC	CAA	GAT	TTG	AAA	TTT	GAC	TCA	AGT	738			
Glu	Leu	Val	Ser	Thr	Lys	Thr	Pro	Gln	Asp	Leu	Lys	Phe	Asp	Ser	Ser				
	200					205					210								
TAC	CTT	AAT	GAT	ATT	GAA	AAC	AAC	ATT	CTT	AAA	GAA	ATC	AAG	CTC	GCT	786			
Tyr	Leu	Asn	Asp	Ile	Glu	Asn	Asn	Ile	Leu	Lys	Glu	Ile	Lys	Leu	Ala				
215					220					225					230				
CAA	AGC	AAG	CAA	AAA	ACC	TTG	ATT	GTT	TTT	CCA	GAA	ACC	GCC	TAC	CCC	834			
Gln	Ser	Lys	Gln	Lys	Thr	Leu	Ile	Val	Phe	Pro	Glu	Thr	Ala	Tyr	Pro				
				235					240					245					
ATC	GCT	TTA	GAA	AAC	TCC	CCC	TTT	AAA	GCG	AAG	CTA	GAA	GAT	TTA	AGC	882			
Ile	Ala	Leu	Glu	Asn	Ser	Pro	Phe	Lys	Ala	Lys	Leu	Glu	Asp	Leu	Ser				
			250					255					260						
GAT	AAT	ATT	GCT	ATT	TTA	ATA	GGG	ACA	TTA	CGG	ACT	CAA	GGC	TAT	AAT	930			
Asp	Asn	Ile	Ala	Ile	Leu	Ile	Gly	Thr	Leu	Arg	Thr	Gln	Gly	Tyr	Asn				
		265					270					275							
CTT	TAT	AAC	AGC	TCG	TTT	TTA	TTT	TCT	AAA	GAA	AGC	GTT	CAG	ATC	GCT	978			
Leu	Tyr	Asn	Ser	Ser	Phe	Leu	Phe	Ser	Lys	Glu	Ser	Val	Gln	Ile	Ala				
	280					285					290								
GAT	AAA	GTA	ATT	TTA	GCC	CCC	TTT	GGC	GAG	ACC	ATG	CCT	TTA	CCG	GAA	1026			
Asp	Lys	Val	Ile	Leu	Ala	Pro	Phe	Gly	Glu	Thr	Met	Pro	Leu	Pro	Glu				
295					300					305					310				
TTT	CTT	CAA	AAA	CCC	CTT	GAA	AAG	CTC	TTT	TTT	GGC	GAG	AGC	ACT	TAT	1074			
Phe	Leu	Gln	Lys	Pro	Leu	Glu	Lys	Leu	Phe	Phe	Gly	Glu	Ser	Thr	Tyr				
				315					320					325					
TTA	TAC	CGC	AAT	GCT	CCT	CAT	TTC	AGC	GAT	TTT	ACA	TTA	GAC	GAT	TTT	1122			
Leu	Tyr	Arg	Asn	Ala	Pro	His	Phe	Ser	Asp	Phe	Thr	Leu	Asp	Asp	Phe				
			330					335					340						
ACT	TTT	CGC	CCC	CTG	ATT	TGC	TAT	GAA	GGC	ACT	TCC	AAA	CCC	GCT	TAT	1170			
Thr	Phe	Arg	Pro	Leu	Ile	Cys	Tyr	Glu	Gly	Thr	Ser	Lys	Pro	Ala	Tyr				
		345					350					355							
TCA	AAC	AGC	CCT	TCA	AAA	ATT	TTT	ATC	GTG	ATG	AGC	AAT	AAC	GCA	TGG	1218			
Ser	Asn	Ser	Pro	Ser	Lys	Ile	Phe	Ile	Val	Met	Ser	Asn	Asn	Ala	Trp				
	360					365					370								
TTT	AGC	CCA	AGC	ATT	GAA	CCC	ACC	TTA	CAA	AGA	ACG	CTT	TTA	AAA	TAC	1266			
Phe	Ser	Pro	Ser	Ile	Glu	Pro	Thr	Leu	Gln	Arg	Thr	Leu	Leu	Lys	Tyr				
375					380					385					390				
TAC	GCA	AGG	CGT	TAT	GAT	AAG	ATC	ATC	TTG	CAC	AGC	GCG	AAC	TTT	TCA	1314			
Tyr	Ala	Arg	Arg	Tyr	Asp	Lys	Ile	Ile	Leu	His	Ser	Ala	Asn	Phe	Ser				
				395					400					405					
ACT	TCT	TAC	ATC	TTA	AGC	CCT	AGT	TTA	TTA	GGC	GAT	ATT	CTT	TTT	AGG	1362			
Thr	Ser	Tyr	Ile	Leu	Ser	Pro	Ser	Leu	Leu	Gly	Asp	Ile	Leu	Phe	Arg				
			410					415					420						

AAA CGA TCA TGATTAAAGC GATTAATATT TCTCATGCTT TTGAAAAGCC TCTTTATAA 1420
 Lys Arg Ser
 425

TGGCG

1425

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Arg	Leu	Leu	Leu	Phe	Asn	Gln	Asn	Ala	Phe	Leu	Leu	Ala	Cys	Met
1				5					10					15	
Phe	Val	Ser	Ser	Val	Tyr	Val	Asn	Ala	Val	Leu	Asp	Ala	Tyr	Ala	Ile
			20					25					30		
Glu	Asn	Pro	Tyr	Ile	Ser	Ile	Thr	Leu	Thr	Ser	Leu	Leu	Ala	Pro	Leu
			35				40					45			
Ser	Met	Leu	Ala	Phe	Leu	Lys	Thr	Pro	Arg	Asn	Ser	Ala	Phe	Ala	Leu
	50					55				60					
Gly	Phe	Phe	Val	Gly	Ala	Leu	Leu	Phe	Tyr	Trp	Cys	Ala	Leu	Ser	Phe
65				70					75					80	
Arg	Tyr	Ser	Asp	Phe	Thr	Tyr	Leu	Leu	Pro	Leu	Ile	Ile	Val	Leu	Ile
				85					90				95		
Ala	Leu	Val	Tyr	Gly	Val	Leu	Phe	Tyr	Leu	Leu	Leu	Tyr	Phe	Glu	Asn
			100					105					110		
Pro	Tyr	Phe	Arg	Leu	Leu	Ser	Phe	Leu	Gly	Ser	Ser	Phe	Ile	His	Pro
		115					120					125			
Phe	Gly	Phe	Asp	Trp	Leu	Val	Pro	Asp	Ser	Phe	Phe	Ser	Tyr	Ser	Val
	130					135					140				
Phe	Arg	Val	Asp	Lys	Leu	Ser	Leu	Gly	Leu	Val	Phe	Leu	Ala	Cys	Ile
145				150					155					160	
Phe	Leu	Ser	Thr	Lys	Pro	Leu	Lys	Lys	Tyr	Arg	Ile	Ile	Gly	Val	Leu
				165					170					175	
Leu	Leu	Leu	Gly	Ala	Leu	Asp	Phe	Asn	Gly	Phe	Lys	Thr	Ser	Asp	Leu
			180					185					190		
Lys	Lys	Val	Gly	Asn	Ile	Glu	Leu	Val	Ser	Thr	Lys	Thr	Pro	Gln	Asp
		195					200					205			
Leu	Lys	Phe	Asp	Ser	Ser	Tyr	Leu	Asn	Asp	Ile	Glu	Asn	Asn	Ile	Leu
	210					215					220				
Lys	Glu	Ile	Lys	Leu	Ala	Gln	Ser	Lys	Gln	Lys	Thr	Leu	Ile	Val	Phe
225				230					235					240	
Pro	Glu	Thr	Ala	Tyr	Pro	Ile	Ala	Leu	Glu	Asn	Ser	Pro	Phe	Lys	Ala
			245					250					255		
Lys	Leu	Glu	Asp	Leu	Ser	Asp	Asn	Ile	Ala	Ile	Leu	Ile	Gly	Thr	Leu
			260				265						270		
Arg	Thr	Gln	Gly	Tyr	Asn	Leu	Tyr	Asn	Ser	Ser	Phe	Leu	Phe	Ser	Lys
		275				280						285			
Glu	Ser	Val	Gln	Ile	Ala	Asp	Lys	Val	Ile	Leu	Ala	Pro	Phe	Gly	Glu
	290					295				300					
Thr	Met	Pro	Leu	Pro	Glu	Phe	Leu	Gln	Lys	Pro	Leu	Glu	Lys	Leu	Phe

305		310		315		320
Phe Gly Glu Ser Thr Tyr Leu Tyr Arg Asn Ala Pro His Phe Ser Asp						
		325		330		335
Phe Thr Leu Asp Asp Phe Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly						
		340		345		350
Thr Ser Lys Pro Ala Tyr Ser Asn Ser Pro Ser Lys Ile Phe Ile Val						
		355		360		365
Met Ser Asn Asn Ala Trp Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln						
		370		375		380
Arg Thr Leu Leu Lys Tyr Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu						
		385		390		395
His Ser Ala Asn Phe Ser Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu						
		405		410		415
Gly Asp Ile Leu Phe Arg Lys Arg Ser						
		420		425		

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...713
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGTAGTAAGA TACCTAGTTT TCAAATCTAT TAAAAGATAA AGGTTATTAC ATG TTT	56
Met Phe	
1	
TCA CTT TCT TAT GTT TCC AAG AAA TTT TTA AGC GTT TTA TTA TTG ATT	104
Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu Ile	
5 10 15	
TCG CTG TTT TTA AGC GCT TGC AAA TCC AAC AAT AAA GAC AAG TTA GAC	152
Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys Leu Asp	
20 25 30	
GAA AAT CTT TTA AGC TCT GGC TCT CAA AGC TCC AAA GAA TTA AAC GAT	200
Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu Asn Asp	
35 40 45 50	
GAG CGA GAC AAT ATA GAC AAA AAG AGT TAC GCT GGT TTA GAA GAT GTT	248
Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu Asp Val	
55 60 65	
TTT TCA GAC AAT AAG TCC ATT AGT CCT AAC GAT AAA TAC ATG CTT TTA	296
Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met Leu Leu	
70 75 80	

GTT TTT GGC CGT AAT GGT TGC TCC TAT TGC GAA AGG TTT AAA AAA GAT	344
Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys Lys Asp	
85 90 95	
CTC AAA AAT GTC AAA GAA TTG CGC GAC TAC ATT AAA GAG CAT TTT AGC	392
Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His Phe Ser	
100 105 110	
GCT TAC TAT GTC AAT ATC AGC TAC TCC AAA GAG CAT GAT TTT AAA GTC	440
Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe Lys Val	
115 120 125 130	
GGC GAT AAA AAT AAT GAA AAA GAA ATC AAA ATG TCC ACA GAA GAA TTA	488
Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu Glu Leu	
135 140 145	
GCG CAA ATT TAT GCC GTC CAA TCC ACC CCT ACG ATT GTT TTA TCC GAT	536
Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu Ser Asp	
150 155 160	
AAA ACC GGC AAA ACC ATC TAT GAA TTG CCC GGC TAT ATG CCC TCT ACG	584
Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro Ser Thr	
165 170 175	
CAA TTT TTA GCC GTG TTA GAA TTT ATC GGC GAT GGG AAG TAT CAA GAC	632
Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr Gln Asp	
180 185 190	
ACA AAA GAC GAT GAG GAT CTC ACT AAA AAA TTA AAG GCT TAC ATC AAG	680
Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr Ile Lys	
195 200 205 210	
TAT AAA ACC AAC CTT TCT AAA AGC AAG TCT AAC TAGGAAAGCC TAATGAAGAA	733
Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn	
215 220	
TCTCAAAAGC CTGCTTTCTT TTTTGCTGGC TTC	766

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Phe Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu	
1 5 10 15	
Leu Ile Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys	
20 25 30	
Leu Asp Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu	
35 40 45	
Asn Asp Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu	

50		55		60
Asp Val Phe Ser Asp	Asn Lys Ser Ile Ser	Pro Asn Asp Lys Tyr Met		
65	70	75	80	
Leu Leu Val Phe Gly	Arg Asn Gly Cys Ser	Tyr Cys Glu Arg Phe Lys		
	85	90	95	
Lys Asp Leu Lys Asn	Val Lys Glu Leu Arg	Asp Tyr Ile Lys Glu His		
	100	105	110	
Phe Ser Ala Tyr Tyr	Val Asn Ile Ser Tyr	Ser Lys Glu His Asp Phe		
	115	120	125	
Lys Val Gly Asp Lys	Asn Asn Glu Lys Glu	Ile Lys Met Ser Thr Glu		
	130	135	140	
Glu Leu Ala Gln Ile	Tyr Ala Val Gln Ser	Thr Pro Thr Ile Val Leu		
145	150	155	160	
Ser Asp Lys Thr Gly	Lys Thr Ile Tyr Glu	Leu Pro Gly Tyr Met Pro		
	165	170	175	
Ser Thr Gln Phe Leu	Ala Val Leu Glu Phe	Ile Gly Asp Gly Lys Tyr		
	180	185	190	
Gln Asp Thr Lys Asp	Asp Glu Asp Leu Thr	Lys Lys Leu Lys Ala Tyr		
	195	200	205	
Ile Lys Tyr Lys Thr	Asn Leu Ser Lys Ser	Lys Ser Asn		
210	215	220		

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 980 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...931
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGAATGAAAT CCTAGATTCT AACGCCATTG TATATTATCT CGCTAAAAAT TC ATG AGA	58
	Met Arg
	1
TTG TTA TTC TTG TTA TTG AGT GCT GCT TTT ATG TTA CTG GCT GAA GAA	106
Leu Leu Phe Leu Leu Leu Ser Ala Ala Phe Met Leu Leu Ala Glu Glu	
	5 10 15
AAA ATA TCT TTA AAC GAT GAC GCC CCC ATT AAA CTA GTG CAT TGG CAA	154
Lys Ile Ser Leu Asn Asp Asp Ala Pro Ile Lys Leu Val His Trp Gln	
	20 25 30
AAT GCA TTA AAA GAA GTC CAA CCT GAT TCA AAC GCT CCA GCA ACA CCA	202
Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala Thr Pro	
	35 40 45 50
CCT ATA AAA GCC GTG CAA ACC ACG CTC ACT TTT GAA ACG CCT TTT AAC	250
Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro Phe Asn	

55										60					65					
AAA	ACG	CCT	AAA	ATC	ATG	GAA	GTT	GAA	GGG	CAA	AAG	GTG	ATC	GTC	TTA	298				
Lys	Thr	Pro	Lys	Ile	Met	Glu	Val	Glu	Gly	Gln	Lys	Val	Ile	Val	Leu					
			70					75					80							
AAA	AAC	GCT	AAA	CTG	GAT	TCT	AAA	AAA	ACC	ATG	GAT	TTT	AAA	GAA	GCC	346				
Lys	Asn	Ala	Lys	Leu	Asp	Ser	Lys	Lys	Thr	Met	Asp	Phe	Lys	Glu	Ala					
		85					90					95								
TCT	TTG	AAT	GCT	TTA	GAA	ATG	TTT	TCC	TAC	CAA	AAT	GAC	ATC	TAC	CTC	394				
Ser	Leu	Asn	Ala	Leu	Glu	Met	Phe	Ser	Tyr	Gln	Asn	Asp	Ile	Tyr	Leu					
	100					105					110									
TTG	TCT	AAA	AAA	GCT	AAA	GTG	GAA	TTA	GAA	ATC	CAA	GCT	TCA	AAC	AGC	442				
Leu	Ser	Lys	Lys	Ala	Lys	Val	Glu	Leu	Glu	Ile	Gln	Ala	Ser	Asn	Ser					
115					120					125					130					
AAG	GAT	AAA	AAA	CGG	CTC	CGC	TTT	CTC	TTT	TTA	CCC	AAA	GGT	TTT	CAT	490				
Lys	Asp	Lys	Lys	Arg	Leu	Arg	Phe	Leu	Phe	Leu	Pro	Lys	Gly	Phe	His					
				135					140					145						
TTA	GCC	CCA	CCG	CCT	AAC	CTG	AAA	GAA	AAA	TCT	CAG	CAA	ACT	AAC	CTT	538				
Leu	Ala	Pro	Pro	Pro	Asn	Leu	Lys	Glu	Lys	Ser	Gln	Gln	Thr	Asn	Leu					
			150					155					160							
GCA	CAA	AAA	GAC	ACC	AAC	GAG	CAA	CCC	CAA	AGC	CCT	TTA	AAC	ACT	CTA	586				
Ala	Gln	Lys	Asp	Thr	Asn	Glu	Gln	Pro	Gln	Ser	Pro	Leu	Asn	Thr	Leu					
		165					170					175								
GAG	TTA	AAA	CCC	CCA	CTA	AAT	TTA	AGC	CAT	GCT	TAT	AAG	GCG	CTA	GCG	634				
Glu	Leu	Lys	Pro	Pro	Leu	Asn	Leu	Ser	His	Ala	Tyr	Lys	Ala	Leu	Ala					
	180					185					190									
GTT	ATT	GCT	GCC	TTA	CTC	TTA	ATA	TTG	TAT	GTC	ATC	AAA	AAA	AAA	ATT	682				
Val	Ile	Ala	Ala	Leu	Leu	Ile	Leu	Tyr	Val	Val	Ile	Lys	Lys	Lys	Ile					
195					200					205					210					
GTT	CCC	ACA	CAA	GGG	TCT	TTT	TCT	GCA	AAA	GAT	TTT	AAG	TTA	GAA	ATT	730				
Val	Pro	Thr	Gln	Gly	Ser	Phe	Ser	Ala	Lys	Asp	Phe	Lys	Leu	Glu	Ile					
				215					220					225						
AGC	GTT	TTG	GGT	CGT	GTT	GAT	GCG	AAC	CAT	AAA	ATC	ATT	TCA	ATA	GAA	778				
Ser	Val	Leu	Gly	Arg	Val	Asp	Ala	Asn	His	Lys	Ile	Ile	Ser	Ile	Glu					
			230					235					240							
ACC	AAT	AAG	GAG	CGT	TAC	TTG	GTC	TTA	CTA	AGC	GAT	AAA	TAC	GGC	CTG	826				
Thr	Asn	Lys	Glu	Arg	Tyr	Leu	Val	Leu	Leu	Ser	Asp	Lys	Tyr	Gly	Leu					
		245					250					255								
CTT	TTA	GAC	AAA	ATA	AGC	CCA	AAA	ACA	TCT	AAA	GAA	GAA	CTG	ATT	AAA	874				
Leu	Leu	Asp	Lys	Ile	Ser	Pro	Lys	Thr	Ser	Lys	Glu	Glu	Leu	Ile	Lys					
	260					265					270									
GAA	GCT	GAA	AAT	AAT	ATA	AAG	AAT	TCA	AAA	TTA	GGA	AAT	TTA	TAT	GCC	922				
Glu	Ala	Glu	Asn	Asn	Ile	Lys	Asn	Ser	Lys	Leu	Gly	Asn	Leu	Tyr	Ala					
275					280					285					290					

GGA AAA TTC TAAACTACAA CCTGCTAAGT TAGGGAAAAA TTTTGACCCT GTGGATCAT 980
Gly Lys Phe

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met	Arg	Leu	Leu	Phe	Leu	Leu	Leu	Ser	Ala	Ala	Phe	Met	Leu	Leu	Ala	1	5	10	15
Glu	Glu	Lys	Ile	Ser	Leu	Asn	Asp	Asp	Ala	Pro	Ile	Lys	Leu	Val	His	20	25	30	
Trp	Gln	Asn	Ala	Leu	Lys	Glu	Val	Gln	Pro	Asp	Ser	Asn	Ala	Pro	Ala	35	40	45	
Thr	Pro	Pro	Ile	Lys	Ala	Val	Gln	Thr	Thr	Leu	Thr	Phe	Glu	Thr	Pro	50	55	60	
Phe	Asn	Lys	Thr	Pro	Lys	Ile	Met	Glu	Val	Glu	Gly	Gln	Lys	Val	Ile	65	70	75	80
Val	Leu	Lys	Asn	Ala	Lys	Leu	Asp	Ser	Lys	Lys	Thr	Met	Asp	Phe	Lys	85	90	95	
Glu	Ala	Ser	Leu	Asn	Ala	Leu	Glu	Met	Phe	Ser	Tyr	Gln	Asn	Asp	Ile	100	105	110	
Tyr	Leu	Leu	Ser	Lys	Lys	Ala	Lys	Val	Glu	Leu	Glu	Ile	Gln	Ala	Ser	115	120	125	
Asn	Ser	Lys	Asp	Lys	Lys	Arg	Leu	Arg	Phe	Leu	Phe	Leu	Pro	Lys	Gly	130	135	140	
Phe	His	Leu	Ala	Pro	Pro	Asn	Leu	Lys	Glu	Lys	Ser	Gln	Gln	Thr		145	150	155	160
Asn	Leu	Ala	Gln	Lys	Asp	Thr	Asn	Glu	Gln	Pro	Gln	Ser	Pro	Leu	Asn	165	170	175	
Thr	Leu	Glu	Leu	Lys	Pro	Pro	Leu	Asn	Leu	Ser	His	Ala	Tyr	Lys	Ala	180	185	190	
Leu	Ala	Val	Ile	Ala	Ala	Leu	Leu	Ile	Leu	Tyr	Val	Ile	Lys	Lys		195	200	205	
Lys	Ile	Val	Pro	Thr	Gln	Gly	Ser	Phe	Ser	Ala	Lys	Asp	Phe	Lys	Leu	210	215	220	
Glu	Ile	Ser	Val	Leu	Gly	Arg	Val	Asp	Ala	Asn	His	Lys	Ile	Ile	Ser	225	230	235	240
Ile	Glu	Thr	Asn	Lys	Glu	Arg	Tyr	Leu	Val	Leu	Leu	Ser	Asp	Lys	Tyr	245	250	255	
Gly	Leu	Leu	Leu	Asp	Lys	Ile	Ser	Pro	Lys	Thr	Ser	Lys	Glu	Glu	Leu	260	265	270	
Ile	Lys	Glu	Ala	Glu	Asn	Asn	Ile	Lys	Asn	Ser	Lys	Leu	Gly	Asn	Leu	275	280	285	
Tyr	Ala	Gly	Lys	Phe												290			

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...567
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
CTAGCGCGAT CTTTGGTCTC ACACAAGCTA TAACAAGCTT GAGAATCGCA TAATATATTC      60
TTGTTCTAC ATG CTA TCA CCA GCA ACT TTC AAA CAA ATA ACT CTA GCA TTA      111
    Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu
      1             5             10

ATC GCT TCA AGA CTA ATC GTT GTA ATC CTA TAT GCT TTT ATC TTT ATT      159
Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile
  15             20             25             30

GTT CTC TCT TTT TAT ATG CTC AAT ATC ATC ACT ATT CTT AAT TTT AAA      207
Val Leu Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys
             35             40             45

GCG CTT ATT TTG GGG TTT GTT AGT GTT TTT TCA AGC GCA TTG TTT TGT      255
Ala Leu Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys
             50             55             60

TTT TGC TTG GCA ATT TTT GTA GCT AGA ATT TTT CAA AAC GAA CAA AGC      303
Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser
             65             70             75

ATC TTA GGA TTT TGT AAT ATC ATC AAT CTC TAT GCG CTA ATG TCT TGT      351
Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys
             80             85             90

AAT GTT TTT GTT CCT TTA GAA TAC CTA CCT AGT ATT GGT CAA TTA TTT      399
Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe
  95             100             105             110

ATC AAA ACA TCT ATT TTT TAC TAC CTT AAT CAA CTT CTA ATC AAA GCT      447
Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala
             115             120             125

TTT CAA GGG ATT GAT ACT ATA CTG GTT TTA GCA ACT TCA ACA TTT TTC      495
Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe
             130             135             140

ATT ATT GGT GGC ATT ATT TTA TTT TTA CTA AGC GCT AAT CGC ATG TTA      543
Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu
             145             150             155

CTA ACA CCA AAA GAA CGC ATG CGT TAAAGGCTTA GTCCCACCAT TGATTTATTT      597
```

Leu Thr Pro Lys Glu Arg Met Arg
160 165

AATGGCTCAA AAAAGGGGTA AGC

620

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu Ile Ala
1 5 10 15
Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile Val Leu
20 25 30
Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys Ala Leu
35 40 45
Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys Phe Cys
50 55 60
Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser Ile Leu
65 70 75 80
Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys Asn Val
85 90 95
Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe Ile Lys
100 105 110
Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala Phe Gln
115 120 125
Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe Ile Ile
130 135 140
Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu Leu Thr
145 150 155 160
Pro Lys Glu Arg Met Arg
165

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1366
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

215						220						225						
ATT	TTA	TAT	CTC	TAC	CCC	TCT	AGC	ACC	ACG	CTA	GAG	CTT	ATT	GGC	GCG	778		
Ile	Leu	Tyr	Leu	Tyr	Pro	Ser	Ser	Thr	Thr	Leu	Glu	Leu	Ile	Gly	Ala			
		230					235					240						
ATT	GAA	AGT	TCG	CCC	ATT	TTT	CAA	AAT	TAT	TTT	GAC	ATG	CCC	ATC	CAG	826		
Ile	Glu	Ser	Ser	Pro	Ile	Phe	Gln	Asn	Tyr	Phe	Asp	Met	Pro	Ile	Gln			
	245					250					255							
CAC	ATC	AGC	GAC	TCC	ATG	CTC	AAA	AAG	ATG	CGG	CGC	AAC	TCT	AGC	CAA	874		
His	Ile	Ser	Asp	Ser	Met	Leu	Lys	Lys	Met	Arg	Arg	Asn	Ser	Ser	Gln			
260					265					270					275			
GCG	CAC	CAT	TTA	AAG	CTT	TTA	GAT	GCC	ATG	AAG	CAG	GTT	AAA	GAA	AGC	922		
Ala	His	His	Leu	Lys	Leu	Leu	Asp	Ala	Met	Lys	Gln	Val	Lys	Glu	Ser			
				280					285					290				
TTT	ATC	AGA	AGC	ACG	ATC	ATT	GTA	GGG	CAT	CCG	GAA	GAA	AAT	GAG	AGC	970		
Phe	Ile	Arg	Ser	Thr	Ile	Ile	Val	Gly	His	Pro	Glu	Glu	Asn	Glu	Ser			
			295					300					305					
GAA	TTT	GAA	GAA	TTG	AGC	GCG	TTT	TTA	GAC	GAG	TTC	CAG	TTT	GAT	AGA	1018		
Glu	Phe	Glu	Glu	Leu	Ser	Ala	Phe	Leu	Asp	Glu	Phe	Gln	Phe	Asp	Arg			
		310					315					320						
TTG	AAT	ATT	TTT	GCT	TTC	AGC	GCT	GAA	GAA	AAC	ACG	CAT	GCC	TAT	TCT	1066		
Leu	Asn	Ile	Phe	Ala	Phe	Ser	Ala	Glu	Glu	Asn	Thr	His	Ala	Tyr	Ser			
	325					330					335							
TTA	GAA	AAA	GTG	CCT	AAA	AAA	ACC	ATC	AAC	GCT	CGC	ATC	AAA	GCC	TTG	1114		
Leu	Glu	Lys	Val	Pro	Lys	Lys	Thr	Ile	Asn	Ala	Arg	Ile	Lys	Ala	Leu			
340					345					350					355			
AAT	AAA	ATC	GCT	TTA	AAG	CAC	CAA	AAC	CAT	TCC	TTT	AAG	GCT	TTG	TTG	1162		
Asn	Lys	Ile	Ala	Leu	Lys	His	Gln	Asn	His	Ser	Phe	Lys	Ala	Leu	Leu			
				360					365					370				
AAT	AAG	CCC	ATT	AAG	GCG	TTA	GTG	GAA	AAT	AAA	GAG	GGC	GAG	TAT	TTT	1210		
Asn	Lys	Pro	Ile	Lys	Ala	Leu	Val	Glu	Asn	Lys	Glu	Gly	Glu	Tyr	Phe			
			375					380					385					
TAC	AAA	GCA	AGG	GAT	CTC	AGA	TGG	GCG	CCT	GAA	GTG	GAT	GGG	GAA	ATC	1258		
Tyr	Lys	Ala	Arg	Asp	Leu	Arg	Trp	Ala	Pro	Glu	Val	Asp	Gly	Glu	Ile			
		390					395					400						
TTG	ATC	AAT	GAT	AGC	GAA	CTA	ACC	ACC	CCC	TTA	AAA	CCC	GGG	CAT	TAT	1306		
Leu	Ile	Asn	Asp	Ser	Glu	Leu	Thr	Thr	Pro	Leu	Lys	Pro	Gly	His	Tyr			
	405					410					415							
ACG	ATT	GCA	CCT	AGC	GAA	TTT	AAA	GAT	AAT	ATC	CTA	CTC	GCT	AAG	GTT	1354		
Thr	Ile	Ala	Pro	Ser	Glu	Phe	Lys	Asp	Asn	Ile	Leu	Leu	Ala	Lys	Val			
420					425					430				435				
TTA	AGC	CCT	TTT	TAAAGTTAG			CCATAAGGCT			AAAAGCACGG			CTAAAGCGT			1405		
Leu	Ser	Pro	Phe															

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Gln	Val	Lys	Glu	Asn	Lys	Gln	Leu	Cys	Leu	Ile	Ser	Leu	Gly	Cys
1				5					10					15	
Ser	Lys	Asn	Leu	Val	Asp	Ser	Glu	Val	Met	Leu	Gly	Lys	Leu	Tyr	Asn
		20					25					30			
Tyr	Thr	Leu	Thr	Asn	Asp	Ala	Lys	Ser	Ala	Asp	Val	Ile	Leu	Ile	Asn
		35					40					45			
Thr	Cys	Gly	Phe	Ile	Glu	Ser	Ala	Lys	Gln	Glu	Ser	Ile	Gln	Thr	Ile
	50					55					60				
Leu	Asn	Ala	Ala	Lys	Asp	Lys	Lys	Glu	Gly	Ala	Ile	Leu	Ile	Ala	Ser
65					70					75				80	
Gly	Cys	Leu	Ser	Glu	Arg	Tyr	Lys	Asp	Glu	Ile	Lys	Glu	Leu	Ile	Pro
				85					90					95	
Glu	Val	Asp	Ile	Phe	Thr	Gly	Val	Gly	Asp	Tyr	Asp	Lys	Ile	Asp	Ile
			100					105					110		
Met	Ile	Ala	Lys	Lys	Gln	Asn	Gln	Phe	Ser	Glu	Gln	Val	Phe	Leu	Ser
		115					120					125			
Glu	His	Tyr	Asn	Ala	Arg	Ile	Ile	Thr	Gly	Ser	Ser	Val	His	Ala	Tyr
	130					135						140			
Val	Lys	Ile	Ser	Glu	Gly	Cys	Asn	Gln	Lys	Cys	Ser	Phe	Cys	Ala	Ile
145					150					155				160	
Pro	Ser	Phe	Lys	Gly	Lys	Leu	Gln	Ser	Arg	Glu	Leu	Asp	Ser	Ile	Leu
				165					170					175	
Lys	Glu	Val	Glu	Asn	Leu	Ala	Leu	Lys	Gly	Tyr	Thr	Asp	Met	Thr	Phe
			180					185					190		
Ile	Ala	Gln	Asp	Ser	Ser	Ser	Phe	Leu	Tyr	Asp	Lys	Gly	Gln	Lys	Asp
		195					200					205			
Gly	Leu	Ile	Gln	Leu	Ile	Arg	Ala	Ile	Asp	Lys	Gln	Gln	Ala	Leu	Lys
	210					215					220				
Ser	Ala	Arg	Ile	Leu	Tyr	Leu	Tyr	Pro	Ser	Ser	Thr	Thr	Leu	Glu	Leu
225				230						235				240	
Ile	Gly	Ala	Ile	Glu	Ser	Ser	Pro	Ile	Phe	Gln	Asn	Tyr	Phe	Asp	Met
				245					250					255	
Pro	Ile	Gln	His	Ile	Ser	Asp	Ser	Met	Leu	Lys	Lys	Met	Arg	Arg	Asn
			260					265					270		
Ser	Ser	Gln	Ala	His	His	Leu	Lys	Leu	Leu	Asp	Ala	Met	Lys	Gln	Val
		275					280					285			
Lys	Glu	Ser	Phe	Ile	Arg	Ser	Thr	Ile	Ile	Val	Gly	His	Pro	Glu	Glu
	290					295					300				
Asn	Glu	Ser	Glu	Phe	Glu	Glu	Leu	Ser	Ala	Phe	Leu	Asp	Glu	Phe	Gln
305				310						315				320	
Phe	Asp	Arg	Leu	Asn	Ile	Phe	Ala	Phe	Ser	Ala	Glu	Glu	Asn	Thr	His
				325					330					335	
Ala	Tyr	Ser	Leu	Glu	Lys	Val	Pro	Lys	Lys	Thr	Ile	Asn	Ala	Arg	Ile
			340					345					350		
Lys	Ala	Leu	Asn	Lys	Ile	Ala	Leu	Lys	His	Gln	Asn	His	Ser	Phe	Lys

355 360 365
 Ala Leu Leu Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly
 370 375 380
 Glu Tyr Phe Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp
 385 390 395 400
 Gly Glu Ile Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro
 405 410 415
 Gly His Tyr Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu
 420 425 430
 Ala Lys Val Leu Ser Pro Phe
 435

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 200...1366
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TGCGCGTTAT RTGGTTTTGA TTGAAAAGTT AGGCATTAAA GACAGATAAT TTTTATCGGT	60
TTTAGGGTGT GCGGAGTTTG TGTTGAAAGA GCGTTTGAAG GCCTTTTTTTA GTGCGGACTC	120
TGTTTTCACT TTAATTTTTG CCCTTTTCTT TCTCACTTCG TTTAAAAAAC CTTTAACTCA	180
AGTCTTGTTG ATTGTTTTTA ATG GTT TTT TTG TTT TTT AGG TGT TAT TTC CAA	232
Met Val Phe Leu Phe Phe Arg Cys Tyr Phe Gln	
1 5 10	
GCG TCT TTG AAA GAA ACT TTC GCA ATT AAT CAT TTA AAA ACA ATG TCT	280
Ala Ser Leu Lys Glu Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser	
15 20 25	
TTT AAA TGG CTC ACT CTG GCT TTT TTG GGC GTG TTT TTA AGC ATC TTC	328
Phe Lys Trp Leu Thr Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe	
30 35 40	
CCT AAC ATG TTT AAC ATG CAT GAT AGC CAA ACT TTC CGC TAC AAT TTA	376
Pro Asn Met Phe Asn Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu	
45 50 55	
TTC GCT CTA AAC ATG TCC TTA ACT TAT GCT TGC GGG GCG TTA TGC TTG	424
Phe Ala Leu Asn Met Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu	
60 65 70 75	
CTT TTT GCC AGT TGC TTA AGA ATC AAA TTG AAT CAA AAA ATC CTT TTT	472
Leu Phe Ala Ser Cys Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe	
80 85 90	

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- ```
(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:
```

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 89...1198  
(D) OTHER INFORMATION:

## 85







|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTT AGC AAA TAC CCT TTA AAA AAG TTT TTA TGG CTT AAT GTT TTT TCC   | 210 |
| Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser   |     |
| 25 30 35                                                          |     |
| AGT TTT TTG TGG GCG CTC ATC GTG GGG AGC GTT TCT TTT CAA GCG AGC   | 258 |
| Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser   |     |
| 40 45 50                                                          |     |
| GAT TGG GTG AAA ACG CTG TAT GAA AGG CTT TCT CAT TAC ACT TCG TTT   | 306 |
| Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe   |     |
| 55 60 65                                                          |     |
| TTT ATC ATA AGT TTT GTT CTT ATA GCG CTT TTA ATA TGG TTT TTA TTG   | 354 |
| Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu   |     |
| 70 75 80                                                          |     |
| AAA CGA TAT TCG CGC AAA ATG GGT TTT TAAGCAAGAT GTTTAATTAA ATGCGCT | 408 |
| Lys Arg Tyr Ser Arg Lys Met Gly Phe                               |     |
| 85 90                                                             |     |
| AGACTACGCC CACAAGCATT CGC                                         | 431 |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro |  |
| 1 5 10 15                                                       |  |
| Leu Ala Val Gly Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu |  |
| 20 25 30                                                        |  |
| Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser |  |
| 35 40 45                                                        |  |
| Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His |  |
| 50 55 60                                                        |  |
| Tyr Thr Ser Phe Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile |  |
| 65 70 75 80                                                     |  |
| Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly Phe             |  |
| 85 90                                                           |  |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 70...1227  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAGCATCAAT ACCCCTTAAA TAAAAGATAT AATGCTGTAT TATAAGCTAG TTTTAATTAC | 60  |
| AATTTTCAA ATG TTA AGG AAA AAC ATT TTA GCT TAC TAT GGG GCG AAT TTT | 111 |
| Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe           |     |
| 1 5 10                                                            |     |
| CTC TTA ATC ATC GCT CAA AGC TTA CCC CAT GCG ATT TTA ACC CCC TTG   | 159 |
| Leu Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu   |     |
| 15 20 25 30                                                       |     |
| TTG CTT TCT AAA GGG CTT AGT TTG AGT GAA ATC TTG CTC GTG CAA ACC   | 207 |
| Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr   |     |
| 35 40 45                                                          |     |
| TTT TTT AGC TTT TGC GTG CTA GTG GCT GAA TAC CCA AGC GGC GTT TTA   | 255 |
| Phe Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu   |     |
| 50 55 60                                                          |     |
| GCG GAT TTG ATG AGC CGA AAA AAT TTA TTC CTG GTT TCT AAT GCC TTT   | 303 |
| Ala Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe   |     |
| 65 70 75                                                          |     |
| TTA ATC GCT AGT TTT TCG TTT GTG CTG TTT TTT GAT AGC TTT ATT TTC   | 351 |
| Leu Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe   |     |
| 80 85 90                                                          |     |
| ATG CTT TTA GCG TGG GGG TTG TAT GGT TTG TAT AGC GCA TGC TCT AGC   | 399 |
| Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser   |     |
| 95 100 105 110                                                    |     |
| GGC ACG ATT GAA GCT TCA CTC ATC ACA GAC ATT AAG GAA AAC AAA AAA   | 447 |
| Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys   |     |
| 115 120 125                                                       |     |
| GAT TTA TCC AAG TTT TTA GCC AAA AAC AAT CAA ATT ACT TAT TTA GGC   | 495 |
| Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly   |     |
| 130 135 140                                                       |     |
| ATG ATT ATA GGG AGT TCT TTG GGA TCG TTT TTG TAT CTC AAA GTC CAT   | 543 |
| Met Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His   |     |
| 145 150 155                                                       |     |
| GCG ATG CTG TAT ATT GTG GGG ATT TTT TTA ATC ATG CTC TGT GTG CTA   | 591 |
| Ala Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu   |     |
| 160 165 170                                                       |     |
| ACG ATC ATT TTT TAT TTT AAA GAG AAA GAA GGG GAT TTT AAA AGC CAA   | 639 |
| Thr Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln   |     |
| 175 180 185 190                                                   |     |
| AAA AGC CTG AAA CTC CTT AAA GAG CAA GTC AAA GGC AGT CTT AAA GAG   | 687 |





(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Arg | Lys | Asn | Ile | Leu | Ala | Tyr | Tyr | Gly | Ala | Asn | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ile | Ala | Gln | Ser | Leu | Pro | His | Ala | Ile | Leu | Thr | Pro | Leu | Leu | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Lys | Gly | Leu | Ser | Leu | Ser | Glu | Ile | Leu | Leu | Val | Gln | Thr | Phe | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Cys | Val | Leu | Val | Ala | Glu | Tyr | Pro | Ser | Gly | Val | Leu | Ala | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Met | Ser | Arg | Lys | Asn | Leu | Phe | Leu | Val | Ser | Asn | Ala | Phe | Leu | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ser | Phe | Ser | Phe | Val | Leu | Phe | Phe | Asp | Ser | Phe | Ile | Phe | Met | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Ala | Trp | Gly | Leu | Tyr | Gly | Leu | Tyr | Ser | Ala | Cys | Ser | Ser | Gly | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Glu | Ala | Ser | Leu | Ile | Thr | Asp | Ile | Lys | Glu | Asn | Lys | Lys | Asp | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Lys | Phe | Leu | Ala | Lys | Asn | Asn | Gln | Ile | Thr | Tyr | Leu | Gly | Met | Ile |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Gly | Ser | Ser | Leu | Gly | Ser | Phe | Leu | Tyr | Leu | Lys | Val | His | Ala | Met |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Tyr | Ile | Val | Gly | Ile | Phe | Leu | Ile | Met | Leu | Cys | Val | Leu | Thr | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Phe | Tyr | Phe | Lys | Glu | Lys | Glu | Gly | Asp | Phe | Lys | Ser | Gln | Lys | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Lys | Leu | Leu | Lys | Glu | Gln | Val | Lys | Gly | Ser | Leu | Lys | Glu | Leu | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Asn | Pro | Lys | Leu | Lys | Ile | Leu | Leu | Val | Gly | His | Leu | Ile | Thr | Pro |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Val | Phe | Phe | Met | Ser | His | Phe | Gln | Met | Trp | Gln | Ala | Tyr | Phe | Leu | Lys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Gln | Gly | Val | Lys | Glu | Gln | Tyr | Leu | Phe | Val | Phe | Tyr | Ile | Ala | Phe | Gln |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ile | Ser | Ile | Leu | Ile | His | Phe | Leu | Lys | Ala | Ser | Ser | Tyr | Ser | Gln |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Ile | Ala | Leu | Ser | Ser | Leu | Val | Val | Leu | Leu | Gly | Val | Ser | Pro | Leu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Leu | Leu | Ser | Asn | Ile | Pro | Tyr | Cys | Phe | Ile | Gly | Val | Tyr | Ala | Leu | Met |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Val | Ala | Phe | Phe | Thr | Tyr | Met | Ser | Tyr | Cys | Leu | Asn | Tyr | Gln | Phe | Ser |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Lys | Phe | Val | Ser | Lys | Asn | Asn | Ile | Ser | Ser | Leu | Ser | Ser | Leu | Leu | Ser |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Cys | Val | Arg | Val | Val | Ser | Val | Leu | Ile | Leu | Ser | Leu | Ser | Ser | Leu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Leu | Arg | Tyr | Phe | Ser | Pro | Leu | Thr | Ile | Ile | Thr | Met | His | Phe | Ala |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Leu | Thr | Leu | Ile | Ile | Leu | Phe | Phe | Phe | Leu | Tyr | Lys | Ala | Lys | Pro | Phe |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 385 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 77...2167
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
GAAGTTTATG AGCCGTTTTG CCACTATTCA AAGAAATTTT GGATTATAAT AAAAAAACTG 60
GCTGAAATTA ACAACA ATG ATT AAA CAA TCA TTA AAT GGA GAG GAC ATG CAA 112
 Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln
 1 5 10

AAA AGT TTA GTT TCT TTG GCT TGG GTT TTT GTA GCT ATT TTA GGG GCG 160
Lys Ser Leu Val Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala
 15 20 25

ATC TGT TTA GGG GTG TTA GCC TTA CAC AAG GGT GAG AGC ATT AAC ACG 208
Ile Cys Leu Gly Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr
 30 35 40

CTA TGG CTT GTA GTA GCG AGC GCT TGT ATT TAT AGC ATA GGC TAT CGT 256
Leu Trp Leu Val Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg
 45 50 55 60

TTT TAT AGC CAT TTT ATC GCT TAT AAG GTG TTA AAG CTA GAT GAT AGC 304
Phe Tyr Ser His Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser
 65 70 75

AGA GCC ACG CCC GCA TGC GTA AGG AAT GAT GGC AAG GAT TTT GTG CCA 352
Arg Ala Thr Pro Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro
 80 85 90

ACC GAT AAA GCG ATC ACT TTT GGG CAC CAT TTC GCC GCT ATT GCT GGG 400
Thr Asp Lys Ala Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly
 95 100 105

GCT GGC CCT TTA GTA GGC CCG ATA CTA GCC GCT CAA ATG GGT TAC TTG 448
Ala Gly Pro Leu Val Gly Pro Ile Leu Ala Ala Gln Met Gly Tyr Leu
 110 115 120

CCC TCT ATC TTA TGG ATT TTG ATA GGC TCG GTT TTA GGG GGT TGC GTG 496
Pro Ser Ile Leu Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val
 125 130 135 140

CAT GAT TTT GTG GTG CTT TTT GCT TCT ATT AGG CGC GAT GGC AAG TCT 544
His Asp Phe Val Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser
```









|                                                                 |  |     |  |     |  |     |
|-----------------------------------------------------------------|--|-----|--|-----|--|-----|
| 625                                                             |  | 630 |  | 635 |  | 640 |
| Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile Asp Ala Ile Leu |  |     |  |     |  |     |
|                                                                 |  | 645 |  | 650 |  | 655 |
| Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu Ile Val Ser Val |  |     |  |     |  |     |
|                                                                 |  | 660 |  | 665 |  | 670 |
| Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile Tyr Pro Pro Leu |  |     |  |     |  |     |
|                                                                 |  | 675 |  | 680 |  | 685 |
| Ala Glu Thr Pro Tyr Ile Lys Ala Ser                             |  |     |  |     |  |     |
| 690                                                             |  | 695 |  |     |  |     |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 121...861
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAAGGGGCTT TGCATTTTTT ACTCATTTCA TGCCTCTTTT TCTTTATTTA GACAGATTAT | 60  |
| TATCTTAAAA TAATTGTAAT ATCATTATTA TTATATCAAC TCAATAAAAA AGGAGAAGGT | 120 |
| ATG CAA AAA ACT TCT AAC ACT CTG GCG CTG GGG AGT TTG ACA GCG CTA   | 168 |
| Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu   |     |
| 1 5 10 15                                                         |     |
| TTC TTT CTA ATG GGT TTT ATC ACG GTT TTA AAC GAT ATT TTA ATC CCA   | 216 |
| Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro   |     |
| 20 25 30                                                          |     |
| CAC TTA AAG CCC ATT TTT GAC TTG ACC TAT TTT GAA GCT TCA CTC ATT   | 264 |
| His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile   |     |
| 35 40 45                                                          |     |
| CAA TTT TGC TTT TTT GGG GCG TAT TTC ATC ATG GGA GGA GTT TTT GGG   | 312 |
| Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly   |     |
| 50 55 60                                                          |     |
| AAT GTG ATC AGT AAA ATC GGC TAC CCT TTT GGC GTG GTG CTT GGT TTT   | 360 |
| Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe   |     |
| 65 70 75 80                                                       |     |
| GTG ATC ACA GCG ACG GGG TGC GCG TTG TTT TAT CCG GCG GCG CAT TTT   | 408 |
| Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe   |     |
| 85 90 95                                                          |     |
| GGA TCC TAT GGG TTT TTT TTA GGA GCG TTG TTT ATT TTA GCG AGC GGG   | 456 |
| Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly   |     |
| 100 105 110                                                       |     |



|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATT GTG TGC TTG CAA ACC GCT GGT AAT CCC TTT GTA ACC TTG CTT TCT   | 504 |
| Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser   |     |
| 115 120 125                                                       |     |
| AAA GGT AAA GAA GCC AGA AAT TTG GTT TTA GTC CAG GCG TTC AAT TCG   | 552 |
| Lys Gly Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser   |     |
| 130 135 140                                                       |     |
| CTT GGC ACA ACT TTA GGG CCT ATT TTT GGG AGC TTG TTG ATT TTT AGC   | 600 |
| Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser   |     |
| 145 150 155 160                                                   |     |
| ACG ACT AAA ATG GGC GAT AAT GCA AGT TTG ATA GAT AAA TTA GCG GAC   | 648 |
| Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp   |     |
| 165 170 175                                                       |     |
| GCT AAA AGC GTT CAA ATG CCT TAT TTG GGC TTG GCG GTG TTT TCG CTT   | 696 |
| Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu   |     |
| 180 185 190                                                       |     |
| CTT TTA GCG CTC ATC ATG TAT CTT TTG AAA TTG CCT GAT GTG GAA AAA   | 744 |
| Leu Leu Ala Leu Ile Met Tyr Leu Leu Lys Leu Pro Asp Val Glu Lys   |     |
| 195 200 205                                                       |     |
| GAA ATG CCC AAA GAG ACG ACT CAA AAA AGC TTG TTT TCG CAC AAA CAC   | 792 |
| Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His   |     |
| 210 215 220                                                       |     |
| TTT GTT TTT GGG GCT TGG GGA TCT TTT TTT ATG TGG GGG GAG AAN TGG   | 840 |
| Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp   |     |
| 225 230 235 240                                                   |     |
| CGA TTG GCT CAT TCT TGG TGC TAAGCTTTGA AAAGCTTTTG AATTTAGACT CTCA | 895 |
| Arg Leu Ala His Ser Trp Cys                                       |     |
| 245                                                               |     |
| ATCAAGCGCG CATTAC                                                 | 911 |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu |  |
| 1 5 10 15                                                       |  |
| Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro |  |
| 20 25 30                                                        |  |
| His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile |  |
| 35 40 45                                                        |  |
| Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  | Asn | Val | Ile | Ser | Lys | Ile | Gly | Tyr | Pro | Phe | Gly | Val | Val | Leu | Gly | Phe |
| 65  | Val | Ile | Thr | Ala | Thr | Gly | Cys | Ala | Leu | Phe | Tyr | Pro | Ala | Ala | His | Phe |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
|     | Gly | Ser | Tyr | Gly | Phe | Phe | Leu | Gly | Ala | Leu | Phe | Ile | Leu | Ala | Ser | Gly |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
|     | Ile | Val | Cys | Leu | Gln | Thr | Ala | Gly | Asn | Pro | Phe | Val | Thr | Leu | Leu | Ser |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
|     | Lys | Gly | Lys | Glu | Ala | Arg | Asn | Leu | Val | Leu | Val | Gln | Ala | Phe | Asn | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
|     | Leu | Gly | Thr | Thr | Leu | Gly | Pro | Ile | Phe | Gly | Ser | Leu | Leu | Ile | Phe | Ser |
| 145 |     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
|     | Thr | Thr | Lys | Met | Gly | Asp | Asn | Ala | Ser | Leu | Ile | Asp | Lys | Leu | Ala | Asp |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
|     | Ala | Lys | Ser | Val | Gln | Met | Pro | Tyr | Leu | Gly | Leu | Ala | Val | Phe | Ser | Leu |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
|     | Leu | Leu | Ala | Leu | Ile | Met | Tyr | Leu | Leu | Lys | Leu | Pro | Asp | Val | Glu | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
|     | Glu | Met | Pro | Lys | Glu | Thr | Thr | Gln | Lys | Ser | Leu | Phe | Ser | His | Lys | His |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
|     | Phe | Val | Phe | Gly | Ala | Trp | Gly | Ser | Phe | Phe | Met | Trp | Gly | Glu | Xaa | Trp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
|     | Arg | Leu | Ala | His | Ser | Trp | Cys |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...3027
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|            |            |            |            |          |     |     |     |     |
|------------|------------|------------|------------|----------|-----|-----|-----|-----|
| GAATTAATGC | ATTAAATAAC | TCAAAATTTT | TGATCAAAGG | CTTGAAAT | ATG | TCA | AAA | 57  |
|            |            |            |            |          | Met | Ser | Lys |     |
|            |            |            |            |          | 1   |     |     |     |
| AAA        | ATT        | CCC        | CTA        | AAA      | AAC | CGC | TTG | AGA |
| GCT        | GAT        | TTT        | ACA        | AAA      | ACC | CCA |     | 105 |
| Lys        | Ile        | Pro        | Leu        | Lys      | Asn | Arg | Leu | Arg |
| Ala        | Asp        | Phe        | Thr        | Lys      | Thr | Pro |     |     |
| 5          |            |            |            |          | 10  |     |     |     |
|            |            |            |            |          | 15  |     |     |     |
| ACA        | GAT        | TTA        | GAA        | GTC      | CCT | AAT | TTA | TTA |
| TTA        | TTA        | CAA        | CGA        | GAC      | AGC | TAT |     | 153 |
| Thr        | Asp        | Leu        | Glu        | Val      | Pro | Asn | Leu | Leu |
| Leu        | Gln        | Arg        | Asp        | Ser      | Tyr |     |     |     |
| 20         |            |            | 25         |          |     | 30  |     | 35  |
| GAT        | TCT        | TTC        | TTG        | TAT      | TCT | AAA | GAG | GGT |
| AAA        | GAG        | AGC        | GGG        | ATT      | GAA | AAG |     | 201 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Phe | Leu | Tyr | Ser | Lys | Glu | Gly | Lys | Glu | Ser | Gly | Ile | Glu | Lys |     |
|     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |     |
| GTT | TTT | AAA | TCC | ATT | TTC | CCT | ATC | CAA | GAT | GAG | CAT | AAC | CGC | ATC | ACT | 249 |
| Val | Phe | Lys | Ser | Ile | Phe | Pro | Ile | Gln | Asp | Glu | His | Asn | Arg | Ile | Thr |     |
|     |     |     | 55  |     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |
| TTA | GAA | TAC | GCG | GGT | TGC | GAA | TTT | GGC | AAG | TCT | AAA | TAC | ACC | GTT | AGA | 297 |
| Leu | Glu | Tyr | Ala | Gly | Cys | Glu | Phe | Gly | Lys | Ser | Lys | Tyr | Thr | Val | Arg |     |
|     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     |
| GAA | GCG | ATG | GAG | AGG | GGC | ATT | ACC | TAC | TCT | ATC | CCT | CTC | AAA | ATT | AAG | 345 |
| Glu | Ala | Met | Glu | Arg | Gly | Ile | Thr | Tyr | Ser | Ile | Pro | Leu | Lys | Ile | Lys |     |
|     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |     |
| GTG | CGC | TTG | ATC | TTG | TGG | GAA | AAA | GAT | ACC | AAG | AGT | GGC | GAA | AAG | AAC | 393 |
| Val | Arg | Leu | Ile | Leu | Trp | Glu | Lys | Asp | Thr | Lys | Ser | Gly | Glu | Lys | Asn |     |
| 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |
| GGC | ATT | AAG | GAT | ATT | AAA | GAA | CAA | AGC | ATT | TTC | ATT | CGT | GAG | ATC | CCT | 441 |
| Gly | Ile | Lys | Asp | Ile | Lys | Glu | Gln | Ser | Ile | Phe | Ile | Arg | Glu | Ile | Pro |     |
|     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |     |
| TTG | ATG | ACA | GAA | CGC | ACT | TCA | TTT | ATT | ATT | AAT | GGG | GTG | GAG | CGC | GTG | 489 |
| Leu | Met | Thr | Glu | Arg | Thr | Ser | Phe | Ile | Ile | Asn | Gly | Val | Glu | Arg | Val |     |
|     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |
| GTG | GTC | AAT | CAA | CTC | CAC | AGA | AGC | CCC | GGT | GTG | ATT | TTC | AAA | GAA | GAA | 537 |
| Val | Val | Asn | Gln | Leu | His | Arg | Ser | Pro | Gly | Val | Ile | Phe | Lys | Glu | Glu |     |
|     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     |
| GAG | TCT | AGC | ACT | TCT | TTA | AAC | AAG | CTC | ATT | TAC | ACA | GGG | CAA | ATC | ATT | 585 |
| Glu | Ser | Ser | Thr | Ser | Leu | Asn | Lys | Leu | Ile | Tyr | Thr | Gly | Gln | Ile | Ile |     |
|     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     |     |
| CCT | GAT | AGG | GGT | TCG | TGG | TTG | TAT | TTT | GAA | TAC | GAT | TCT | AAA | GAT | GTT | 633 |
| Pro | Asp | Arg | Gly | Ser | Trp | Leu | Tyr | Phe | Glu | Tyr | Asp | Ser | Lys | Asp | Val |     |
| 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |
| TTA | TAC | GCT | CGT | ATC | AAT | AAA | CGC | CGT | AAA | GTG | CCT | GTT | ACC | ATT | TTA | 681 |
| Leu | Tyr | Ala | Arg | Ile | Asn | Lys | Arg | Arg | Lys | Val | Pro | Val | Thr | Ile | Leu |     |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |
| TTC | AGG | GCG | ATG | GAT | TAT | CAA | AAA | CAA | GAC | ATC | ATC | AAA | ATG | TTC | TAC | 729 |
| Phe | Arg | Ala | Met | Asp | Tyr | Gln | Lys | Gln | Asp | Ile | Ile | Lys | Met | Phe | Tyr |     |
|     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |
| CCG | CTT | GTT | AAA | GTG | CGT | TAT | GAA | AAC | GAT | AAA | TAT | TTG | ATC | CCG | TTT | 777 |
| Pro | Leu | Val | Lys | Val | Arg | Tyr | Glu | Asn | Asp | Lys | Tyr | Leu | Ile | Pro | Phe |     |
|     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |     |
| GCT | TCA | TTA | GAC | GCC | AAT | CAA | AGA | ATG | GAA | TTT | GAC | TTG | AAA | GAT | CCT | 825 |
| Ala | Ser | Leu | Asp | Ala | Asn | Gln | Arg | Met | Glu | Phe | Asp | Leu | Lys | Asp | Pro |     |
|     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     |     |
| CAA | GGC | AAG | GTT | ATT | CTT | TTA | GCG | GGT | AAA | AAG | CTC | ACT | TCA | AGA | AAG | 873 |
| Gln | Gly | Lys | Val | Ile | Leu | Leu | Ala | Gly | Lys | Lys | Leu | Thr | Ser | Arg | Lys |     |
| 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |

ATT AAA GAG CTT AAA GAA AAC CAT TTA GAA TGG GTG GAA TAC CCT ATG 921  
Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met  
280 285 290

GAT ATT TTA CTC AAT CGC CAT TTA GCT GAG CCT GTT ATG GTA GGG AAA 969  
Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys  
295 300 305

GAA GTC TTA TTG GAC ATG CTC ACT CAG CTA GAT AAA AAC AAA TTA GAA 1017  
Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu  
310 315 320

AAA ATC CAC GAT TTA GGC GTG CAA GAA TTT GTG ATC ATC AAC GAT CTG 1065  
Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu  
325 330 335

GCG TTA GGG CAT GAC GCT TCC ATT ATC CAA TCT TTT TCA GCC GAT TCT 1113  
Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser  
340 345 350 355

GAG TCT TTG AAA TTA CTC AAG CAA ACC GAA AAA ATT GAT GAT GAA AAC 1161  
Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn  
360 365 370

GCT CTA GCG GCG ATT CGT ATC CAT AAG GTT ATG AAA CCA GGC GAT CCC 1209  
Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro  
375 380 385

GTT ACG ACT GAA GTG GCT AAG CAG TTT GTC AAA AAA CTT TTC TTT GAT 1257  
Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp  
390 395 400

CCA GAA CGC TAT GAT TTG ACC ATG GTG GGC CGC ATG AAA ATG AAT CAC 1305  
Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His  
405 410 415

AAG TTA GGC TTG CAT GTG CCT GAT TAC ATT ACG ACT TTA ACG CAT GAA 1353  
Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu Thr His Glu  
420 425 430 435

GAT ATT ATC ACC ACC GTT AAA TAC CTC ATG AAG ATC AAA AAC AAT CAA 1401  
Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys Asn Asn Gln  
440 445 450

GGC AAG ATT GAT GAC AGG GAC CAC TTG GGC AAT CGT AGG ATT AGG GCG 1449  
Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg Ile Arg Ala  
455 460 465

GTA GGG GAA TTG TTG GCC AAT GAA TTG CAT TCA GGT TTA GTG AAA ATG 1497  
Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu Val Lys Met  
470 475 480

CAA AAG ACC ATT AAA GAC AAG CTC ACT ACC ATG AGC GGG GCT TTT GAT 1545  
Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly Ala Phe Asp  
485 490 495

TCG CTC ATG CCC CAT GAC TTG GTC AAT TCT AAA ATG ATC ACA AGC ACC 1593  
Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile Thr Ser Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| 500 |     |     |     |     | 505 |     |     |     |     |     | 510 |     |     |     |     | 515  |  |
| ATC | ATG | GAA | TTT | TTC | ATG | GGC | GGT | CAG | CTC | TCG | CAA | TTT | ATG | GAT | CAA | 1641 |  |
| Ile | Met | Glu | Phe | Phe | Met | Gly | Gly | Gln | Leu | Ser | Gln | Phe | Met | Asp | Gln |      |  |
|     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |     | 530 |     |      |  |
| ACG | AAT | CCC | TTG | AGT | GAG | GTT | ACG | CAC | AAG | CGC | CGC | CTT | TCA | GCG | CTC | 1689 |  |
| Thr | Asn | Pro | Leu | Ser | Glu | Val | Thr | His | Lys | Arg | Arg | Leu | Ser | Ala | Leu |      |  |
|     |     |     | 535 |     |     |     |     | 540 |     |     |     |     | 545 |     |     |      |  |
| GGC | GAA | GGG | GGG | TTG | GTG | AAA | GAC | AGA | GTG | GGG | TTT | GAA | GCC | AGG | GAT | 1737 |  |
| Gly | Glu | Gly | Gly | Leu | Val | Lys | Asp | Arg | Val | Gly | Phe | Glu | Ala | Arg | Asp |      |  |
|     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |     |     |     |      |  |
| GTG | CAC | CCC | ACG | CAT | TAT | GGC | CGA | ATT | TGT | CCC | ATT | GAG | ACC | CCA | GAA | 1785 |  |
| Val | His | Pro | Thr | His | Tyr | Gly | Arg | Ile | Cys | Pro | Ile | Glu | Thr | Pro | Glu |      |  |
|     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |     |     |     |      |  |
| GGT | CAA | AAT | ATC | GGT | CTG | ATC | AAC | ACC | CTT | TCC | ACT | TTC | ACA | AGA | GTG | 1833 |  |
| Gly | Gln | Asn | Ile | Gly | Leu | Ile | Asn | Thr | Leu | Ser | Thr | Phe | Thr | Arg | Val |      |  |
| 580 |     |     |     |     | 585 |     |     |     | 590 |     |     |     |     |     | 595 |      |  |
| AAT | GAT | TTA | GGC | TTT | ATT | GAA | GCC | CCT | TAT | AAA | AAG | GTT | GTG | GAT | GGC | 1881 |  |
| Asn | Asp | Leu | Gly | Phe | Ile | Glu | Ala | Pro | Tyr | Lys | Lys | Val | Val | Asp | Gly |      |  |
|     |     |     | 600 |     |     |     |     | 605 |     |     |     |     | 610 |     |     |      |  |
| AAG | GTC | GTG | GGT | GAG | ACG | ATT | TAT | TTG | ACC | GCT | ATT | CAA | GAA | GAC | AGC | 1929 |  |
| Lys | Val | Val | Gly | Glu | Thr | Ile | Tyr | Leu | Thr | Ala | Ile | Gln | Glu | Asp | Ser |      |  |
|     |     |     | 615 |     |     |     |     | 620 |     |     |     |     | 625 |     |     |      |  |
| CAC | ATC | ATC | GCT | CCC | GCA | AGC | ACC | CCC | ATT | GAT | GAA | GAG | GGG | AAT | ATT | 1977 |  |
| His | Ile | Ile | Ala | Pro | Ala | Ser | Thr | Pro | Ile | Asp | Glu | Glu | Gly | Asn | Ile |      |  |
|     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |     |     |     |      |  |
| TTG | GGC | GAT | TTG | ATT | GAA | ACG | CGC | GTG | GAA | GGC | GAG | ATC | GTT | TTA | AAC | 2025 |  |
| Leu | Gly | Asp | Leu | Ile | Glu | Thr | Arg | Val | Glu | Gly | Glu | Ile | Val | Leu | Asn |      |  |
|     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |     |     |     |      |  |
| GAA | AAA | AGC | AAA | GTA | ACC | TTA | ATG | GAT | TTA | AGC | TCT | AGC | ATG | CTA | GTG | 2073 |  |
| Glu | Lys | Ser | Lys | Val | Thr | Leu | Met | Asp | Leu | Ser | Ser | Ser | Met | Leu | Val |      |  |
| 660 |     |     |     |     | 665 |     |     |     | 670 |     |     |     |     | 675 |     |      |  |
| GGG | GTA | GCC | GCA | TCG | CTC | ATT | CCT | TTC | TTA | GAG | CAT | GAT | GAC | GCC | AAC | 2121 |  |
| Gly | Val | Ala | Ala | Ser | Leu | Ile | Pro | Phe | Leu | Glu | His | Asp | Asp | Ala | Asn |      |  |
|     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |     | 690 |     |      |  |
| CGT | GCC | TTA | ATG | GGG | ACT | AAC | ATG | CAG | CGC | CAA | GCG | GTG | CCC | TTA | TTA | 2169 |  |
| Arg | Ala | Leu | Met | Gly | Thr | Asn | Met | Gln | Arg | Gln | Ala | Val | Pro | Leu | Leu |      |  |
|     |     |     | 695 |     |     |     |     | 700 |     |     |     |     | 705 |     |     |      |  |
| AGA | AGC | GAC | GCT | CCC | ATT | GTA | GGC | ACG | GGG | ATT | GAA | AAA | ATT | ATT | GCT | 2217 |  |
| Arg | Ser | Asp | Ala | Pro | Ile | Val | Gly | Thr | Gly | Ile | Glu | Lys | Ile | Ile | Ala |      |  |
|     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |     |     |     |      |  |
| AGG | GAT | TCT | TGG | GGA | GCG | ATC | AAA | GCC | AAT | CGC | GCA | GGC | GTT | GTA | GAA | 2265 |  |
| Arg | Asp | Ser | Trp | Gly | Ala | Ile | Lys | Ala | Asn | Arg | Ala | Gly | Val | Val | Glu |      |  |
|     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |     |     |     |      |  |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAA ATT GAT TCT AAA AAT ATT TAT ATT TTA GGC GAA AGC AAA GAA GAA | 2313 |
| Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu |      |
| 740 745 750 755                                                 |      |
| GCC TAT ATT GAT GCG TAT TCT TTG CAA AAA AAC TTG CGC ACC AAC CAA | 2361 |
| Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln |      |
| 760 765 770                                                     |      |
| AAC ACC AGT TTC AAT CAA GTC CCT ATC GTT AAA GTG GGC GAT AAA GTG | 2409 |
| Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val |      |
| 775 780 785                                                     |      |
| GGA GCC GGG CAA ATC ATC GCT GAT GGC CCT AGC ATG GAT AGA GGC GAG | 2457 |
| Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu |      |
| 790 795 800                                                     |      |
| TTG GCG TTA GGG AAA AAT GTG CGC GTG GCG TTC ATG CCT TGG AAT GGC | 2505 |
| Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly |      |
| 805 810 815                                                     |      |
| TAT AAC TTT GAA GAC GCG ATC GTG GTG AGT GAG TGC ATC ACT AAA GAT | 2553 |
| Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp |      |
| 820 825 830 835                                                 |      |
| GAT ATT TTC ACT TCC ACC CAC ATT TAT GAA AAA GAA GTG GAT GCT AGG | 2601 |
| Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg |      |
| 840 845 850                                                     |      |
| GAG CTT AAG CAT GGT GTG GAA GAA TTT ACC GCT GAT ATT CCT GAT GTG | 2649 |
| Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val |      |
| 855 860 865                                                     |      |
| AAA GAA GAA GCG CTC GCT CAT CTT GAT GAA AGC GGG ATC GTT AAA GTC | 2697 |
| Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val |      |
| 870 875 880                                                     |      |
| GGT ACT TAT GTG AGC GCT GGC ATG ATT TTG GTG GGC AAA ACT TCT CCT | 2745 |
| Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro |      |
| 885 890 895                                                     |      |
| AAA GGC GAG ATT AAA AGC ACG CCT GAA GAG CGG CTT TTA AGG GCT ATT | 2793 |
| Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile |      |
| 900 905 910 915                                                 |      |
| TTT GGG GAT AAA GCC GGG CAT GTG GTC AAT AAG AGT TTG TAT TGC CCT | 2841 |
| Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro |      |
| 920 925 930                                                     |      |
| CCC AGT TTG GAA GGC ACG GTG ATT GAT GTG AAA GTC TTC ACT AAA AAA | 2889 |
| Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys |      |
| 935 940 945                                                     |      |
| GGC TAT GAG AAA GAC GCG CGA GTT TTG AGC GCG TAT GAA GAA GAA AAA | 2937 |
| Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys |      |
| 950 955 960                                                     |      |
| GCC AAG CTT GAT ATG GAG CAT TTT GAT CGC TTG ACC ATG CTC AAT AGA | 2985 |
| Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg |      |



|                         |                     |                         |                     |     |                         |
|-------------------------|---------------------|-------------------------|---------------------|-----|-------------------------|
| 290                     | Val Gly Lys Glu Val | 295                     | Leu Asp Met Leu Thr | 300 | Gln Leu Asp Lys Asn     |
| 305                     | Lys Leu Glu Lys Ile | 310                     | His Asp Leu Gly Val | 315 | Gln Glu Phe Val Ile Ile |
|                         | 325                 |                         | 330                 |     | 335                     |
| Asn Asp Leu Ala Leu     | Gly His Asp Ala Ser | Ile Ile Gln Ser Phe Ser |                     |     |                         |
|                         | 340                 |                         | 345                 |     | 350                     |
| Ala Asp Ser Glu Ser Leu | Lys Leu Lys Gln Thr | Glu Lys Ile Asp         |                     |     |                         |
|                         | 355                 |                         | 360                 |     | 365                     |
| Asp Glu Asn Ala Leu Ala | Ala Ile Arg Ile His | Lys Val Met Lys Pro     |                     |     |                         |
|                         | 370                 |                         | 375                 |     | 380                     |
| Gly Asp Pro Val Thr Thr | Glu Val Ala Lys Gln | Phe Val Lys Lys Leu     |                     |     |                         |
|                         | 385                 |                         | 390                 |     | 400                     |
| Phe Phe Asp Pro Glu Arg | Tyr Asp Leu Thr Met | Val Gly Arg Met Lys     |                     |     |                         |
|                         | 405                 |                         | 410                 |     | 415                     |
| Met Asn His Lys Leu Gly | Leu His Val Pro Asp | Tyr Ile Thr Thr Leu     |                     |     |                         |
|                         | 420                 |                         | 425                 |     | 430                     |
| Thr His Glu Asp Ile Ile | Thr Thr Val Lys Tyr | Leu Met Lys Ile Lys     |                     |     |                         |
|                         | 435                 |                         | 440                 |     | 445                     |
| Asn Asn Gln Gly Lys Ile | Asp Asp Arg Asp His | Leu Gly Asn Arg Arg     |                     |     |                         |
|                         | 450                 |                         | 455                 |     | 460                     |
| Ile Arg Ala Val Gly Glu | Leu Leu Ala Asn Glu | Leu His Ser Gly Leu     |                     |     |                         |
|                         | 465                 |                         | 470                 |     | 475                     |
| Val Lys Met Gln Lys Thr | Ile Lys Asp Lys Leu | Thr Thr Met Ser Gly     |                     |     |                         |
|                         | 485                 |                         | 490                 |     | 495                     |
| Ala Phe Asp Ser Leu Met | Pro His Asp Leu Val | Asn Ser Lys Met Ile     |                     |     |                         |
|                         | 500                 |                         | 505                 |     | 510                     |
| Thr Ser Thr Ile Met Glu | Phe Phe Met Gly Gly | Gln Leu Ser Gln Phe     |                     |     |                         |
|                         | 515                 |                         | 520                 |     | 525                     |
| Met Asp Gln Thr Asn Pro | Leu Ser Glu Val Thr | His Lys Arg Arg Leu     |                     |     |                         |
|                         | 530                 |                         | 535                 |     | 540                     |
| Ser Ala Leu Gly Glu Gly | Gly Gly Leu Val Lys | Asp Arg Val Gly Phe Glu |                     |     |                         |
|                         | 545                 |                         | 550                 |     | 555                     |
| Ala Arg Asp Val His Pro | Thr His Tyr Gly Arg | Ile Cys Pro Ile Glu     |                     |     |                         |
|                         | 565                 |                         | 570                 |     | 575                     |
| Thr Pro Glu Gly Gln Asn | Ile Gly Leu Ile Asn | Thr Leu Ser Thr Phe     |                     |     |                         |
|                         | 580                 |                         | 585                 |     | 590                     |
| Thr Arg Val Asn Asp Leu | Gly Phe Ile Glu Ala | Pro Tyr Lys Lys Val     |                     |     |                         |
|                         | 595                 |                         | 600                 |     | 605                     |
| Val Asp Gly Lys Val Val | Gly Glu Thr Ile Tyr | Leu Thr Ala Ile Gln     |                     |     |                         |
|                         | 610                 |                         | 615                 |     | 620                     |
| Glu Asp Ser His Ile Ile | Ala Pro Ala Ser Thr | Pro Ile Asp Glu Glu     |                     |     |                         |
|                         | 625                 |                         | 630                 |     | 635                     |
| Gly Asn Ile Leu Gly Asp | Leu Ile Glu Thr Arg | Val Glu Gly Glu Ile     |                     |     |                         |
|                         | 645                 |                         | 650                 |     | 655                     |
| Val Leu Asn Glu Lys Ser | Lys Val Thr Leu Met | Asp Leu Ser Ser Ser     |                     |     |                         |
|                         | 660                 |                         | 665                 |     | 670                     |
| Met Leu Val Gly Val Ala | Ala Ser Leu Ile Pro | Phe Leu Glu His Asp     |                     |     |                         |
|                         | 675                 |                         | 680                 |     | 685                     |
| Asp Ala Asn Arg Ala Leu | Met Gly Thr Asn Met | Gln Arg Gln Ala Val     |                     |     |                         |
|                         | 690                 |                         | 695                 |     | 700                     |
| Pro Leu Leu Arg Ser Asp | Ala Pro Ile Val Gly | Thr Gly Ile Glu Lys     |                     |     |                         |
|                         | 705                 |                         | 710                 |     | 715                     |
| Ile Ile Ala Arg Asp Ser | Trp Gly Ala Ile Lys | Ala Asn Arg Ala Gly     |                     |     |                         |
|                         | 725                 |                         | 730                 |     | 735                     |
| Val Val Glu Lys Ile Asp | Ser Lys Asn Ile Tyr | Ile Leu Gly Glu Ser     |                     |     |                         |
|                         | 740                 |                         | 745                 |     | 750                     |
| Lys Glu Glu Ala Tyr Ile | Asp Ala Tyr Ser Leu | Gln Lys Asn Leu Arg     |                     |     |                         |



$$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}, \quad \frac{d}{dt} \left( \frac{\partial L}{\partial \dot{y}} \right) = \frac{\partial L}{\partial y}, \quad \frac{d}{dt} \left( \frac{\partial L}{\partial \dot{z}} \right) = \frac{\partial L}{\partial z}$$

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(A) NAME/KEY: Coding Sequence

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

107

CGT GAA AAA ATG CGT TTA TGC CCC TTG TAT TGG CGC ATC TTA GCG TTT 153  
 Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile Leu Ala Phe  
 20 25 30 35

TTA ACC GAT GGT TTG TTA GTG GCG TTT TTA TTG AGC GAT CTT TTA GAC 201  
 Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp Leu Leu Asp  
 40 45 50

GCA TGC GAT TTC TTG CAT TCT TTA TAT TGG CTA GCT AAC CCT ATT TAT 249  
 Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn Pro Ile Tyr  
 55 60 65

CAC AGC GCA TTT GTT GCG ATG GGT TTT ATC ATC TTG TAT GGC GTT TAT 297  
 His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr Gly Val Tyr  
 70 75 80

GAA ATC TTT TTT GTG TGT TTG TGC AAG ATG AGC TTG GCT AAA CTG GTT 345  
 Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala Lys Leu Val  
 85 90 95

TTT AGG ATT AAG ATT ATT GAT ATT TAT TTG GCA GAT TGC CCC AGT AGG 393  
 Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys Pro Ser Arg  
 100 105 110 115

GCT ATT TTA TTG AAG CGT TTA GGG TTA AAG ATC GTG GTT TTT CTA TGC 441  
 Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val Phe Leu Cys  
 120 125 130

CCC TTT TTA TGG TTT GTT GCG TTT AAA AAC CCC TAT CAT AGG GCG TGG 489  
 Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His Arg Ala Trp  
 135 140 145

CAT GAA GAA AAA AGC AAA AGT CTT TTG GTA TTG TTT TAATCATGAT TTATTG 541  
 His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe  
 150 155

GTTGTATTTG GCGGTCTTTT TTTTGTGAG CGCATTAGAC 581

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met His Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr  
 1 5 10 15  
 Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile  
 20 25 30  
 Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp  
 35 40 45  
 Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn

50 55 60  
 Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr  
 65 70 75 80  
 Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala  
 85 90 95  
 Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys  
 100 105 110  
 Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val  
 115 120 125  
 Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His  
 130 135 140  
 Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe  
 145 150 155

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...852
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTTAAGC GGCAGAGGGG ATAAGGATTT AAGCACCGTT TATAACGCTT TAAAAGGAGG 60  
 TTTAAA ATG AGG TAT CAA AAC ATG TTT GAA ACC TTA AAA AAA CAC GAA 108  
 Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu  
 1 5 10  
 AAA ATG GCG TTT ATC CCG TTT GTA ACC TTG GGC GAT CCT AAT TAT GAA 156  
 Lys Met Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu  
 15 20 25 30  
 TTG AGT TTT GAA ATC ATT AAA ACC CTA ATT ATT AGC GGG GTG AGC GCT 204  
 Leu Ser Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala  
 35 40 45  
 TTA GAA TTG GGT CTT GCT TTT TCT GAT CCT GTG GCG GAT GGC ATT ACC 252  
 Leu Glu Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr  
 50 55 60  
 ATA CAA GCG AGC CAT TTA AGG GCG TTA AAA CAC GCT AGC ATG GCT AAA 300  
 Ile Gln Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys  
 65 70 75  
 AAT TTC CAG CTT TTA AAA AAG ATT AGA GAT TAC AAC CAC AAT ATT CCC 348  
 Asn Phe Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro  
 80 85 90

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ATA GGG CTT TTA GCG TAT GCG AAT TTA ATT TTT TCT TAT GGC GTT GAT  | 396 |
| Ile Gly Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp  |     |
| 95 100 105 110                                                   |     |
| GGC TTT TAC GCT CAA GCT AAA GAA TGC GGT ATA GAT AGC GTT TTA ATA  | 444 |
| Gly Phe Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile  |     |
| 115 120 125                                                      |     |
| GCG GAC ATG CCC CTA ATA GAA AAA GAA TTA GTC ATC AAA TCC GCT CAA  | 492 |
| Ala Asp Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln  |     |
| 130 135 140                                                      |     |
| AAA CAC CAA ATC AAG CAA ATC TTT ATC GCC AGC CCC AAT GCG AGC AGT  | 540 |
| Lys His Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser  |     |
| 145 150 155                                                      |     |
| AAA GAT TTA GAA CAA GTC GCT ACG CAT TCG CAA GGC TAT ATC TAC GCT  | 588 |
| Lys Asp Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala  |     |
| 160 165 170                                                      |     |
| TTA GCC AGG AGT GGG GTT ACA GGG GCG AGC CGT ATT TTA GAG AAT GAT  | 636 |
| Leu Ala Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp  |     |
| 175 180 185 190                                                  |     |
| TCG AGT GCT ATT ATT AAA ACC TTA AAA GCT TTT AGC CCT ACC CCA GCC  | 684 |
| Ser Ser Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala  |     |
| 195 200 205                                                      |     |
| TTA CTG GGC TTT GGC ATT TCC AAA AAA GAA CAC ATC ACA AAC GCT AAA  | 732 |
| Leu Leu Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys  |     |
| 210 215 220                                                      |     |
| GGC ATG GGT GCT GAT GGC GTG ATT TGC GGA TCA GCG TTA GTC AAA ATC  | 780 |
| Gly Met Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile  |     |
| 225 230 235                                                      |     |
| ATA GAA GAA AAT TTA AAC AAT GAA AAC GCC ATG CTG GAA AAA ATT AAA  | 828 |
| Ile Glu Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys  |     |
| 240 245 250                                                      |     |
| GGG TTT ATA GGA GGA ATG ATT TTT TAAGGCTTTT AGGCTTTGTT GCGTTAAAAA | 882 |
| Gly Phe Ile Gly Gly Met Ile Phe                                  |     |
| 255 260                                                          |     |
| TTAAAGATCA CAGATTAAC                                             | 901 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu Lys Met  
1 5 10 15  
Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu Leu Ser  
20 25 30  
Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala Leu Glu  
35 40 45  
Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr Ile Gln  
50 55 60  
Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys Asn Phe  
65 70 75 80  
Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro Ile Gly  
85 90 95  
Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp Gly Phe  
100 105 110  
Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile Ala Asp  
115 120 125  
Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln Lys His  
130 135 140  
Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser Lys Asp  
145 150 155 160  
Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala Leu Ala  
165 170 175  
Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp Ser Ser  
180 185 190  
Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala Leu Leu  
195 200 205  
Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys Gly Met  
210 215 220  
Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile Ile Glu  
225 230 235 240  
Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys Gly Phe  
245 250 255  
Ile Gly Gly Met Ile Phe  
260

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...954
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AAGTAATGCC CCTGTTGTAT CAGCTTGATT TAAGAGGAAT AAGTTATT ATG AAT AAA 57  
Met Asn Lys  
1  
GCT ATT GCT AGT AAG ATA CTC ATC ACT TTG GGT TTT TTA TTT CTC TAC 105

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ile | Ala | Ser | Lys | Ile | Leu | Ile | Thr | Leu | Gly | Phe | Leu | Phe | Leu | Tyr |     |
| 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     |     |
| AGA | GTC | TTA | GCT | TAT | ATC | CCC | ATT | CCT | GGC | GTA | GAT | TTA | GCA | GCG | ATC | 153 |
| Arg | Val | Leu | Ala | Tyr | Ile | Pro | Ile | Pro | Gly | Val | Asp | Leu | Ala | Ala | Ile |     |
| 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |     | 35  |     |
| AAG | GCT | TTT | TTT | GAC | AGC | AAT | TCC | AAC | AAC | GCT | TTG | GGG | TTG | TTT | AAT | 201 |
| Lys | Ala | Phe | Phe | Asp | Ser | Asn | Ser | Asn | Asn | Ala | Leu | Gly | Leu | Phe | Asn |     |
|     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     | 50  |     |     |
| ATG | TTT | AGC | GGG | AAT | GCG | GTT | TCT | CGC | TTG | AGC | ATC | ATC | TCG | TTG | GGT | 249 |
| Met | Phe | Ser | Gly | Asn | Ala | Val | Ser | Arg | Leu | Ser | Ile | Ile | Ser | Leu | Gly |     |
|     |     |     | 55  |     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |
| ATC | ATG | CCC | TAT | ATC | ACT | TCT | TCA | ATT | ATC | ATG | GAG | CTT | TTG | AGC | GCG | 297 |
| Ile | Met | Pro | Tyr | Ile | Thr | Ser | Ser | Ile | Ile | Met | Glu | Leu | Leu | Ser | Ala |     |
|     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     |
| ACT | TTC | CCT | AAC | CTG | GCT | AAA | ATG | AAA | AAA | GAG | CGG | GAT | GGC | ATG | CAA | 345 |
| Thr | Phe | Pro | Asn | Leu | Ala | Lys | Met | Lys | Lys | Glu | Arg | Asp | Gly | Met | Gln |     |
|     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |     |
| AAA | TAC | ATG | CAA | ATC | GTG | CGT | TAT | TTG | ACC | ATT | TTA | ATC | ACC | CTA | ATC | 393 |
| Lys | Tyr | Met | Gln | Ile | Val | Arg | Tyr | Leu | Thr | Ile | Leu | Ile | Thr | Leu | Ile |     |
| 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |
| CAA | GCG | GTG | AGC | GTT | TCA | GTA | GGC | TTA | AGG | AGC | ATT | AGT | GGA | GGA | GCC | 441 |
| Gln | Ala | Val | Ser | Val | Ser | Val | Gly | Leu | Arg | Ser | Ile | Ser | Gly | Gly | Ala |     |
|     |     |     |     | 120 |     |     |     | 125 |     |     |     |     | 130 |     |     |     |
| AAT | GGG | GCG | ATC | ATG | ATT | GAT | ATG | CAA | GTT | TTT | ATG | ATC | GTT | TCA | GCG | 489 |
| Asn | Gly | Ala | Ile | Met | Ile | Asp | Met | Gln | Val | Phe | Met | Ile | Val | Ser | Ala |     |
|     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |
| TTT | TCT | ATG | CTT | ACA | GGA | ACG | ATG | CTA | CTC | ATG | TGG | ATA | GGG | GAG | CAA | 537 |
| Phe | Ser | Met | Leu | Thr | Gly | Thr | Met | Leu | Leu | Met | Trp | Ile | Gly | Glu | Gln |     |
|     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     |
| ATC | ACG | CAA | AGG | GGC | GTG | GGG | AAT | GGG | ATC | AGT | CTC | ATT | ATT | TTT | GCC | 585 |
| Ile | Thr | Gln | Arg | Gly | Val | Gly | Asn | Gly | Ile | Ser | Leu | Ile | Ile | Phe | Ala |     |
|     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     |     |
| GGG | ATT | GTT | TCA | GGG | ATC | CCA | TCA | GCT | ATT | TCA | GGC | ACA | TTC | AAT | TTG | 633 |
| Gly | Ile | Val | Ser | Gly | Ile | Pro | Ser | Ala | Ile | Ser | Gly | Thr | Phe | Asn | Leu |     |
| 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |
| GTC | AAT | ACG | GGC | GTT | ATT | AAT | ATC | TTA | ATG | CTC | ATT | GGT | ATT | GTG | CTG | 681 |
| Val | Asn | Thr | Gly | Val | Ile | Asn | Ile | Leu | Met | Leu | Ile | Gly | Ile | Val | Leu |     |
|     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |     | 210 |     |     |
| ATT | GTT | TTA | GCG | ACT | ATT | TTT | GCG | ATT | ATC | TAT | GTG | GAA | TTA | GCT | GAG | 729 |
| Ile | Val | Leu | Ala | Thr | Ile | Phe | Ala | Ile | Ile | Tyr | Val | Glu | Leu | Ala | Glu |     |
|     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |
| CGC | AGG | ATC | CCT | ATT | TCT | TAT | GCG | CGT | AAA | GTG | GTG | ATG | CAA | AAC | CAA | 777 |
| Arg | Arg | Ile | Pro | Ile | Ser | Tyr | Ala | Arg | Lys | Val | Val | Met | Gln | Asn | Gln |     |
|     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |     |

AAC AAG CGC ATC ATG AAT TAC ATT CCT ATT AAG TTG AAT TTA AGT GGG 825  
Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn Leu Ser Gly  
245 250 255  
  
GTG ATC CCC CCT ATT TTC GCT TCA GCT TTG CTC GTG TTC CCT TCT ACG 873  
Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe Pro Ser Thr  
260 265 270 275  
  
ATT TTG CAG CAA GCC ACA AGC AAC AAA ACC TTG CAA GCG GTT GCG NAT 921  
Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala Val Ala Xaa  
280 285 290  
  
TTT TTA AGC CCG CAA GGT ATG CGT ATA ATA TTT TGATGTTCTT GCTCATCATC 974  
Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe  
295 300  
  
TTTTTTGCTT ACTTTTATTC TTCTATTGTG TTCAATTCTA AGGATATTGC GGATAATTTG 1034  
AGGCGTAATG GCGGGTATAT TCCAGGGCTT AGGCCTGGAG AGGGGAC 1081

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Asn Lys Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu  
1 5 10 15  
Phe Leu Tyr Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu  
20 25 30  
Ala Ala Ile Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly  
35 40 45  
Leu Phe Asn Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile  
50 55 60  
Ser Leu Gly Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu  
65 70 75 80  
Leu Ser Ala Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp  
85 90 95  
Gly Met Gln Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile  
100 105 110  
Thr Leu Ile Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser  
115 120 125  
Gly Gly Ala Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile  
130 135 140  
Val Ser Ala Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile  
145 150 155 160  
Gly Glu Gln Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile  
165 170 175  
Ile Phe Ala Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr  
180 185 190  
Phe Asn Leu Val Asn Thr Gly Val Ile Asn Ile Leu Met Leu Ile Gly  
195 200 205

Ile Val Leu Ile Val Leu Ala Thr Ile Phe Ala Ile Ile Tyr Val Glu  
 210 215 220  
 Leu Ala Glu Arg Arg Ile Pro Ile Ser Tyr Ala Arg Lys Val Val Met  
 225 230 235 240  
 Gln Asn Gln Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn  
 245 250 255  
 Leu Ser Gly Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe  
 260 265 270  
 Pro Ser Thr Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala  
 275 280 285  
 Val Ala Xaa Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe  
 290 295 300

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 109...363
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AATGGGGCAA TTCAAGGCGA TAGAAGCTTG AATGAGGGCT TCTTCTAAGG TTTTGGCTTT 60  
 GATTTCAATA AAATTTTGCA TCAATGTTCC TTTTGTGTTT GCGCATGC ATG CGT TTT 117  
 Met Arg Phe  
 1

TTA TTC TCT AAG ACT TTA TTG ATG ATG AGT TGT TGC AAC ACC GAA AGG 165  
 Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn Thr Glu Arg  
 5 10 15

ATG TTG TTC GTG GTC CAA TAC AAG ACT AAC CCT GCC GGG AAA GTG ATT 213  
 Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly Lys Val Ile  
 20 25 30 35

AAA AAG ATT GTG AAT AAT AGG GGT AAG AGT TTA AAA ATC TTT GCT TGC 261  
 Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile Phe Ala Cys  
 40 45 50

ATG GGA TCG GTC ATG GTG TTT GGC GTA ACG CTT TGG TGC CAA TAC ATA 309  
 Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys Gln Tyr Ile  
 55 60 65

GAC GCT CCC ATA AGA AGC GGT AAA ATA AAA TAC GGA TCC ATG ATG GAT 357  
 Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser Met Met Asp  
 70 75 80

AAA TCA TGAATCCATA AGATCCACTC TGAGCTTTTC AATTCACAG CGTTATAAAG CA 415  
 Lys Ser



CTCTATAA

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Phe | Leu | Phe | Ser | Lys | Thr | Leu | Leu | Met | Met | Ser | Cys | Cys | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Glu | Arg | Met | Leu | Phe | Val | Val | Gln | Tyr | Lys | Thr | Asn | Pro | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Val | Ile | Lys | Lys | Ile | Val | Asn | Asn | Arg | Gly | Lys | Ser | Leu | Lys | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ala | Cys | Met | Gly | Ser | Val | Met | Val | Phe | Gly | Val | Thr | Leu | Trp | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Tyr | Ile | Asp | Ala | Pro | Ile | Arg | Ser | Gly | Lys | Ile | Lys | Tyr | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Met | Asp | Lys | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 85  |

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...688
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

|                                                                 |            |            |            |            |          |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|----------|----|
| TTTAAATTA                                                       | GAAACAGATG | TATCTGTTTT | AAATTTTGAA | TAGGGAGTTT | CTATCATT | 58 |
| ATG TTA TTG AAA ACA AAA TTA AAA ATT ATA AGC TCG GTG ATT TTG AGC | 106        |            |            |            |          |    |
| Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser |            |            |            |            |          |    |
| 1 5 10 15                                                       |            |            |            |            |          |    |
| GCT TTA TTG TGG GTG GGT TGC TCA AGC GAA ATG GCA ACT TAT CAA AAC | 154        |            |            |            |          |    |
| Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn |            |            |            |            |          |    |

| 20  |     |            |     |     |     |            |     |            |     | 25         |     |               |     |     | 30  |     |  |  |  |  |
|-----|-----|------------|-----|-----|-----|------------|-----|------------|-----|------------|-----|---------------|-----|-----|-----|-----|--|--|--|--|
| GTG | AAT | GAT        | GCC | ACT | AAA | AAT        | ACG | ACT        | GCA | AGC        | ATT | AAT           | AGC | ACG | GAT | 202 |  |  |  |  |
| Val | Asn | Asp        | Ala | Thr | Lys | Asn        | Thr | Thr        | Ala | Ser        | Ile | Asn           | Ser | Thr | Asp |     |  |  |  |  |
| 35  |     |            | 40  |     |     |            |     | 45         |     |            |     |               |     |     |     |     |  |  |  |  |
| TTA | TTG | CTA        | ACC | GCT | AAC | GCG        | ATG | TTA        | GAT | TCC        | ATG | TTT           | AGC | GAC | CCT | 250 |  |  |  |  |
| Leu | Leu | Leu        | Thr | Ala | Asn | Ala        | Met | Leu        | Asp | Ser        | Met | Phe           | Ser | Asp | Pro |     |  |  |  |  |
| 50  |     | 55         |     |     |     |            | 60  |            |     |            |     |               |     |     |     |     |  |  |  |  |
| AAT | TTT | GAG        | CAA | CTC | AAG | GCG        | AAG | CAT        | TTG | ATT        | GAA | GTT           | TCA | GAT | GTG | 298 |  |  |  |  |
| Asn | Phe | Glu        | Gln | Leu | Lys | Gly        | Lys | His        | Leu | Ile        | Glu | Val           | Ser | Asp | Val |     |  |  |  |  |
| 65  |     | 70         |     |     |     |            | 75  |            |     |            | 80  |               |     |     |     |     |  |  |  |  |
| ATT | AAC | GAC        | ACC | ACG | CAG | CCC        | AAT | TTG        | GAC | ATG        | AAT | CTT           | TTG | ACG | ACT | 346 |  |  |  |  |
| Ile | Asn | Asp        | Thr | Thr | Gln | Pro        | Asn | Leu        | Asp | Met        | Asn | Leu           | Leu | Thr | Thr |     |  |  |  |  |
| 85  |     |            |     | 90  |     |            |     |            | 95  |            |     |               |     |     |     |     |  |  |  |  |
| GAA | ATC | GCG        | CGG | CAG | TTG | CGG        | TTG | CGA        | TCT | AAT        | GGG | AGG           | TTC | AAT | ATC | 394 |  |  |  |  |
| Glu | Ile | Ala        | Arg | Gln | Leu | Arg        | Leu | Arg        | Ser | Asn        | Gly | Arg           | Phe | Asn | Ile |     |  |  |  |  |
| 100 |     |            | 105 |     |     |            |     | 110        |     |            |     |               |     |     |     |     |  |  |  |  |
| ACA | AGG | GCG        | AGC | GGA | GGG | AGT        | GGC | ATT        | GCA | GCC        | GAT | AGC           | AGA | ATG | GTG | 442 |  |  |  |  |
| Thr | Arg | Ala        | Ser | Gly | Gly | Ser        | Gly | Ile        | Ala | Ala        | Asp | Ser           | Arg | Met | Val |     |  |  |  |  |
| 115 |     | 120        |     |     |     |            | 125 |            |     |            |     |               |     |     |     |     |  |  |  |  |
| AAA | CAG | CGC        | GAA | AAA | GAA | CGA        | GAG | AGC        | GAA | GAG        | TAT | AAT           | CAA | GAC | ACC | 490 |  |  |  |  |
| Lys | Gln | Arg        | Glu | Lys | Glu | Arg        | Glu | Ser        | Glu | Glu        | Tyr | Asn           | Gln | Asp | Thr |     |  |  |  |  |
| 130 |     | 135        |     |     |     |            | 140 |            |     |            |     |               |     |     |     |     |  |  |  |  |
| ACT | GTA | GAA        | AAA | GGC | ACT | TTA        | AAA | GCC        | GCT | GAT        | TTA | TCT           | TTA | AGT | GGT | 538 |  |  |  |  |
| Thr | Val | Glu        | Lys | Gly | Thr | Leu        | Lys | Ala        | Ala | Asp        | Leu | Ser           | Leu | Ser | Gly |     |  |  |  |  |
| 145 |     | 150        |     |     |     |            | 155 |            |     |            | 160 |               |     |     |     |     |  |  |  |  |
| AAA | GTA | TCT        | AGT | ATC | GCA | GCC        | TCT | ATT        | AGT | AGT        | TCT | AGG           | CAG | CGC | TTG | 586 |  |  |  |  |
| Lys | Val | Ser        | Ser | Ile | Ala | Ala        | Ser | Ile        | Ser | Ser        | Ser | Arg           | Gln | Arg | Leu |     |  |  |  |  |
| 165 |     |            |     | 170 |     |            |     |            | 175 |            |     |               |     |     |     |     |  |  |  |  |
| GAC | TAT | GAC        | TTC | ACC | CTA | AGC        | CTT | ACC        | AAC | AGG        | AAA | ACG           | GGT | GAA | GAG | 634 |  |  |  |  |
| Asp | Tyr | Asp        | Phe | Thr | Leu | Ser        | Leu | Thr        | Asn | Arg        | Lys | Thr           | Gly | Glu | Glu |     |  |  |  |  |
| 180 |     |            | 185 |     |     |            |     | 190        |     |            |     |               |     |     |     |     |  |  |  |  |
| GTA | TGG | AGC        | GAT | GTT | AAG | CCT        | ATT | GTG        | AAG | AAC        | GCT | AGC           | AAT | AAG | CGT | 682 |  |  |  |  |
| Val | Trp | Ser        | Asp | Val | Lys | Pro        | Ile | Val        | Lys | Asn        | Ala | Ser           | Asn | Lys | Arg |     |  |  |  |  |
| 195 |     | 200        |     |     |     |            | 205 |            |     |            |     |               |     |     |     |     |  |  |  |  |
| ATG | TTT | TAAATTTATA |     |     |     | TTTGAAAGGA |     | TGAACAATGA |     | AAAATCAAGT |     | TAAAAAAATT TT |     |     |     | 740 |  |  |  |  |
| Met | Phe |            |     |     |     |            |     |            |     |            |     |               |     |     |     |     |  |  |  |  |
| 210 |     |            |     |     |     |            |     |            |     |            |     |               |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Lys | Thr | Lys | Leu | Lys | Ile | Ile | Ser | Ser | Val | Ile | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Leu | Trp | Val | Gly | Cys | Ser | Ser | Glu | Met | Ala | Thr | Tyr | Gln | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asn | Asp | Ala | Thr | Lys | Asn | Thr | Thr | Ala | Ser | Ile | Asn | Ser | Thr | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Leu | Thr | Ala | Asn | Ala | Met | Leu | Asp | Ser | Met | Phe | Ser | Asp | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Phe | Glu | Gln | Leu | Lys | Gly | Lys | His | Leu | Ile | Glu | Val | Ser | Asp | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Asn | Asp | Thr | Thr | Gln | Pro | Asn | Leu | Asp | Met | Asn | Leu | Leu | Thr | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Ile | Ala | Arg | Gln | Leu | Arg | Leu | Arg | Ser | Asn | Gly | Arg | Phe | Asn | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Arg | Ala | Ser | Gly | Gly | Ser | Gly | Ile | Ala | Ala | Asp | Ser | Arg | Met | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gln | Arg | Glu | Lys | Glu | Arg | Glu | Ser | Glu | Glu | Tyr | Asn | Gln | Asp | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Val | Glu | Lys | Gly | Thr | Leu | Lys | Ala | Ala | Asp | Leu | Ser | Leu | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Val | Ser | Ser | Ile | Ala | Ala | Ser | Ile | Ser | Ser | Ser | Arg | Gln | Arg | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Tyr | Asp | Phe | Thr | Leu | Ser | Leu | Thr | Asn | Arg | Lys | Thr | Gly | Glu | Glu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Val | Trp | Ser | Asp | Val | Lys | Pro | Ile | Val | Lys | Asn | Ala | Ser | Asn | Lys | Arg |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Met | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 84...1214
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| TTATCATTTGT | GTAAAAATAG | TCGTTTAAAC  | AAACAAATT   | TTGTTAATAG  | ATTTTACCTA | 60  |
| ATCTGAGAGA  | GAATTATATT | TTA ATG AAG | ACA GAG AAA | CAA AAA TTT | TTA GAG    | 113 |
|             |            | Met Lys Thr | Glu Lys Gln | Lys Phe Leu | Glu        |     |
|             |            | 1           | 5           |             | 10         |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | CGT | AAA | GAT | GGG | GCG | AAC | TCT | GTG | CTG | ATT | TTA | AGA | GGG | GAT | TGG | 161 |
| Met | Arg | Lys | Asp | Gly | Ala | Asn | Ser | Val | Leu | Ile | Leu | Arg | Gly | Asp | Trp |     |
|     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
| GAT | TTT | AAA | ACG | AGC | GTG | TTT | CGT | TTA | GAT | GAG | TTG | AAA | AAA | AAT | TTA | 209 |
| Asp | Phe | Lys | Thr | Ser | Val | Phe | Arg | Leu | Asp | Glu | Leu | Lys | Lys | Asn | Leu |     |
|     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |
| TTA | GAT | CAT | CAA | GGG | CCT | TTA | AAA | ATG | GAT | TTT | TCA | GGG | TGC | CAA | AAA | 257 |
| Leu | Asp | His | Gln | Gly | Pro | Leu | Lys | Met | Asp | Phe | Ser | Gly | Cys | Gln | Lys |     |
|     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |
| GTG | GAT | TTT | GTT | TTT | GGC | ATG | TTT | TTA | TTT | GAT | TTA | GTT | AAG | GAG | CGT | 305 |
| Val | Asp | Phe | Val | Phe | Gly | Met | Phe | Leu | Phe | Asp | Leu | Val | Lys | Glu | Arg |     |
|     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     |
| TCT | TTA | AAC | ATT | GAA | TTG | TGT | AAC | GTG | AGT | GAG | AAT | AAC | GCA | TGC | GCT | 353 |
| Ser | Leu | Asn | Ile | Glu | Leu | Cys | Asn | Val | Ser | Glu | Asn | Asn | Ala | Cys | Ala |     |
| 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |
| TTG | AAA | GTG | GTT | AAA | GAC | TGG | CTT | GAA | AAA | GAA | GAG | GAT | TTA | GAG | TCT | 401 |
| Leu | Lys | Val | Val | Lys | Asp | Trp | Leu | Glu | Lys | Glu | Glu | Asp | Leu | Glu | Ser |     |
|     |     |     |     | 95  |     |     |     | 100 |     |     |     |     |     | 105 |     |     |
| AAA | AAA | GCG | GGC | AAA | CAC | TAC | GAA | CTT | TTG | ATC | ACT | AAA | TTG | GGT | AAG | 449 |
| Lys | Lys | Ala | Gly | Lys | His | Tyr | Glu | Leu | Leu | Ile | Thr | Lys | Leu | Gly | Lys |     |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |
| AGT | ATC | GTA | GAG | ACT | TAT | AAT | ACC | TTT | TTA | AAC | GCA | TTC | AAT | TTT | TGC | 497 |
| Ser | Ile | Val | Glu | Thr | Tyr | Asn | Thr | Phe | Leu | Asn | Ala | Phe | Asn | Phe | Cys |     |
|     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |
| GGC | ATG | ATT | TTA | TTC | TAC | TTC | ATT | AAA | AGC | GTT | TTC | AAC | CCC | AAA | CGC | 545 |
| Gly | Met | Ile | Leu | Phe | Tyr | Phe | Ile | Lys | Ser | Val | Phe | Asn | Pro | Lys | Arg |     |
|     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     |     |
| TTT | TGT | ATC | ACT | CCT | TTG | CTC | TAT | CAT | ATC | AAT | GAA | TCC | GGG | TTT | AAG | 593 |
| Phe | Cys | Ile | Thr | Pro | Leu | Leu | Tyr | His | Ile | Asn | Glu | Ser | Gly | Phe | Lys |     |
| 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |
| GTT | TTG | CCA | GTG | AGT | ATT | TTA | ACG | GTG | TTT | ATC | GTG | GGG | TTT | GCC | GTT | 641 |
| Val | Leu | Pro | Val | Ser | Ile | Leu | Thr | Val | Phe | Ile | Val | Gly | Phe | Ala | Val |     |
|     |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |
| GCT | TTA | CAA | GGG | GCT | TTA | CAA | TTA | CAA | GAC | ATG | GGC | GCG | CCT | TTA | ATG | 689 |
| Ala | Leu | Gln | Gly | Ala | Leu | Gln | Leu | Gln | Asp | Met | Gly | Ala | Pro | Leu | Met |     |
|     |     | 190 |     |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |
| TCG | GTG | GAA | ATG | ACG | GCT | AAA | CTC | GCT | TTA | AGA | GAA | ATC | GGC | CCT | TTT | 737 |
| Ser | Val | Glu | Met | Thr | Ala | Lys | Leu | Ala | Leu | Arg | Glu | Ile | Gly | Pro | Phe |     |
|     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |
| ATT | TTA | ACC | CTT | GTG | GTG | GCC | GGG | AGG | AGC | GCG | AGC | AGT | TTT | ACC | GCG | 785 |
| Ile | Leu | Thr | Leu | Val | Val | Ala | Gly | Arg | Ser | Ala | Ser | Ser | Phe | Thr | Ala |     |
|     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     |     |
| CAA | ATT | GGG | GTG | ATG | AAG | ATC | ACT | GAG | GAA | TTA | GAC | GCG | ATG | AAA | ACC | 833 |
| Gln | Ile | Gly | Val | Met | Lys | Ile | Thr | Glu | Glu | Leu | Asp | Ala | Met | Lys | Thr |     |

|                                                                   |  |     |  |     |  |     |      |
|-------------------------------------------------------------------|--|-----|--|-----|--|-----|------|
| 235                                                               |  | 240 |  | 245 |  | 250 |      |
| ATG GGC TTT AAC CCT TTT GAA TTT TTA GTG TTG CCT AGG GTG TTA GCC   |  |     |  |     |  |     | 881  |
| Met Gly Phe Asn Pro Phe Glu Phe Leu Val Leu Pro Arg Val Leu Ala   |  |     |  |     |  |     |      |
|                                                                   |  | 255 |  | 260 |  | 265 |      |
| TTA GTG ATT GTT TTG CCT TTA TTG GTG TTT ATT GCC GAT GCG TTC GCC   |  |     |  |     |  |     | 929  |
| Leu Val Ile Val Leu Pro Leu Leu Val Phe Ile Ala Asp Ala Phe Ala   |  |     |  |     |  |     |      |
|                                                                   |  | 270 |  | 275 |  | 280 |      |
| ATT CTT GGG GGC ATG TTT GCG ATT AAA TAC CAA TTG GAT TTA GGC TTC   |  |     |  |     |  |     | 977  |
| Ile Leu Gly Gly Met Phe Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe   |  |     |  |     |  |     |      |
|                                                                   |  | 285 |  | 290 |  | 295 |      |
| CCG AGC TAT ATT GAC AGA TTC CAT GAC ACA GTG GGT TGG AAC CAT TTT   |  |     |  |     |  |     | 1025 |
| Pro Ser Tyr Ile Asp Arg Phe His Asp Thr Val Gly Trp Asn His Phe   |  |     |  |     |  |     |      |
|                                                                   |  | 300 |  | 305 |  | 310 |      |
| TTG GTA GGG ATT GTC AAA GCC CCT TTT TGG GGG TTT GCG ATT GCG ATG   |  |     |  |     |  |     | 1073 |
| Leu Val Gly Ile Val Lys Ala Pro Phe Trp Gly Phe Ala Ile Ala Met   |  |     |  |     |  |     |      |
|                                                                   |  | 315 |  | 320 |  | 325 | 330  |
| GTA GGG TGC ATG CGC GGG TTT GAA GTC AAG GGG GAT ACT GAG AGC ATT   |  |     |  |     |  |     | 1121 |
| Val Gly Cys Met Arg Gly Phe Glu Val Lys Gly Asp Thr Glu Ser Ile   |  |     |  |     |  |     |      |
|                                                                   |  | 335 |  | 340 |  | 345 |      |
| GGG CGC TTG ACC ACT ATT AGC GTC GTG AAC GCT TTG TTT TGG ATC ATT   |  |     |  |     |  |     | 1169 |
| Gly Arg Leu Thr Thr Ile Ser Val Val Asn Ala Leu Phe Trp Ile Ile   |  |     |  |     |  |     |      |
|                                                                   |  | 350 |  | 355 |  | 360 |      |
| TTC TTA GAC GCT ATT TTT TCT ATC ATC TTT TCT AAG TTG AAC ATA TAATG |  |     |  |     |  |     | 1219 |
| Phe Leu Asp Ala Ile Phe Ser Ile Ile Phe Ser Lys Leu Asn Ile       |  |     |  |     |  |     |      |
|                                                                   |  | 365 |  | 370 |  | 375 |      |
| AACGCTACTA ACAATCAAGT CTTAATTGAA GTGAAGGATC TCCATAGCGC            |  |     |  |     |  |     | 1269 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Glu | Lys | Gln | Lys | Phe | Leu | Glu | Met | Arg | Lys | Asp | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ser | Val | Leu | Ile | Leu | Arg | Gly | Asp | Trp | Asp | Phe | Lys | Thr | Ser | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Arg | Leu | Asp | Glu | Leu | Lys | Lys | Asn | Leu | Leu | Asp | His | Gln | Gly | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Lys | Met | Asp | Phe | Ser | Gly | Cys | Gln | Lys | Val | Asp | Phe | Val | Phe | Gly |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Met | Phe | Leu | Phe | Asp | Leu | Val | Lys | Glu | Arg | Ser | Leu | Asn | Ile | Glu | Leu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Asn | Val | Ser | Glu | Asn | Asn | Ala | Cys | Ala | Leu | Lys | Val | Val | Lys | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Leu | Glu | Lys | Glu | Glu | Asp | Leu | Glu | Ser | Lys | Lys | Ala | Gly | Lys | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Glu | Leu | Leu | Ile | Thr | Lys | Leu | Gly | Lys | Ser | Ile | Val | Glu | Thr | Tyr |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Asn | Thr | Phe | Leu | Asn | Ala | Phe | Asn | Phe | Cys | Gly | Met | Ile | Leu | Phe | Tyr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Phe | Ile | Lys | Ser | Val | Phe | Asn | Pro | Lys | Arg | Phe | Cys | Ile | Thr | Pro | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Tyr | His | Ile | Asn | Glu | Ser | Gly | Phe | Lys | Val | Leu | Pro | Val | Ser | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Thr | Val | Phe | Ile | Val | Gly | Phe | Ala | Val | Ala | Leu | Gln | Gly | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Leu | Gln | Asp | Met | Gly | Ala | Pro | Leu | Met | Ser | Val | Glu | Met | Thr | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Leu | Ala | Leu | Arg | Glu | Ile | Gly | Pro | Phe | Ile | Leu | Thr | Leu | Val | Val |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Gly | Arg | Ser | Ala | Ser | Ser | Phe | Thr | Ala | Gln | Ile | Gly | Val | Met | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Thr | Glu | Glu | Leu | Asp | Ala | Met | Lys | Thr | Met | Gly | Phe | Asn | Pro | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Phe | Leu | Val | Leu | Pro | Arg | Val | Leu | Ala | Leu | Val | Ile | Val | Leu | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Val | Phe | Ile | Ala | Asp | Ala | Phe | Ala | Ile | Leu | Gly | Gly | Met | Phe |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Ile | Lys | Tyr | Gln | Leu | Asp | Leu | Gly | Phe | Pro | Ser | Tyr | Ile | Asp | Arg |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | His | Asp | Thr | Val | Gly | Trp | Asn | His | Phe | Leu | Val | Gly | Ile | Val | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Pro | Phe | Trp | Gly | Phe | Ala | Ile | Ala | Met | Val | Gly | Cys | Met | Arg | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Glu | Val | Lys | Gly | Asp | Thr | Glu | Ser | Ile | Gly | Arg | Leu | Thr | Thr | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Val | Val | Asn | Ala | Leu | Phe | Trp | Ile | Ile | Phe | Leu | Asp | Ala | Ile | Phe |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Ile | Ile | Phe | Ser | Lys | Leu | Asn | Ile |     |     |     |     |     |     |     |
|     |     |     | 370 |     |     |     | 375 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...503
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CACAAGAGAA AATTTGCAAG CGTTTTTACA ACAAATAAG ATAAATTAGG GAGAGTGGT 59  
  
 ATG GGA TTT TTG AAT GGG TAT TTT TTA TGG GTT AAG GCT TTC CAT GTG 107  
 Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val  
 1 5 10 15  
  
 ATA GCG GTC ATT TCG TGG ATG GCA GCG TTG TTT TAT TTG CCG CGC CTT 155  
 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu  
 20 25 30  
  
 TTT GTC TAT CAT GCA GAA AAC GCG CAT AAA AAA GAG TTT GTA GGA GTG 203  
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val  
 35 40 45  
  
 GTT CAA ATC CAA GAA AAA AAG CTT TAT TCC TTT ATC GCT TCA CCG GCT 251  
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala  
 50 55 60  
  
 ATG GGT TTT ACG CTT ATT ACA GGG ATT TTA ATG CTG TTG ATA GAG CCT 299  
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro  
 65 70 75 80  
  
 ACG CTC TTT AAA AGT GGG GGT TGG TTG CAT GCT AAA TTG GCT TTA GTG 347  
 Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val  
 85 90 95  
  
 GTT TTA CTT TTA GCC TAT CAT TTT TAT TGC AAA AAA TGC ATG CGC GAG 395  
 Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu  
 100 105 110  
  
 CTG GAA AAA GAC CCC ACA AGG AGA AAC GCA AGG TTT TAT CGC GTG TTT 443  
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe  
 115 120 125  
  
 AAT GAG GCG CCA ACG ATT TTA ATG ATC CTC ATT GTG ATT TTA GTG GTT 491  
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val  
 130 135 140  
  
 GTC AAG CCT TTT TAAAGACAAG CCATGAAAAA AGAAAAGTCA TGAAAAAAGA AAAGCA 549  
 Val Lys Pro Phe  
 145  
  
 TCTCAAGC 557

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:





| 55                                                                                                                                                    | 60 | 65 |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|-----|
| GAA TAC AAC GCT AAA AAG CAA AAT ATC TTG CTT AAA GAT ATT AAA TCC<br>Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp Ile Lys Ser<br>70 75 80        |    |    | 298 |
| AAT TTA GAA GGG ATC AGT TTT GAG CTT TTA GAT GAA GAT GAA GCG AAA<br>Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp Glu Ala Lys<br>85 90 95        |    |    | 346 |
| AAA TTA GAC GCG CTT TTA TTG GAA TTG CAA GGC CAT AGC CAG TTT GAA<br>Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser Gln Phe Glu<br>100 105 110 115 |    |    | 394 |
| ATC AAA AAG GAA GCG GGG TTT TAT AGC GTG AAT CTC ACC CCT TTA GAG<br>Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr Pro Leu Glu<br>120 125 130     |    |    | 442 |
| CAA GAA GAA TTG CGT AAA AAC ACG ATT TTG CAA GTG ATA GGG ATC ATT<br>Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile Gly Ile Ile<br>135 140 145     |    |    | 490 |
| CGT AAC CGC TTG GAT CAA TTT GGT TTG GCA GAG CCT GTA GTC ATT CAG<br>Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val Val Ile Gln<br>150 155 160     |    |    | 538 |
| CAA GGT AAA GAA GAA ATT TCG GTG CAA TTG CCT GGC ATT AAG ACT TTA<br>Gln Gly Lys Glu Glu Ile Ser Val Gln Leu Pro Gly Ile Lys Thr Leu<br>165 170 175     |    |    | 586 |
| GAA GAA GAA CGG CGC GCT AAA GAC TTG ATT TCA AGA TCC GCT CAT TTG<br>Glu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Arg Ser Ala His Leu<br>180 185 190 195 |    |    | 634 |
| CAG ATG ATG GCG GTG GAT GAA GAA CAC AAT AAA GAT GCG ATG AAA ATG<br>Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala Met Lys Met<br>200 205 210     |    |    | 682 |
| ACG GAT TTA GAG GCT CAA AAA TTA GGC AGC GTG TTG TTG TCT GAT GTG<br>Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu Ser Asp Val<br>215 220 225     |    |    | 730 |
| GAA ATG GGG GGT AAA ATC TTG CTC AAA GCG ATC CCC ATT TTA GAT GGC<br>Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile Leu Asp Gly<br>230 235 240     |    |    | 778 |
| GAA ATG CTT ACA GAT GCG AAA GTG GTG TAT GAC CAA AAC AAC CAG CCG<br>Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn Asn Gln Pro<br>245 250 255     |    |    | 826 |
| GTG GTG AGC TTC ACG CTG GAT GCG CAA GGG GCT AAG ATT TTT GGG GAT<br>Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile Phe Gly Asp<br>260 265 270 275 |    |    | 874 |
| TTC TCA GGT GCG AAT GTG GGC AAA CGC ATG GCG ATT GTT TTA GAC AAT<br>Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val Leu Asp Asn<br>280 285 290     |    |    | 922 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AAG GTC TAT TCA GCC CCG GTG ATT AGG GAG CGT ATC GGT GGG GGG AGC   | 970  |
| Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly Gly Gly Ser   |      |
| 295 300 305                                                       |      |
| GGG CAG ATT AGC GGG AAT TTT AGC GTG GCT CAA GCG AGC GAT TTA GCG   | 1018 |
| Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser Asp Leu Ala   |      |
| 310 315 320                                                       |      |
| ATC GCT TTA AGG AGT GGG GCG ATG AGC GCT CCC ATT CAG GTT TTA GAA   | 1066 |
| Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln Val Leu Glu   |      |
| 325 330 335                                                       |      |
| AAA AGA ATT ATA GGC CCA AGT TTA GGG AAA GAC AGC GTT AAA ACT TCC   | 1114 |
| Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val Lys Thr Ser   |      |
| 340 345 350 355                                                   |      |
| ATT ATC GCT CTA GTT GGG GGC TTT ATT TTA GTG ATG GGC TTT ATG GTG   | 1162 |
| Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly Phe Met Val   |      |
| 360 365 370                                                       |      |
| CTT TAT TAC TCT ATG GCG GGG GTG ATC GCT TGT TTG GCG TTA GTG GTC   | 1210 |
| Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala Leu Val Val   |      |
| 375 380 385                                                       |      |
| AAT CTT TTT TTG ATT GTG GCG GTC ATG GCG ATT TTT GGA GCG ACG CTG   | 1258 |
| Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly Ala Thr Leu   |      |
| 390 395 400                                                       |      |
| ACT TTA CCG GGA ATG GCG GGG ATT GTT TTA ACC GTG GGG ATT GCC GTG   | 1306 |
| Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly Ile Ala Val   |      |
| 405 410 415                                                       |      |
| GAT GCT AAT ATC ATC ATC AAC GAG CGC ATT AGA GAA GTC TTA AGA GAG   | 1354 |
| Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val Leu Arg Glu   |      |
| 420 425 430 435                                                   |      |
| AAT GAG GGC ATC GCT AAA GCG ATC CAT TTA GGC TAT ATC AAT GCG AGC   | 1402 |
| Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile Asn Ala Ser   |      |
| 440 445 450                                                       |      |
| CGG GCG ATT TTT GAT TCT AAT ATC ACT TCT TTG ATC GCT TCA GTG TTA   | 1450 |
| Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala Ser Val Leu   |      |
| 455 460 465                                                       |      |
| TTA TAC GCT TAT GGC ACA GGA GCG ATT AAA GGC TTT GCC CTA ACT ACA   | 1498 |
| Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala Leu Thr Thr   |      |
| 470 475 480                                                       |      |
| GGC ATT GGG ATT TTA GCC TCT ATT ATC ACC GCT ATT GTT GGC ACG CAA   | 1546 |
| Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val Gly Thr Gln   |      |
| 485 490 495                                                       |      |
| GGG ATT TAT CAA GCC CTT TTA CCT AAA CTC ACT CAA ACA AAA AGC CTT   | 1594 |
| Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr Lys Ser Leu   |      |
| 500 505 510 515                                                   |      |
| TAC TTT TGG TTT GGC GTG AAT AAA AGA GCT TAGGAGGTTT TATGGAATTA TTC | 1647 |
| Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala                           |      |

AAACGAACTA GAATCTTAAG CTTC

1671

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Phe | Asn | Ala | Arg | Leu | Ile | Val | Phe | Ile | Gly | Ala | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gly | Val | Gly | Phe | Ser | Val | Pro | Ser | Leu | Leu | Glu | Thr | Lys | Gly | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Thr | Leu | Gly | Leu | Asp | Leu | Arg | Gly | Gly | Leu | Asn | Met | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Val | Gln | Thr | Asp | Glu | Ala | Leu | Lys | Asn | Lys | Tyr | Leu | Ser | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ala | Leu | Glu | Tyr | Asn | Ala | Lys | Lys | Gln | Asn | Ile | Leu | Leu | Lys | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ile | Lys | Ser | Asn | Leu | Glu | Gly | Ile | Ser | Phe | Glu | Leu | Leu | Asp | Glu | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Ala | Lys | Lys | Leu | Asp | Ala | Leu | Leu | Glu | Leu | Gln | Gly | His | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gln | Phe | Glu | Ile | Lys | Lys | Glu | Ala | Gly | Phe | Tyr | Ser | Val | Asn | Leu | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Glu | Gln | Glu | Glu | Leu | Arg | Lys | Asn | Thr | Ile | Leu | Gln | Val | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ile | Ile | Arg | Asn | Arg | Leu | Asp | Gln | Phe | Gly | Leu | Ala | Glu | Pro | Val |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Val | Ile | Gln | Gln | Gly | Lys | Glu | Glu | Ile | Ser | Val | Gln | Leu | Pro | Gly | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Lys | Thr | Leu | Glu | Glu | Arg | Arg | Ala | Lys | Asp | Leu | Ile | Ser | Arg | Ser |     |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ala | His | Leu | Gln | Met | Met | Ala | Val | Asp | Glu | Glu | His | Asn | Lys | Asp | Ala |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Met | Lys | Met | Thr | Asp | Leu | Glu | Ala | Gln | Lys | Leu | Gly | Ser | Val | Leu | Leu |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Ser | Asp | Val | Glu | Met | Gly | Gly | Lys | Ile | Leu | Leu | Lys | Ala | Ile | Pro | Ile |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Asp | Gly | Glu | Met | Leu | Thr | Asp | Ala | Lys | Val | Val | Tyr | Asp | Gln | Asn |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asn | Gln | Pro | Val | Val | Ser | Phe | Thr | Leu | Asp | Ala | Gln | Gly | Ala | Lys | Ile |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Phe | Gly | Asp | Phe | Ser | Gly | Ala | Asn | Val | Gly | Lys | Arg | Met | Ala | Ile | Val |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Leu | Asp | Asn | Lys | Val | Tyr | Ser | Ala | Pro | Val | Ile | Arg | Glu | Arg | Ile | Gly |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Gly | Gly | Ser | Gly | Gln | Ile | Ser | Gly | Asn | Phe | Ser | Val | Ala | Gln | Ala | Ser |
| 305 |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |     |
| Asp | Leu | Ala | Ile | Ala | Leu | Arg | Ser | Gly | Ala | Met | Ser | Ala | Pro | Ile | Gln |



|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTA GAA AAT TTT AAA GCG TTT CAA ATC AAC GAT AAA ATC CTT GAT CTG     | 252 |
| Leu Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu     |     |
| 50 55 60                                                            |     |
| TCC ATA GAG GGC AAA AAA GCC CTA CAA TAC GAT GAT CAT GAA ATC TTT     | 300 |
| Ser Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe     |     |
| 65 70 75                                                            |     |
| TTT GAT TCC AAA ATC AAG CGC TAT GAT GAA GAC ACC ATT GAA AGC GTT     | 348 |
| Phe Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val     |     |
| 80 85 90 95                                                         |     |
| GAG TCT CCT AAG GCC AAA CGG CAG CAG GAT TTG TAT TTC TTC CCT AAT     | 396 |
| Glu Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn     |     |
| 100 105 110                                                         |     |
| GGG GTT ACT TAT AAA AGA AGC GAT GAT TCC AGT TTT TGG AGT GAA ACA     | 444 |
| Gly Val Thr Tyr Lys Arg Ser Asp Ser Ser Phe Trp Ser Glu Thr         |     |
| 115 120 125                                                         |     |
| GGG ATT TAT AAC CAT AAG GAG CAA AAT TTT AAA GGC AAG GGC CGT TTC     | 492 |
| Gly Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe     |     |
| 130 135 140                                                         |     |
| ATT CTC ACT TCA AAG GAC AGC AAG ATT GAA GGG CTT GAC ATT TCT TAT     | 540 |
| Ile Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr     |     |
| 145 150 155                                                         |     |
| TCG CAT GCA TTA GCT ATT ATT GAA GCT CAA AGC ATT CAA GCG CAT TTA     | 588 |
| Ser His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu     |     |
| 160 165 170 175                                                     |     |
| TTC TTA GAT GAA ATC AAA CAA AGC CAA AAA GAA AAG AAA AAA TTC CCC     | 636 |
| Phe Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro     |     |
| 180 185 190                                                         |     |
| ACT TTC AAA GGA GGT TTT TAATGCGTTG GTGGTGT TTTT TTGGTGTGTT GTTTTGGT | 692 |
| Thr Phe Lys Gly Gly Phe                                             |     |
| 195                                                                 |     |
| ATTTTAAGCG TGAT                                                     | 706 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ser | Ser | Phe | Thr | Ser | Asn | Ser | Val | Leu | Asn | Phe | Phe | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Leu | Ser | Phe | Ile | Thr | Ile | Gly | Leu | Val | Phe | Phe | Phe | Leu | Arg | Ser |



|     |     |     |     |     |     |            |            |            |          |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|------------|------------|------------|----------|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Ser | Phe | Asp | Lys | Ala        | Asn        | Arg        | Thr      | Ser | Leu | Glu | Ser | Tyr | Arg |     |
|     |     |     | 50  |     |     |            |            | 55         |          |     |     |     | 60  |     |     |     |
| GGG | CCT | GGT | TTA | GAA | AAA | GGC        | CTA        | GAA        | ATG      | TTA | CAA | ACG | ATC | AAA | GAG | 363 |
| Gly | Pro | Gly | Leu | Glu | Lys | Gly        | Leu        | Glu        | Met      | Leu | Gln | Thr | Ile | Lys | Glu |     |
|     |     | 65  |     |     |     |            | 70         |            |          |     |     | 75  |     |     |     |     |
| GAA | TTT | GGT | TAT | AAA | ATC | TTA        | ACC        | GAT        | GTG      | CAT | GAG | AGT | TAT | CAA | GCA | 411 |
| Glu | Phe | Gly | Tyr | Lys | Ile | Leu        | Thr        | Asp        | Val      | His | Glu | Ser | Tyr | Gln | Ala |     |
|     | 80  |     |     |     |     | 85         |            |            |          |     | 90  |     |     |     |     |     |
| AGC | GTG | GCA | GCC | AAA | GTG | GCG        | GAT        | ATT        | TTA      | CAA | ATC | CCG | GCG | TTT | TTG | 459 |
| Ser | Val | Ala | Ala | Lys | Val | Ala        | Asp        | Ile        | Leu      | Gln | Ile | Pro | Ala | Phe | Leu |     |
| 95  |     |     |     |     | 100 |            |            |            |          | 105 |     |     |     |     | 110 |     |
| TGC | CGC | CAA | ACG | GAT | CTG | ATT        | GTA        | GAA        | GTG      | AGC | CAG | ACT | AAC | GCT | ATT | 507 |
| Cys | Arg | Gln | Thr | Asp | Leu | Ile        | Val        | Glu        | Val      | Ser | Gln | Thr | Asn | Ala | Ile |     |
|     |     |     |     | 115 |     |            |            | 120        |          |     |     |     |     | 125 |     |     |
| GTC | AAT | ATC | AAA | AAA | GGG | CAA        | TTC        | ATG        | AAC      | CCA | AAA | GAC | ATG | CAA | TAT | 555 |
| Val | Asn | Ile | Lys | Lys | Gly | Gln        | Phe        | Met        | Asn      | Pro | Lys | Asp | Met | Gln | Tyr |     |
|     |     |     | 130 |     |     |            |            | 135        |          |     |     |     | 140 |     |     |     |
| TCT | GTT | CTA | AAG | GCC | CTT | AAA        | ACG        | AGA        | GAT      | AAA | AGC | ATT | CAA | AGC | CCC | 603 |
| Ser | Val | Leu | Lys | Ala | Leu | Lys        | Thr        | Arg        | Asp      | Lys | Ser | Ile | Gln | Ser | Pro |     |
|     |     | 145 |     |     |     |            | 150        |            |          |     |     | 155 |     |     |     |     |
| ACT | TAT | GAA | ACA | GCG | TTA | AAA        | AAT        | GGC        | GTG      | TGG | CTG | TGT | GAA | AGG | GGG | 651 |
| Thr | Tyr | Glu | Thr | Ala | Leu | Lys        | Asn        | Gly        | Val      | Trp | Leu | Cys | Glu | Arg | Gly |     |
|     | 160 |     |     |     |     | 165        |            |            |          |     | 170 |     |     |     |     |     |
| AGC | AGC | TTT | GGG | TAT | GGG | AAT        | TTA        | GTG        | GTG      | GAT | ATG | CGC | TCT | TTA | AAA | 699 |
| Ser | Ser | Phe | Gly | Tyr | Gly | Asn        | Leu        | Val        | Val      | Asp | Met | Arg | Ser | Leu | Lys |     |
| 175 |     |     |     |     | 180 |            |            |            |          | 185 |     |     |     |     | 190 |     |
| ATC | ATG | CGA | GAA | TTT | GCC | CCT        | GTG        | ATT        | TTT      | GAC | GCT | ACC | CAT | AGC | GTG | 747 |
| Ile | Met | Arg | Glu | Phe | Ala | Pro        | Val        | Ile        | Phe      | Asp | Ala | Thr | His | Ser | Val |     |
|     |     |     |     | 195 |     |            |            |            | 200      |     |     |     |     | 205 |     |     |
| CAA | ATG | CCA | GGG | GGA | GCG | AAC        | GGG        | AAA        | AGT      | TCA | GGA | GAC | AGC | TCT | TTT | 795 |
| Gln | Met | Pro | Gly | Gly | Ala | Asn        | Gly        | Lys        | Ser      | Ser | Gly | Asp | Ser | Ser | Phe |     |
|     |     |     | 210 |     |     |            |            | 215        |          |     |     |     | 220 |     |     |     |
| GCC | CCT | ATT | TTA | GCG | AGA | GCT        | GCG        | GCG        | GCG      | GTG | GGG | ATT | GAT | GGG | TTG | 843 |
| Ala | Pro | Ile | Leu | Ala | Arg | Ala        | Ala        | Ala        | Ala      | Val | Gly | Ile | Asp | Gly | Leu |     |
|     |     | 225 |     |     |     |            | 230        |            |          |     |     | 235 |     |     |     |     |
| TTT | GCT | GAA | ACG | CAT | GTT | GAT        | CCT        | AAA        | AAC      | GCC | CTA | AGC | GAT | GGA | GCA | 891 |
| Phe | Ala | Glu | Thr | His | Val | Asp        | Pro        | Lys        | Asn      | Ala | Leu | Ser | Asp | Gly | Ala |     |
|     | 240 |     |     |     |     | 245        |            |            |          |     | 250 |     |     |     |     |     |
| AAC | ATG | CTA | AAA | CCT | GAC | GAG        | CTA        | GAA        | CAA      | TTA | GTA | ACC | GAC | ATG | TTA | 939 |
| Asn | Met | Leu | Lys | Pro | Asp | Glu        | Leu        | Glu        | Gln      | Leu | Val | Thr | Asp | Met | Leu |     |
| 255 |     |     |     |     | 260 |            |            |            |          | 265 |     |     |     |     | 270 |     |
| AAA | ATC | CAA | AAT | TTA | TTT | TAAAGGAATT | TCATGCAAAT | CATAGAAGGG | AAATTGCA |     |     |     |     |     |     | 995 |
| Lys | Ile | Gln | Asn | Leu | Phe |            |            |            |          |     |     |     |     |     |     |     |
|     |     |     |     | 275 |     |            |            |            |          |     |     |     |     |     |     |     |

ATTACAAGGG AATGA

1010

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Thr | Ser | Lys | Thr | Lys | Thr | Pro | Lys | Ser | Val | Leu | Ile | Ala | Gly |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Cys | Val | Ile | Glu | Ser | Leu | Glu | Asn | Leu | Arg | Ser | Ile | Ala | Thr | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Gln | Pro | Leu | Ala | Asn | Asn | Glu | Arg | Leu | Asp | Phe | Tyr | Phe | Lys | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Phe | Asp | Lys | Ala | Asn | Arg | Thr | Ser | Leu | Glu | Ser | Tyr | Arg | Gly | Pro |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Leu | Glu | Lys | Gly | Leu | Glu | Met | Leu | Gln | Thr | Ile | Lys | Glu | Glu | Phe |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly | Tyr | Lys | Ile | Leu | Thr | Asp | Val | His | Glu | Ser | Tyr | Gln | Ala | Ser | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ala | Ala | Lys | Val | Ala | Asp | Ile | Leu | Gln | Ile | Pro | Ala | Phe | Leu | Cys | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Thr | Asp | Leu | Ile | Val | Glu | Val | Ser | Gln | Thr | Asn | Ala | Ile | Val | Asn |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Ile | Lys | Lys | Gly | Gln | Phe | Met | Asn | Pro | Lys | Asp | Met | Gln | Tyr | Ser | Val |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Lys | Ala | Leu | Lys | Thr | Arg | Asp | Lys | Ser | Ile | Gln | Ser | Pro | Thr | Tyr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Glu | Thr | Ala | Leu | Lys | Asn | Gly | Val | Trp | Leu | Cys | Glu | Arg | Gly | Ser | Ser |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Phe | Gly | Tyr | Gly | Asn | Leu | Val | Val | Asp | Met | Arg | Ser | Leu | Lys | Ile | Met |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Arg | Glu | Phe | Ala | Pro | Val | Ile | Phe | Asp | Ala | Thr | His | Ser | Val | Gln | Met |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Pro | Gly | Gly | Ala | Asn | Gly | Lys | Ser | Ser | Gly | Asp | Ser | Ser | Phe | Ala | Pro |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |
| Ile | Leu | Ala | Arg | Ala | Ala | Ala | Ala | Val | Gly | Ile | Asp | Gly | Leu | Phe | Ala |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Glu | Thr | His | Val | Asp | Pro | Lys | Asn | Ala | Leu | Ser | Asp | Gly | Ala | Asn | Met |  |
|     |     |     | 245 |     |     |     |     |     |     | 250 |     |     |     | 255 |     |  |
| Leu | Lys | Pro | Asp | Glu | Leu | Glu | Gln | Leu | Val | Thr | Asp | Met | Leu | Lys | Ile |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |  |
| Gln | Asn | Leu | Phe |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single





(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 91...1329  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
ACCACCCCTT AATCTCAAAA AACCCCAATC ATAAAAAGCT TTATGCTACA ATGAAAGCTC 60
TTTAACACGA TAAAAGGGCG GTTTAATAGC ATG GCA CAA GAA AAA GCA GTT CCA 114
 Met Ala Gln Glu Lys Ala Val Pro
 1 5

AGA GAT CCT AAA AAA CTC AAT GCG TTT GAT TTG CGT TGG ATG GTG TCC 162
Arg Asp Pro Lys Lys Leu Asn Ala Phe Asp Leu Arg Trp Met Val Ser
 10 15 20

TTA TTT GGC ACG GCG GTG GGG GCT GGG ATT TTA TTT TTG CCT ATT AGA 210
Leu Phe Gly Thr Ala Val Gly Ala Gly Ile Leu Phe Leu Pro Ile Arg
 25 30 35 40

GCC GGT GGG CAT GGG GTA TGG GCT ATT GTG GTA ATG AGC GCG ATC ATT 258
Ala Gly Gly His Gly Val Trp Ala Ile Val Val Met Ser Ala Ile Ile
 45 50 55

TTC CCT TTA ACT TAT CTA GGG CAT AGA GCT TTA GCT TAT TTC ATA GGA 306
Phe Pro Leu Thr Tyr Leu Gly His Arg Ala Leu Ala Tyr Phe Ile Gly
 60 65 70

TCT AAA GAC AAA GAA GAC ATT ACC ATG GTC GTT CGC TCT CAT TTT GGC 354
Ser Lys Asp Lys Glu Asp Ile Thr Met Val Val Arg Ser His Phe Gly
 75 80 85

GCT CAA TGG GGT TTT CTT ATC ACT TTG CTT TAT TTC TTA GCG ATT TAT 402
Ala Gln Trp Gly Phe Leu Ile Thr Leu Leu Tyr Phe Leu Ala Ile Tyr
 90 95 100

CCT ATT TGC TTG GTT TAT GGG GTG GGT ATC ACT AAC GTG TTT GAT CAT 450
Pro Ile Cys Leu Val Tyr Gly Val Gly Ile Thr Asn Val Phe Asp His
 105 110 115 120

TTT TTC ACT AAC CAG TTG CAT TTA GCG CCT TTT CAT CGG GGA TTA TTG 498
Phe Phe Thr Asn Gln Leu His Leu Ala Pro Phe His Arg Gly Leu Leu
 125 130 135

GCT GTA GCG TTA GTT TCT TTA ATG ATG TTG GTG ATG GTT TTT AAC GCT 546
Ala Val Ala Leu Val Ser Leu Met Met Leu Val Met Val Phe Asn Ala
 140 145 150

ACG ATT GTT ACG CGC ATT TGT AAC GCT TTA GTG TAT CCT TTA TGC TTG 594
Thr Ile Val Thr Arg Ile Cys Asn Ala Leu Val Tyr Pro Leu Cys Leu
 155 160 165

ATT TTA TTG CTT TTT TCT TTG TAT CTT ATC CCT TAT TGG CAA GGC GCT 642
Ile Leu Leu Leu Phe Ser Leu Tyr Leu Ile Pro Tyr Trp Gln Gly Ala
 170 175 180
```



## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Glu | Lys | Ala | Val | Pro | Arg | Asp | Pro | Lys | Lys | Leu | Asn | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Asp | Leu | Arg | Trp | Met | Val | Ser | Leu | Phe | Gly | Thr | Ala | Val | Gly | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Leu | Phe | Leu | Pro | Ile | Arg | Ala | Gly | Gly | His | Gly | Val | Trp | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Val | Val | Met | Ser | Ala | Ile | Ile | Phe | Pro | Leu | Thr | Tyr | Leu | Gly | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ala | Leu | Ala | Tyr | Phe | Ile | Gly | Ser | Lys | Asp | Lys | Glu | Asp | Ile | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | Val | Val | Arg | Ser | His | Phe | Gly | Ala | Gln | Trp | Gly | Phe | Leu | Ile | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Tyr | Phe | Leu | Ala | Ile | Tyr | Pro | Ile | Cys | Leu | Val | Tyr | Gly | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ile | Thr | Asn | Val | Phe | Asp | His | Phe | Phe | Thr | Asn | Gln | Leu | His | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Phe | His | Arg | Gly | Leu | Leu | Ala | Val | Ala | Leu | Val | Ser | Leu | Met |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Leu | Val | Met | Val | Phe | Asn | Ala | Thr | Ile | Val | Thr | Arg | Ile | Cys | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Leu | Val | Tyr | Pro | Leu | Cys | Leu | Ile | Leu | Leu | Leu | Phe | Ser | Leu | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ile | Pro | Tyr | Trp | Gln | Gly | Ala | Asn | Leu | Phe | Val | Val | Pro | Ser | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Lys | Glu | Phe | Val | Leu | Ala | Ile | Trp | Leu | Thr | Leu | Pro | Val | Leu | Val | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Phe | Asp | His | Ser | Pro | Ile | Ile | Ser | Thr | Phe | Thr | Gln | Asn | Val | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Glu | Tyr | Gly | Val | Phe | Lys | Glu | Tyr | Lys | Leu | Asn | Gln | Ile | Glu | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Thr | Ser | Leu | Met | Leu | Leu | Gly | Phe | Val | Met | Phe | Phe | Val | Phe | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Cys | Val | Met | Cys | Leu | Asn | Ala | Asp | Asp | Phe | Val | Lys | Ala | Arg | Glu | Gln |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Ile | Pro | Ile | Leu | Ser | Tyr | Leu | Ala | Asn | Thr | Leu | Asn | Asn | Pro | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Asn | Tyr | Ala | Gly | Pro | Val | Val | Ala | Phe | Leu | Ala | Ile | Phe | Ser | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Phe | Gly | His | Tyr | Tyr | Gly | Ala | Lys | Glu | Gly | Leu | Glu | Gly | Ile | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ile | Gln | Ser | Leu | Lys | Leu | Lys | Lys | Ala | Ser | Lys | Pro | Leu | Ser | Val | Ser |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 63...827  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

135









TTGAATTTAT AAAATAATTG TGT

1160

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Lys | Thr | Asn | Asn | Ala | Arg | Met | Pro | Lys | Ile | Gly | Ile | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ile | Lys | Thr | Gly | Arg | Ile | Arg | Tyr | Arg | Tyr | Ile | Thr | Leu | Ile | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Arg | His | Ser | Phe | Tyr | Tyr | Cys | Asn | Leu | Leu | Leu | Leu | Ser | Arg | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Val | Thr | Leu | Thr | Ala | His | Asn | Glu | Phe | Cys | Pro | Thr | His | Arg | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Ala | Pro | Asn | Phe | Arg | Val | Val | Ser | Ile | Ile | Ala | Asn | Asn | Gln | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Phe | Gln | Ala | Leu | Arg | Pro | Ile | Asn | His | Ile | Ser | Phe | Ile | Pro | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Pro | Thr | Phe | Asn | Arg | Ala | Pro | Arg | Gln | Asp | Phe | Ala | Val | Phe | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Asp | Leu | Thr | Leu | Ile | Ile | Asp | Lys | Asn | Gln | Ser | Val | Ile | Gly | Ile |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Phe | Gly | Leu | Leu | Val | Phe | Phe | Pro | Cys | Gln | Arg | Glu | His | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Leu | Val | Phe | Leu | Thr | Ser | Phe | Ser | Lys | Asp | Arg | Gly | Phe | Phe | Ser |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Arg | Asn | Ala | Cys | Gly | Cys | Ile | Lys | His | Phe | Leu | Ser | Val | Ile | His | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Met | Arg | Ala | Val | Phe | Arg | Glu | Asn | Asn | Gln | Ile | Gln | Pro | Arg | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Leu | Phe | Asp | Pro | Thr | Asn | His | Leu | Ser | Asp | Ile | Ala | Thr | Ile | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | His | Leu | Ile | Leu | Ser | Val | Glu | Ser | Arg | His | Leu | Ile | Ile | Asn | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Arg | Tyr | Thr | His | Ser | Ile | Trp | Ala | Ala | Thr | Asn | Ile | Ser | Met | Ser | His |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Met | Phe | Leu | Val | Phe |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...1611
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGCTTTTATAA AAAATGTTAG AAACCCTTAC AAAACAAGCT AATATATTCT ATTCAATTTG | 60  |
| CCTCAAGGAC AAACAAAC ATG AAA AAA CTT CTT TAT ACC ATA CTC GCG CTT    | 111 |
| Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu                        |     |
| 1 5 10                                                             |     |
| CTT TTA ATC GGC CTT TTA ACA ATC TAT CTC ATC CTT TTT ACA GAA TGG    | 159 |
| Leu Leu Ile Gly Leu Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp    |     |
| 15 20 25                                                           |     |
| GGG AAT AAG ATC ATC GCT TCG TAT ATA GAG AAA AAA ATC AAC CCG AAC    | 207 |
| Gly Asn Lys Ile Ile Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn    |     |
| 30 35 40                                                           |     |
| GAG CAC TAC TTG AGC GTT AAA ACC TTT AAA TTG AGA TTC AAC TCT TTG    | 255 |
| Glu His Tyr Leu Ser Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu    |     |
| 45 50 55                                                           |     |
| GAT TTT AAA GCT CAA GCC AAC GAT GAT TCC ACG CTC ATT CTT AAG GGG    | 303 |
| Asp Phe Lys Ala Gln Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly    |     |
| 60 65 70 75                                                        |     |
| GAT TTT TCA CTT TTA AAG CAA AGC GTA AAT TTG AAT TAC CAT ATA GAT    | 351 |
| Asp Phe Ser Leu Leu Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp    |     |
| 80 85 90                                                           |     |
| ATT AAA GAT TTA CGC TCT TTC AAA GAA TGG ATA CCC TAC CCT TTA AGG    | 399 |
| Ile Lys Asp Leu Arg Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg    |     |
| 95 100 105                                                         |     |
| GGG GCT GTT ATC ACT TCT GGG AAT ATT AAA GGG CAT AGA AAA GCC CTT    | 447 |
| Gly Ala Val Ile Thr Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu    |     |
| 110 115 120                                                        |     |
| ATG ATT CAA GGC GTC TCT AAT GTG GCT CAA TCC CAC ACT GCC TAC AAT    | 495 |
| Met Ile Gln Gly Val Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn    |     |
| 125 130 135                                                        |     |
| GCC CTT TTA GAT GAT TTC AAG CTT TCT CGC TTA AAT TTG AAC GCA CAA    | 543 |
| Ala Leu Leu Asp Asp Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln    |     |
| 140 145 150 155                                                    |     |
| GAC GCC AAT TTA GAA GAT TTG CTT TAT TTA ATC AAT CGC CCC GCT TAT    | 591 |
| Asp Ala Asn Leu Glu Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr    |     |
| 160 165 170                                                        |     |
| GCG AAC GCA AAA GTG TCC TTA CAG GCG GAT TTT AAC TCT CTA AAG CCT    | 639 |
| Ala Asn Ala Lys Val Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro    |     |
| 175 180 185                                                        |     |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| TTA GAG GGG CAT TTG ATC CTA ACA GCT AAT AAC GCT TTA ATC AAT AAC | 687  |
| Leu Glu Gly His Leu Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn |      |
| 190 195 200                                                     |      |
| GCC CTA ATC AAT CAA ATT TTT CAT TTA AAC CTT AAA GAC ACG CTT GTT | 735  |
| Ala Leu Ile Asn Gln Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val |      |
| 205 210 215                                                     |      |
| TTC AGC CTC TCG CAT TCA AGC GAC TTT AAA GGA AAC AAA GCC ATC AGC | 783  |
| Phe Ser Leu Ser His Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser |      |
| 220 225 230 235                                                 |      |
| GAT ACC ACC CTG ACT AGC CCT TTA GCC AAT TTC AAA GCC CTA AAA AGC | 831  |
| Asp Thr Thr Leu Thr Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser |      |
| 240 245 250                                                     |      |
| GAA TAC CTT TTC TCT ATT TTA AAA CTC AAC GCC CCC TAC ACT TTA GAA | 879  |
| Glu Tyr Leu Phe Ser Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu |      |
| 255 260 265                                                     |      |
| ATC CCC AAT CTA GCC AAA CTC TAT AAC ATT ACC AAC CAC CCC TTA AAA | 927  |
| Ile Pro Asn Leu Ala Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys |      |
| 270 275 280                                                     |      |
| GGG AGC TTG ACT TTA AAA GGC GCT ATA GAA CAA AGC CCC AAA CTT TTA | 975  |
| Gly Ser Leu Thr Leu Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu |      |
| 285 290 295                                                     |      |
| AAA GTC AGC GGC CAT TCA AAT TTA CTA GAC GGC GCG CTG GAT TTC ACG | 1023 |
| Lys Val Ser Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr |      |
| 300 305 310 315                                                 |      |
| CTT TTA AAT AAA GAT TTG AAA GGG CGT TTT TCC AAT ATT TCC ACT TTA | 1071 |
| Leu Leu Asn Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu |      |
| 320 325 330                                                     |      |
| AAA GCT TTA GAT TTA TTC CAT TAC CCT AAG TTT TTC CAA TCC GTT GCA | 1119 |
| Lys Ala Leu Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala |      |
| 335 340 345                                                     |      |
| GAC GCT AAT TTG GAT TAT GAT CTT ATC GCT AAG CAA GGC GTA TTG AAA | 1167 |
| Asp Ala Asn Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys |      |
| 350 355 360                                                     |      |
| GCC CGC CTA AAA AAC GCA AGA TTC CTC AAA AAT GCA TTC AGC GAT TTT | 1215 |
| Ala Arg Leu Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe |      |
| 365 370 375                                                     |      |
| CTC TAC TCC ATT TCT AAA TTT GAT ATT ACA AAA GAA ATT TAT AAC GAT | 1263 |
| Leu Tyr Ser Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp |      |
| 380 385 390 395                                                 |      |
| GCC AAT CTG GTA AGC CAA ATC AAC CAG CAA CGC CTG CTC TCT GAT CTG | 1311 |
| Ala Asn Leu Val Ser Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu |      |
| 400 405 410                                                     |      |
| AGT TTA AAA AGC CCC AAA ACC CAA TTG AAA ATC CAT AAC GGT TTG TTG | 1359 |
| Ser Leu Lys Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu |      |



|                     |                     |                         |  |     |
|---------------------|---------------------|-------------------------|--|-----|
| 130                 |                     | 135                     |  | 140 |
| Phe Lys Leu Ser Arg | Leu Asn Leu Asn Ala | Gln Asp Ala Asn Leu Glu |  |     |
| 145                 | 150                 | 155                     |  | 160 |
| Asp Leu Leu Tyr Leu | Ile Asn Arg Pro Ala | Tyr Ala Asn Ala Lys Val |  |     |
|                     | 165                 | 170                     |  | 175 |
| Ser Leu Gln Ala Asp | Phe Asn Ser Leu Lys | Pro Leu Glu Gly His Leu |  |     |
|                     | 180                 | 185                     |  | 190 |
| Ile Leu Thr Ala Asn | Asn Ala Leu Ile Asn | Asn Ala Leu Ile Asn Gln |  |     |
|                     | 195                 | 200                     |  | 205 |
| Ile Phe His Leu Asn | Leu Lys Asp Thr Leu | Val Phe Ser Leu Ser His |  |     |
|                     | 210                 | 215                     |  | 220 |
| Ser Ser Asp Phe Lys | Gly Asn Lys Ala Ile | Ser Asp Thr Thr Leu Thr |  |     |
| 225                 | 230                 | 235                     |  | 240 |
| Ser Pro Leu Ala Asn | Phe Lys Ala Leu Lys | Ser Glu Tyr Leu Phe Ser |  |     |
|                     | 245                 | 250                     |  | 255 |
| Ile Leu Lys Leu Asn | Ala Pro Tyr Thr Leu | Glu Ile Pro Asn Leu Ala |  |     |
|                     | 260                 | 265                     |  | 270 |
| Lys Leu Tyr Asn Ile | Thr Asn His Pro Leu | Lys Gly Ser Leu Thr Leu |  |     |
|                     | 275                 | 280                     |  | 285 |
| Lys Gly Ala Ile Glu | Gln Ser Pro Lys Leu | Lys Val Ser Gly His     |  |     |
|                     | 290                 | 295                     |  | 300 |
| Ser Asn Leu Leu Asp | Gly Ala Leu Asp Phe | Thr Leu Leu Asn Lys Asp |  |     |
| 305                 | 310                 | 315                     |  | 320 |
| Leu Lys Gly Arg Phe | Ser Asn Ile Ser Thr | Leu Lys Ala Leu Asp Leu |  |     |
|                     | 325                 | 330                     |  | 335 |
| Phe His Tyr Pro Lys | Phe Phe Gln Ser Val | Ala Asp Ala Asn Leu Asp |  |     |
|                     | 340                 | 345                     |  | 350 |
| Tyr Asp Leu Ile Ala | Lys Gln Gly Val Leu | Lys Ala Arg Leu Lys Asn |  |     |
|                     | 355                 | 360                     |  | 365 |
| Ala Arg Phe Leu Lys | Asn Ala Phe Ser Asp | Phe Leu Tyr Ser Ile Ser |  |     |
|                     | 370                 | 375                     |  | 380 |
| Lys Phe Asp Ile Thr | Lys Glu Ile Tyr Asn | Asp Ala Asn Leu Val Ser |  |     |
| 385                 | 390                 | 395                     |  | 400 |
| Gln Ile Asn Gln Gln | Arg Leu Leu Ser Asp | Leu Ser Leu Lys Ser Pro |  |     |
|                     | 405                 | 410                     |  | 415 |
| Lys Thr Gln Leu Lys | Ile His Asn Gly Leu | Leu Asp Leu Asn Thr Lys |  |     |
|                     | 420                 | 425                     |  | 430 |
| Gln Met Asn Met Leu | Met Asp Ala Glu Ile | Leu Lys Phe Ile Phe Lys |  |     |
|                     | 435                 | 440                     |  | 445 |
| Met Lys Leu Gln Gly | Asn Met His Gln Pro | Lys Phe Ser Leu Ile Leu |  |     |
|                     | 450                 | 455                     |  | 460 |
| Asn Glu Lys Ala Ile | Gln Gln Asn Leu Gln | Gln Gly Leu Lys Glu Ile |  |     |
| 465                 | 470                 | 475                     |  | 480 |
| Leu Lys Asn Asp Thr | Leu Lys Lys Gly Leu | Asp His Leu Leu Lys Asp |  |     |
|                     | 485                 | 490                     |  | 495 |
| Asp Lys Leu Lys Glu | Lys Leu Glu Lys Gly | Leu Lys Gly Leu Phe     |  |     |
|                     | 500                 | 505                     |  | 510 |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 53...352  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTAATTCTGT CTATTACACC AACAAATCAAT CTCAAAACAA AGGACATGAAAG ATG AAA | 58  |
| Met Lys                                                           |     |
| 1                                                                 |     |
| ACA AAA CAT AAA GGA ATA AGA ATG TTT AAG CAA ATT CGT AGA ATG ATG   | 106 |
| Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg Met Met   |     |
| 5 10 15                                                           |     |
| AGT TTG GCA ATA TTA ATG CCT AGT TTT TTA TTG GCG GCA CCA GAT TAC   | 154 |
| Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro Asp Tyr   |     |
| 20 25 30                                                          |     |
| AAA CAA AAA TTC ACT CAA ATA TTG GAT TTC ATA AGC AAT GAC TTT ATC   | 202 |
| Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp Phe Ile   |     |
| 35 40 45 50                                                       |     |
| AAG GCT ATT GGT GGT CTA ATC ATT GTT GGG ACT TGC ATT TAC GCC TAT   | 250 |
| Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr Ala Tyr   |     |
| 55 60 65                                                          |     |
| AAA AAT TGG GAC AGG CTT GGA GAA ATT GGT TGG AAA TGC GTT GGG ATT   | 298 |
| Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val Gly Ile   |     |
| 70 75 80                                                          |     |
| ATC ATT ATA ACC GCT GCT ATT TCT AAT GCT AAA ACT TTA AGT CAA TGG   | 346 |
| Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser Gln Trp   |     |
| 85 90 95                                                          |     |
| TTA TTT TAGATGGCAT TGCATATTGT TTGTGTTGAA AGTATCAACA TTAGA         | 397 |
| Leu Phe                                                           |     |
| 100                                                               |     |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

|                                                                 |
|-----------------------------------------------------------------|
| Met Lys Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg |
| 1 5 10 15                                                       |
| Met Met Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro |
| 20 25 30                                                        |

Asp Tyr Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp  
 35 40 45  
 Phe Ile Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr  
 50 55 60  
 Ala Tyr Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val  
 65 70 75 80  
 Gly Ile Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser  
 85 90 95  
 Gln Trp Leu Phe  
 100

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...318
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CTTGCCAATC CCTTCAATAT CCACCGAATT GATGCCATGC TCAATTAAAA A ATG ATC   | 57  |
| Met Ile                                                            |     |
| 1                                                                  |     |
| CAA AGC GAC GCT GTC TTT AAG ATA AAT TTC TGT CTT GCC CTT CTT GTA    | 105 |
| Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu Leu Val    |     |
| 5 10 15                                                            |     |
| TTT GTA AAG AGG GGC TTG AGC GAT ATA AAC ATG CCC TTG TTC AAT CAG    | 153 |
| Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe Asn Gln    |     |
| 20 25 30                                                           |     |
| CGG GCG CAA ATA ACG ATA GAA AAA AGT CAT CAG CAA GGT TTG GAT ATG    | 201 |
| Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu Asp Met    |     |
| 35 40 45 50                                                        |     |
| GCT CCC ATC CAC ATC AGC ATC GGT CAT GAT AAT GAT TTT ATG ATA GCG    | 249 |
| Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met Ile Ala    |     |
| 55 60 65                                                           |     |
| CAA TCT TTC TAT ATC AAA ACT CTC TTG AAT GCC GCA CCC AAA AGC CGT    | 297 |
| Gln Ser Phe Tyr Ile Lys Thr Leu Leu Asn Ala Ala Pro Lys Ser Arg    |     |
| 70 75 80                                                           |     |
| GAT CAT GTT TTT AAT TTC TTC TGATTTTAGG ATTTTGTGATA AATGGCTTTT TTCC | 352 |
| Asp His Val Phe Asn Phe Phe                                        |     |
| 85                                                                 |     |

ACATTTAAAA TCTTA

367

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ile | Gln | Ser | Asp | Ala | Val | Phe | Lys | Ile | Asn | Phe | Cys | Leu | Ala | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Val | Phe | Val | Lys | Arg | Gly | Leu | Ser | Asp | Ile | Asn | Met | Pro | Leu | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Gln | Arg | Ala | Gln | Ile | Thr | Ile | Glu | Lys | Ser | His | Gln | Gln | Gly | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Met | Ala | Pro | Ile | His | Ile | Ser | Ile | Gly | His | Asp | Asn | Asp | Phe | Met |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Ile | Ala | Gln | Ser | Phe | Tyr | Ile | Lys | Thr | Leu | Leu | Asn | Ala | Ala | Pro | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Ser | Arg | Asp | His | Val | Phe | Asn | Phe | Phe |     |     |     |     |     |     |     |  |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|            |            |            |            |            |     |     |     |     |
|------------|------------|------------|------------|------------|-----|-----|-----|-----|
| TAAAAAGCAC | TTTAGAGAGA | TTTACGAAAG | TGTTTTGAAG | CGAAGAATGT | CTG | ATG |     | 56  |
|            |            |            |            |            | Met |     |     |     |
|            |            |            |            |            | 1   |     |     |     |
| ATT        | ATC        | TTT        | GGA        | AAA        | GAT | TAC | CTA |     |
| Ile        | Ile        | Phe        | Gly        | Lys        | Asp | Tyr | Leu |     |
|            |            | 5          |            |            |     |     | 10  |     |
| ACA        | GAC        | TTG        | CAA        | AAT        | AGC | GCT |     | 104 |
| Thr        | Asp        | Leu        | Gln        | Asn        | Ser | Ala |     |     |
|            |            |            | 15         |            |     |     |     |     |
| AAA        | GAT        | ATT        | CTT        | CTC        | ATC | GCT | TCG |     |
| Lys        | Asp        | Ile        | Leu        | Leu        | Ile | Ala | Ser |     |
|            |            | 20         |            |            |     | 25  |     |     |
| CAA        | ATT        | CTC        | AAA        | GAA        | AGA | CTT | TTT | 152 |
| Gln        | Ile        | Leu        | Lys        | Glu        | Arg | Leu | Phe |     |
|            |            |            | 30         |            |     |     |     |     |



GCC CAC AAA AAT GAG ATT TTC TTT TGC CCT AGA AAT AGC TAC ATT CAA 200  
 Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile Gln  
 35 40 45

GCG TTT AGA ATC TAT CAA GAA AGA AAG ATT ACC ATA AGT TTT CAC GGT 248  
 Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His Gly  
 50 55 60 65

GGA ATA AAT AAT AAT ATC TGC CTT CTC GCC TTG AAA GGC ATC CAC AGT 296  
 Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His Ser  
 70 75 80

GTC TAT TTT GAG CTC ATC AAA ATT CTT GAA GCC GTA TTT TTC CAC TTC T 345  
 Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His Phe  
 85 90 95

GATCGCAAGC ATCTTTTTTTG GGCATTATAA GGTGTGATAA T 386

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser  
 1 5 10 15  
 Ala Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu  
 20 25 30  
 Phe Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile  
 35 40 45  
 Gln Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His  
 50 55 60  
 Gly Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His  
 65 70 75 80  
 Ser Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His  
 85 90 95  
 Phe

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 55...516  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|                                                                   |            |            |            |            |      |     |    |
|-------------------------------------------------------------------|------------|------------|------------|------------|------|-----|----|
| CGCGTTTGGG                                                        | TCTTCATTAA | AAATTCGTTG | CTCACCCCTG | GGTTATAAGC | TTGA | GCT | 57 |
|                                                                   |            |            |            |            |      | Ala |    |
|                                                                   |            |            |            |            |      | 1   |    |
| TCA GAA GTG GCC CCC TCA GAG GTT TTG TTG GAT TCT TCT TGC TTG TCT   | 105        |            |            |            |      |     |    |
| Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu Ser   |            |            |            |            |      |     |    |
| 5 10 15                                                           |            |            |            |            |      |     |    |
| TTT TCT TTG ACT ATA TCC TTA GTT GTT ACT TGT TTA GGA GCG CTT TTT   | 153        |            |            |            |      |     |    |
| Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu Phe   |            |            |            |            |      |     |    |
| 20 25 30                                                          |            |            |            |            |      |     |    |
| TCT TTA GCT TCC TCT TTA GCT TCT TCT TTT TTG GGC TCT TCT TTA GGC   | 201        |            |            |            |      |     |    |
| Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu Gly   |            |            |            |            |      |     |    |
| 35 40 45                                                          |            |            |            |            |      |     |    |
| TCT TCT TTT TTA ACC TCT TCA ACT TTA GGC TCA GGC TTA GGC TCG GGT   | 249        |            |            |            |      |     |    |
| Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser Gly   |            |            |            |            |      |     |    |
| 50 55 60 65                                                       |            |            |            |            |      |     |    |
| TTT GGT TCA GGT TTG GGT TCA GGC TTA GGT TTT GGT TTT GGC TTT GGC   | 297        |            |            |            |      |     |    |
| Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe Gly   |            |            |            |            |      |     |    |
| 70 75 80                                                          |            |            |            |            |      |     |    |
| TTG GGT TTA GGC TTA GGT TTA GGC TTT GTA ACC TCC TTT TTG GGT TCT   | 345        |            |            |            |      |     |    |
| Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly Ser   |            |            |            |            |      |     |    |
| 85 90 95                                                          |            |            |            |            |      |     |    |
| TCT TTT TTT GGC TCT TCT TTC TTG GGT TTT TCT TTA GGC TCT TCT TTG   | 393        |            |            |            |      |     |    |
| Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser Leu   |            |            |            |            |      |     |    |
| 100 105 110                                                       |            |            |            |            |      |     |    |
| GGT TTA GCC GAC TCA GCA TTA GTC TTT GTA TTG GAA TTA GTG TTG ATG   | 441        |            |            |            |      |     |    |
| Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu Met   |            |            |            |            |      |     |    |
| 115 120 125                                                       |            |            |            |            |      |     |    |
| CTG GCT AAA CTC ATG GTA ACC TTA GTG GTC CCG GCT TGC GCT AAA GGC   | 489        |            |            |            |      |     |    |
| Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys Gly   |            |            |            |            |      |     |    |
| 130 135 140 145                                                   |            |            |            |            |      |     |    |
| TCT GGG GCG TCT TCG CGC AGT AAA AAA TAGCCAAACC CTATAGCGTA TAGGGCA | 543        |            |            |            |      |     |    |
| Ser Gly Ala Ser Ser Arg Ser Lys Lys                               |            |            |            |            |      |     |    |
| 150                                                               |            |            |            |            |      |     |    |
| AAAGAGATTA AAAAGCTAAC ACTCGT                                      | 569        |            |            |            |      |     |    |

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Glu | Val | Ala | Pro | Ser | Glu | Val | Leu | Leu | Asp | Ser | Ser | Cys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Ser | Leu | Thr | Ile | Ser | Leu | Val | Val | Thr | Cys | Leu | Gly | Ala | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Leu | Ala | Ser | Ser | Leu | Ala | Ser | Ser | Phe | Leu | Gly | Ser | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ser | Ser | Phe | Leu | Thr | Ser | Ser | Thr | Leu | Gly | Ser | Gly | Leu | Gly | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Phe | Gly | Ser | Gly | Leu | Gly | Ser | Gly | Leu | Gly | Phe | Gly | Phe | Gly | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Leu | Gly | Leu | Gly | Leu | Gly | Leu | Gly | Phe | Val | Thr | Ser | Phe | Leu | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Phe | Phe | Gly | Ser | Ser | Phe | Leu | Gly | Phe | Ser | Leu | Gly | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gly | Leu | Ala | Asp | Ser | Ala | Leu | Val | Phe | Val | Leu | Glu | Leu | Val | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Leu | Ala | Lys | Leu | Met | Val | Thr | Leu | Val | Val | Pro | Ala | Cys | Ala | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ser | Gly | Ala | Ser | Ser | Arg | Ser | Lys | Lys |     |     |     |     |     |     |
| 145 |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 77...310  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

|                                                                 |            |                                                 |            |            |            |     |
|-----------------------------------------------------------------|------------|-------------------------------------------------|------------|------------|------------|-----|
| CCCCACAAAT                                                      | CCTAGCGATA | GTGAAATGCC                                      | CTAATTCATG | GACAAAGATT | AAAAACGCCA | 60  |
| GCATCAAAAC                                                      | CGCTAC     | AAT GAA CAT CAT ACC CCT GCA GGC TCT TTG GTG TTA |            |            |            | 112 |
|                                                                 |            | Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu |            |            |            |     |
|                                                                 | 1          |                                                 | 5          |            | 10         |     |
| GGA TCT TTT ATC ATC GGC TCT TTT AAA GGC GTG GGT GCT ATA GGG GGC |            |                                                 |            |            |            | 160 |
| Gly Ser Phe Ile Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly |            |                                                 |            |            |            |     |
|                                                                 | 15         |                                                 | 20         |            | 25         |     |
| GTG GGT GCT GTG GTT TTT GGG ATT TCT TTA TTT TCT TTT GGG GGT TTT |            |                                                 |            |            |            | 208 |



GGGTTTTGTG AATGACGACT AAAAGAGTGA ATACTGCCAC AAACAAGATA ATG ACA 56  
Met Thr  
1

TTA AAT ACT TTC TTG GAT ACA TGT TTT CTT TTA TTC ATC AGT ATT CTT 104  
Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser Ile Leu  
5 10 15

TTT TAT TTA AGT ATA CCA ATT TAT CCT AAC AAA GTG GTG GTT GTC CCG 152  
Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val Val Pro  
20 25 30

CAA GGT TCG CTC AAA AAA GTG TTT TTT TCT TTA AAA GAG CAA GGC GTG 200  
Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln Gly Val  
35 40 45 50

GAT ATG AAC GCT TTG GAT TTG CTT TTT TTA CGC CTG ATG GGC ATG CCT 248  
Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly Met Pro  
55 60 65

AAA AAA GGT TAT ATT GAT ATG GGC GAT GGG GCT TTA AGG AAG GGG GAT 296  
Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys Gly Asp  
70 75 80

TTT TTA GTC CGT TTG ATT AAG GCA AAA GCG GCA CAA AAA AGT GCG ACT 344  
Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser Ala Thr  
85 90 95

CTA ATC CCT GGG GAA AGC CGC TAT TTT TTC ACG CAA ATT TTG AGC GAG 392  
Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu Ser Glu  
100 105 110

ACT TAC CAA CTA GAA ACA AGC GAT CTC AAT CAG GCT TAT GAA AGC ATC 440  
Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu Ser Ile  
115 120 125 130

GCT CCA CGA TTG AAT GGC GAA GTG ATA GAA GAT GGG GTG ATA TGG CCA 488  
Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile Trp Pro  
135 140 145

GAC ACT TAT CAT TTG CCT TTA GGG GAG GAC GCT TTT AAA ATC ATG CAA 536  
Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile Met Gln  
150 155 160

ACT TTG ATT GGT CAA TCC ATG AAA AAA CAC GAA GCC TTA AGC AAA CAA 584  
Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser Lys Gln  
165 170 175

TGG CTT GGA TAC TAC CAT AAA GAA GAG TGG TTT GAA AAA ATC ATT CTC 632  
Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile Ile Leu  
180 185 190

GCT TCT ATT GTG CAA AAA GAA GCC GCT AAT GTT GAA GAA ATG CCC TTG 680  
Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met Pro Leu  
195 200 205 210

ATT GCG AGC GTG ATT TTT AAC CGC TTG AAA AAA GGC ATG CCT TTA CAA 728  
Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro Leu Gln



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 130 |     | 135 |     | 140 |     |     |     |     |     |     |     |     |     |     |     |
| Trp | Pro | Asp | Thr | Tyr | His | Leu | Pro | Leu | Gly | Glu | Asp | Ala | Phe | Lys | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Gln | Thr | Leu | Ile | Gly | Gln | Ser | Met | Lys | Lys | His | Glu | Ala | Leu | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Lys | Gln | Trp | Leu | Gly | Tyr | Tyr | His | Lys | Glu | Glu | Trp | Phe | Glu | Lys | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Ala | Ser | Ile | Val | Gln | Lys | Glu | Ala | Ala | Asn | Val | Glu | Glu | Met |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Pro | Leu | Ile | Ala | Ser | Val | Ile | Phe | Asn | Arg | Leu | Lys | Lys | Gly | Met | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Leu | Gln | Met | Asp | Gly | Ala | Leu | Asn | Tyr | Gln | Glu | Phe | Ser | His | Ala | Lys |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Val | Thr | Lys | Glu | Arg | Ile | Lys | Thr | Asp | Asn | Thr | Pro | Tyr | Asn | Thr | Tyr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Lys | Phe | Lys | Gly | Leu | Pro | Lys | Asn | Pro | Val | Gly | Ser | Val | Ser | Leu | Glu |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| Ala | Ile | Arg | Ala | Val | Ile | Phe | Pro | Lys | Lys | Thr | Asp | Phe | Leu | Tyr | Phe |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Val | Lys | Met | Pro | Asp | Lys | Lys | His | Ala | Phe | Ser | Ala | Thr | Tyr | Lys | Glu |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| His | Leu | Lys | Asn | Ile | Asn | Leu | Ser | Asn | Asn | His | Phe |     |     |     |     |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...584
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GAAAGTTCGG GGGCGGATTC TATGATTAAT GGCTATGGTT ATACCAAAGA ATG AGT  | 56  |
| Met Ser                                                         |     |
| 1                                                               |     |
| CAA AAA ATC CTA ATT CTA GGT ATT GGC AAT ATC CTT TTT GGC GAT GAA | 104 |
| Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly Asp Glu |     |
| 5 10 15                                                         |     |
| GGG ATT GGG GTG CAT TTA GCC CAC TAC CTC AAA AAA AAT TTT TCT TTT | 152 |
| Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe Ser Phe |     |
| 20 25 30                                                        |     |
| TTC CCT AGC GTG GAT ATT ATA GAT GGG GGG ACA ATG GCC CAG CAG CTC | 200 |
| Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln Gln Leu |     |
| 35 40 45 50                                                     |     |

ATT CCT TTA ATC ACT TCG TAT GAA AAG GTT TTG ATT TTG GAT TGC GTG 248  
 Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp Cys Val  
 55 60 65

AGC GCT GAA GGC GTT GAG ATA GGA TCA GTC TAT GCT TTT GAT TTT AAG 296  
 Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp Phe Lys  
 70 75 80

GAC GCT CCT AAA GAA ATC ACA TGG GCT GGG AGC GCT CAT GAA GTG GAA 344  
 Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu Val Glu  
 85 90 95

ATG CTA CAC ACT TTA AGG CTC ACG GAG TTT TTA GGG GAT TTG CCT AAA 392  
 Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu Pro Lys  
 100 105 110

ACT TTT ATC GTG GGG CTT GTG CCT TTT GTG ATA GGG AGC GAG ACC ACT 440  
 Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu Thr Thr  
 115 120 125 130

TTC AAG CTT TCA AGC AAA ATT TTA AAC GCT TTA GAA ACC GCC TTA AAA 488  
 Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala Leu Lys  
 135 140 145

GCC ATA GAA ACC CAA CTC AAC GCA TGG GGG GTT AAA ATG CAA CGC ACC 536  
 Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln Arg Thr  
 150 155 160

GAT CAT ATC GCT TTA GAA TGT ATC GCT GAA CTT TCT TAT AAG GGT TTT T 585  
 Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys Gly Phe  
 165 170 175

GAATTGGTTT TTGTTTTTCT TTTTAAATGC GTTAATGAAG AAACAAGCCT GA 637

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly  
 1 5 10 15  
 Asp Glu Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe  
 20 25 30  
 Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln  
 35 40 45  
 Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp  
 50 55 60  
 Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp  
 65 70 75 80  
 Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu





(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
Met Met Trp Arg Ser Leu Xaa Val Ala Phe Thr Ile Thr Asp Ile Ser
 1 5 10 15
Lys Thr Phe Gln Ser Gln Pro Lys His Gln Ile Gly Thr Leu Glu
 20 25 30
Leu Asn Phe Ala Phe
 35
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...1523  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
CTGTATTCGC TTCTGTGGAT TACTACCCTC AAAGAAAAGA AAGCCACAGA ATG AAC 56
 Met Asn
 1
ACC ACC ATC TTA GAA GCT TAT GCG GCT GAG CCA AGC AGG CAA ACC CTC 104
Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln Thr Leu
 5 10 15
TCT AAA GTC AGC AAC CGA TTC AAA GAG CAT GGC GCT AAA TTT GAT CTT 152
Ser Lys Val Ser Asn Arg Phe Lys Glu His Gly Ala Lys Phe Asp Leu
 20 25 30
CGT GTG ATG GCA ACG CAT GGA GGC ACC ATT AGT TGG AAA GCT AAA GAA 200
Arg Val Met Ala Thr His Gly Gly Thr Ile Ser Trp Lys Ala Lys Glu
 35 40 45 50
CTC GCT AGG ACT ATT GTG AGC GGC CCT ATT GGA GGC GTG ATT GGA TCT 248
Leu Ala Arg Thr Ile Val Ser Gly Pro Ile Gly Gly Val Ile Gly Ser
 55 60 65
AAA TTG CTA GGC GAA ACG CTT GGT TAT GAC AAT ATT GCA TGC AGT GAT 296
Lys Leu Leu Gly Glu Thr Leu Gly Tyr Asp Asn Ile Ala Cys Ser Asp
 70 75 80
ATT GGK GGC ACG AGC TTT GAT ATG GCG CTT ATC GTT AAG AGC AAT TTT 344
Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser Asn Phe
 85 90 95
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| AAC | ATC | GCT | TCT | GAC | CCT | GAT | ATG | GCA | CGC | CTT | GTT | TTA | TCT | CTA | CCG | 392  |
| Asn | Ile | Ala | Ser | Asp | Pro | Asp | Met | Ala | Arg | Leu | Val | Leu | Ser | Leu | Pro |      |
| 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |     |     |      |
| CTT | GTG | GCT | ATG | GAT | TCT | GTT | GGC | GCA | GGT | GCT | GGG | AGT | TTT | GTG | CGC | 440  |
| Leu | Val | Ala | Met | Asp | Ser | Val | Gly | Ala | Gly | Ala | Gly | Ser | Phe | Val | Arg |      |
| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |      |
| ATT | GAT | CCA | CAC | AGC | CGA | TCT | GTC | AAA | CTA | GGG | CCT | GAC | AGC | GCG | GGG | 488  |
| Ile | Asp | Pro | His | Ser | Arg | Ser | Val | Lys | Leu | Gly | Pro | Asp | Ser | Ala | Gly |      |
|     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |      |
| TAT | AGA | GTT | GGC | ACT | TGT | TGG | AAA | GAC | AGC | GGG | TTA | GAC | ACG | GTT | TCA | 536  |
| Tyr | Arg | Val | Gly | Thr | Cys | Trp | Lys | Asp | Ser | Gly | Leu | Asp | Thr | Val | Ser |      |
|     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |     |     |      |
| GTA | ACC | GAT | TGC | CAT | ATT | GTT | TTA | GGC | TAT | TTG | AAC | CCG | GAT | AAT | TTC | 584  |
| Val | Thr | Asp | Cys | His | Ile | Val | Leu | Gly | Tyr | Leu | Asn | Pro | Asp | Asn | Phe |      |
|     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |     |      |
| TTA | GGC | GGT | TTG | ATC | AAA | TTA | GAT | GTG | GAT | AGG | GCT | AAA | AAA | CAC | ATT | 632  |
| Leu | Gly | Gly | Leu | Ile | Lys | Leu | Asp | Val | Asp | Arg | Ala | Lys | Lys | His | Ile |      |
|     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |      |
| AAA | GAA | CAA | ATC | GCT | GAT | CCG | CTA | GGC | ATT | AGC | GTA | GAA | GAT | GCG | GCT | 680  |
| Lys | Glu | Gln | Ile | Ala | Asp | Pro | Leu | Gly | Ile | Ser | Val | Glu | Asp | Ala | Ala |      |
| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |      |
| GCT | GGT | GTG | ATT | GAA | TTG | CTT | GAT | TTG | GAG | CTT | AAA | GAA | TAC | TTG | CGA | 728  |
| Ala | Gly | Val | Ile | Glu | Leu | Leu | Asp | Leu | Glu | Leu | Lys | Glu | Tyr | Leu | Arg |      |
|     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     | 225 |     |      |
| TCC | AAC | ATT | AGC | GCT | AAA | GGG | TAT | AGC | CCA | TCT | GAT | TTT | GTG | TGC | TTT | 776  |
| Ser | Asn | Ile | Ser | Ala | Lys | Gly | Tyr | Ser | Pro | Ser | Asp | Phe | Val | Cys | Phe |      |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |      |
| TCA | TAT | GGT | GGC | GCA | GGA | CCT | GTG | CAT | ACC | TAT | GGC | TAT | ACA | GAA | GGA | 824  |
| Ser | Tyr | Gly | Gly | Ala | Gly | Pro | Val | His | Thr | Tyr | Gly | Tyr | Thr | Glu | Gly |      |
|     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |      |
| TTA | GGG | TTT | AAG | GAT | GTG | GTA | GTG | CCT | GCG | TGG | GCG | GCT | GGA | TTT | AGC | 872  |
| Leu | Gly | Phe | Lys | Asp | Val | Val | Val | Pro | Ala | Trp | Ala | Ala | Gly | Phe | Ser |      |
|     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |      |
| GCT | TTT | GGT | TGT | GCT | TGC | GCT | GAT | TTT | GAA | TAC | AGA | TAC | GAC | AAG | AGC | 920  |
| Ala | Phe | Gly | Cys | Ala | Cys | Ala | Asp | Phe | Glu | Tyr | Arg | Tyr | Asp | Lys | Ser |      |
| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |      |
| GTG | GAT | ATT | GCC | ATT | CCG | CAG | TAT | TCT | TCA | GAC | AAG | TCA | AAA | ATA | GAC | 968  |
| Val | Asp | Ile | Ala | Ile | Pro | Gln | Tyr | Ser | Ser | Asp | Lys | Ser | Lys | Ile | Asp |      |
|     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     | 305 |     |      |
| GCA | TGC | AAA | ATC | ATT | CAA | GAC | GCA | TGG | GAT | GAA | TTG | ACT | TTG | AAA | GTG | 1016 |
| Ala | Cys | Lys | Ile | Ile | Gln | Asp | Ala | Trp | Asp | Glu | Leu | Thr | Leu | Lys | Val |      |
|     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |      |
| ATT | GAA | GAG | TTC | AAG | ATC | AAT | GGA | TTT | TCT | CAA | AAA | GAT | GTG | ATC | TTA | 1064 |
| Ile | Glu | Glu | Phe | Lys | Ile | Asn | Gly | Phe | Ser | Gln | Lys | Asp | Val | Ile | Leu |      |

| 325                                                               | 330 | 335 |      |
|-------------------------------------------------------------------|-----|-----|------|
| AGA CCT GGA TAC AGG ATG CAG TAT ATG GGG CAA TTG AAT GAT TTA GAG   |     |     | 1112 |
| Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp Leu Glu   |     |     |      |
| 340                                                               | 345 | 350 |      |
| ATC ACT TCT CCT GTG TCA AAA GCT GCA AGC GTG GCT GAT TGG GAA GAG   |     |     | 1160 |
| Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp Glu Glu   |     |     |      |
| 355                                                               | 360 | 365 | 370  |
| ATT GTC AAA GAA TAT GAA AAA ACC TAC GCT CGC GTT TAT TCT GAA TCA   |     |     | 1208 |
| Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser Glu Ser   |     |     |      |
|                                                                   | 375 | 380 | 385  |
| GCG TGT TCT CCA GAG CTT GGT TTT AGC GTG ACT GGC GTG ATC ATG CGT   |     |     | 1256 |
| Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile Met Arg   |     |     |      |
|                                                                   | 390 | 395 | 400  |
| GGT GTT GTG GCT ACG CAA AAA CCT GTG ATT CCG GTT GAA AAA GAG CAT   |     |     | 1304 |
| Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys Glu His   |     |     |      |
|                                                                   | 405 | 410 | 415  |
| GGT GCT ACG CCC CCA AAA GAA GCC AAA ATA GGC GTT AGA AAA TTC TAT   |     |     | 1352 |
| Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys Phe Tyr   |     |     |      |
|                                                                   | 420 | 425 | 430  |
| CGG CAT AAA AAA TGG GTG GAT GCA GAT GTG TGG CAA ATG GAA AAA TTA   |     |     | 1400 |
| Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu Lys Leu   |     |     |      |
|                                                                   | 440 | 445 | 450  |
| CTG CCT GGA AAT GAA GTC ATA GGA CCT GCG ATC GTG GAA TCA GAT GCG   |     |     | 1448 |
| Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser Asp Ala   |     |     |      |
|                                                                   | 455 | 460 | 465  |
| ACC ACT TTC GTG ATA CCC AAA GGC TTT GCG ACA AGA CTA GAC AAA CAC   |     |     | 1496 |
| Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp Lys His   |     |     |      |
|                                                                   | 470 | 475 | 480  |
| CGA TTG TTC CAC TTG AAA GAA ATT AAA TAAAGGAGTT CAAAATGGCA AATTTAT |     |     | 1550 |
| Arg Leu Phe His Leu Lys Glu Ile Lys                               |     |     |      |
|                                                                   | 485 | 490 |      |
| TGAAAAACGG CAAACTTTA AAACAA                                       |     |     | 1576 |

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Asn Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln



[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(A) NAME/KEY: Coding Sequence

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

1

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

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(v) FRAGMENT TYPE: internal
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Gln | Leu | Lys | Ser | Asn | Leu | Asp | Trp | Tyr | Ala | Asp | Tyr | Leu | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Leu | Asp | Arg | Phe | Gly | Glu | Lys | Met | Glu | Glu | Ser | Lys | Glu | Arg | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Leu | Leu | Ile | Ala | Ser | Leu | Ala | Pro | Leu | Ala | Gly | Phe | Ala | Ala | Arg |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Pro | Gly | Leu | Leu | Ser | Leu | Leu | Gly | Leu | Met | Leu | Ala | Met | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Ala | Asn | Phe | Trp | Ile |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...773
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

|                                                                 |         |          |
|-----------------------------------------------------------------|---------|----------|
| TGGCTTAATT GTTAAGCCGG CTAGAAAAAG AGCGTTATTT GCGCCATATC          | ATG CTA | 56       |
|                                                                 | Met Leu |          |
|                                                                 | 1       |          |
| GAA GAT GTG GGC GAA GAG GGT CAA TTG AAG CTT TTA AAA TCT AGC GTT |         | 104      |
| Glu Asp Val Gly Glu Glu Gly Gln Leu Lys Leu Leu Lys Ser Ser Val |         |          |
|                                                                 | 5       | 15       |
| TTA GTC ATT GGG GCT GGG GGT CTT GGA TCG GCG GTT TTG ATG TAT TTG |         | 152      |
| Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met Tyr Leu |         |          |
|                                                                 | 20      | 30       |
| TGT GCC GCT GGG ATA GGA AAA ATC GGT ATT GTA GAT TTT GAT GTA GTA |         | 200      |
| Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp Val Val |         |          |
|                                                                 | 35      | 40 45 50 |
| GAT ATG AGT AAT TTG CAA CGC CAA ATC ATC CAT TCA CAG GAT TTT TTA |         | 248      |
| Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp Phe Leu |         |          |
|                                                                 | 55      | 60 65    |
| AAC CAA TCT AAA GCC TCT AGC GCG AAA GCG CGC TTA AAA CAA CTC AAT |         | 296      |
| Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln Leu Asn |         |          |
|                                                                 | 70      | 75 80    |
| GCG GGT ATT GAA ATA GAG GCT TTT GAA GAA CGC TTT AAG GCT CAT AAC |         | 344      |
| Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala His Asn |         |          |
|                                                                 | 85      | 90 95    |

GCT CTT TCT CTC ATA GAG CCT TAT GAT TTT ATC ATA GAC GCC ACG GAC 392  
 Ala Leu Ser Leu Ile Glu Pro Tyr Asp Phe Ile Ile Asp Ala Thr Asp  
 100 105 110  
 AAT TTT AAC GCT AAA TTT TTG ATC AAT GAC GCT TGC GTG TTA GCC CAA 440  
 Asn Phe Asn Ala Lys Phe Leu Ile Asn Asp Ala Cys Val Leu Ala Gln  
 115 120 125 130  
 AAA CCC TAT TCG CAT GCC GGG GTT TTA GAA TAC AGG GGG CAA AGC ATG 488  
 Lys Pro Tyr Ser His Ala Gly Val Leu Glu Tyr Arg Gly Gln Ser Met  
 135 140 145  
 AGC GTT TTA CCC CAT AGC GCA TGC TTA GCG TGC GTT TTT GAT AAG CCC 536  
 Ser Val Leu Pro His Ser Ala Cys Leu Ala Cys Val Phe Asp Lys Pro  
 150 155 160  
 CCT AAA AAG GGA TTA AAT CCC ATT TCA GGG CTT TTT GGG GTC TTA CCC 584  
 Pro Lys Lys Gly Leu Asn Pro Ile Ser Gly Leu Phe Gly Val Leu Pro  
 165 170 175  
 GGA GTT TTA GGG TGT ATC CAA GCG AGC GAA TGC CTT AAA TAT TTT TTA 632  
 Gly Val Leu Gly Cys Ile Gln Ala Ser Glu Cys Leu Lys Tyr Phe Leu  
 180 185 190  
 GGG TTT GAA ACT TTA CTT ATA AAT ACT TTA CTT ATA GCC GAT ATT AAA 680  
 Gly Phe Glu Thr Leu Leu Ile Asn Thr Leu Leu Ile Ala Asp Ile Lys  
 195 200 205 210  
 ACG ATG GAT TTT AAA AAA ATT CAA GCA CCC AAA AAC CCT GAA TGT AGG 728  
 Thr Met Asp Phe Lys Lys Ile Gln Ala Pro Lys Asn Pro Glu Cys Arg  
 215 220 225  
 GTT TGT GGC ACG CAT AAA ATC ACG CAT TTA CAG GAT TAT GAA ATT TAGAT 778  
 Val Cys Gly Thr His Lys Ile Thr His Leu Gln Asp Tyr Glu Ile  
 230 235 240  
 TAAGGGGTAA GTTTTGGATT TATCAACCAT ATTAGGCTTG GTATTGGC 826

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Leu Glu Asp Val Gly Glu Glu Gly Gln Leu Lys Leu Leu Lys Ser  
 1 5 10 15  
 Ser Val Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met  
 20 25 30  
 Tyr Leu Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp  
 35 40 45  
 Val Val Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |
| Phe | Leu | Asn | Gln | Ser | Lys | Ala | Ser | Ser | Ala | Lys | Ala | Arg | Leu | Lys | Gln |
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Leu | Asn | Ala | Gly | Ile | Glu | Ile | Glu | Ala | Phe | Glu | Glu | Arg | Phe | Lys | Ala |
|     |     | 85  |     | 90  |     | 95  |     |     |     |     |     |     |     |     |     |
| His | Asn | Ala | Leu | Ser | Leu | Ile | Glu | Pro | Tyr | Asp | Phe | Ile | Ile | Asp | Ala |
|     |     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |
| Thr | Asp | Asn | Phe | Asn | Ala | Lys | Phe | Leu | Ile | Asn | Asp | Ala | Cys | Val | Leu |
|     |     | 115 |     | 120 |     | 125 |     |     |     |     |     |     |     |     |     |
| Ala | Gln | Lys | Pro | Tyr | Ser | His | Ala | Gly | Val | Leu | Glu | Tyr | Arg | Gly | Gln |
|     |     | 130 |     | 135 |     | 140 |     |     |     |     |     |     |     |     |     |
| Ser | Met | Ser | Val | Leu | Pro | His | Ser | Ala | Cys | Leu | Ala | Cys | Val | Phe | Asp |
|     |     | 145 |     | 150 |     | 155 |     |     |     |     |     |     |     |     |     |
| Lys | Pro | Pro | Lys | Lys | Gly | Leu | Asn | Pro | Ile | Ser | Gly | Leu | Phe | Gly | Val |
|     |     | 165 |     | 170 |     | 175 |     |     |     |     |     |     |     |     |     |
| Leu | Pro | Gly | Val | Leu | Gly | Cys | Ile | Gln | Ala | Ser | Glu | Cys | Leu | Lys | Tyr |
|     |     | 180 |     | 185 |     | 190 |     |     |     |     |     |     |     |     |     |
| Phe | Leu | Gly | Phe | Glu | Thr | Leu | Leu | Ile | Asn | Thr | Leu | Leu | Ile | Ala | Asp |
|     |     | 195 |     | 200 |     | 205 |     |     |     |     |     |     |     |     |     |
| Ile | Lys | Thr | Met | Asp | Phe | Lys | Lys | Ile | Gln | Ala | Pro | Lys | Asn | Pro | Glu |
|     |     | 210 |     | 215 |     | 220 |     |     |     |     |     |     |     |     |     |
| Cys | Arg | Val | Cys | Gly | Thr | His | Lys | Ile | Thr | His | Leu | Gln | Asp | Tyr | Glu |
|     |     | 225 |     | 230 |     | 235 |     |     |     |     |     |     |     |     |     |
| Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...494
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAATTCATT CTATTTTAGA TAATGAGTTC AATCCCCACA AACAGCAAGA ATG AAT  | 56  |
| Met Asn                                                         |     |
| 1                                                               |     |
| CGC ATG AAT AAA AAT TAT CTT TTA ATC TTT TTG TTG TTA GCG AGT CTT | 104 |
| Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala Ser Leu |     |
| 5 10 15                                                         |     |
| GTT GCT AGA GAG AAG GAC GCT TCT TCA AAC CTT TTT GAT TTG ATT GAT | 152 |
| Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu Ile Asp |     |
| 20 25 30                                                        |     |
| AAG GGG ATC AAC AGA GAA CAA GAA TTA AAA GAG CAG GAG CAA AAA ACG | 200 |



110

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Ser | 100 | Leu | Val | Arg | Asn | Gln | 105 | Ser | Val | Ala | Tyr | Glu | Ile | Leu | Cys |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Glu | Asn | Gln | Pro | Leu | Trp | Ile | Glu | Val | Ser | Thr | Asn | Leu | Gly | Lys | Arg |     |     |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| Thr | Phe | Gln | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1631
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCTTTCTTTA TTCTCATTGC ATCTTGTTGGG ATCATTTTTT TTTTTTATTA ATG CTA | 56  |
| Met Leu                                                         |     |
| 1                                                               |     |
| GCT TCC ATC ATC TCA ATT TTA AGG GTT TTT GTT TTG TTA TTC AAC ACG | 104 |
| Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe Asn Thr |     |
| 5 10 15                                                         |     |
| CCG TTA TTC ATC TTT GCT TTT TTG CCT GTT GGT TTT TTA GGG TAT TTT | 152 |
| Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly Tyr Phe |     |
| 20 25 30                                                        |     |
| ATC TTG CAA GCT TAT GCT AAA AAT CCC CTG TTC CCT AAA CTA TGG CTA | 200 |
| Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu Trp Leu |     |
| 35 40 45 50                                                     |     |
| GTA TTG GCT AGT TTG TTT TTT TAT GCT TTT TGG AAT GTG AAG TAT TTG | 248 |
| Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys Tyr Leu |     |
| 55 60 65                                                        |     |
| CCC TTA TTG GTT GGC TCT ATT GTT TTT AAT TAT TTT GTG GCT TTG AAA | 296 |
| Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala Leu Lys |     |
| 70 75 80                                                        |     |
| ATC CAT CAA ACC CAG CCA AAT GCA TAT AAA AGA TTA TGG CTT ATT TTG | 344 |
| Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu Ile Leu |     |
| 85 90 95                                                        |     |
| GGC TTG ATC GCT AAT GTT TCA CTT TTA GGA TTT TTC AAA TAC ACT GAT | 392 |
| Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr Thr Asp |     |
| 100 105 110                                                     |     |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| TTT TTC TTA ACC AAT TTC AAT CTA ATA TGG AAG AGC CAT TTT GAA ACC | 440  |
| Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe Glu Thr |      |
| 115 120 125 130                                                 |      |
| TTG CAT TTA ATC TTG CCT TTA GCG ATC AGC TTT TTC ACT TTG CAA CAA | 488  |
| Leu His Leu Ile Leu Pro Leu Ala Ile Ser Phe Phe Thr Leu Gln Gln |      |
| 135 140 145                                                     |      |
| ATC GCT TAC TTG ATG GAC ACT TAT AAG CAA AAT CAA ATC ATG CAG CCC | 536  |
| Ile Ala Tyr Leu Met Asp Thr Tyr Lys Gln Asn Gln Ile Met Gln Pro |      |
| 150 155 160                                                     |      |
| AAA ATG AGA GAG AGA GTG AGT GAA AAC GCT CCT ATT TTA TTA AAT CCT | 584  |
| Lys Met Arg Glu Arg Val Ser Glu Asn Ala Pro Ile Leu Leu Asn Pro |      |
| 165 170 175                                                     |      |
| CCC ACT TCA TTT TTT TCA CTT TCG CAT TTT TTA GAT TAC GCT TTA TTT | 632  |
| Pro Thr Ser Phe Phe Ser Leu Ser His Phe Leu Asp Tyr Ala Leu Phe |      |
| 180 185 190                                                     |      |
| GTG AGT TTC TTC CCT CAA CTC ATT GCA GGG CCT ATT GTG CAT CAT AGC | 680  |
| Val Ser Phe Phe Pro Gln Leu Ile Ala Gly Pro Ile Val His His Ser |      |
| 195 200 205 210                                                 |      |
| GAG ATG ATG CCT CAA TTT AAA GAT AAA AAC AAT CAA TAT TTG AAT TAC | 728  |
| Glu Met Met Pro Gln Phe Lys Asp Lys Asn Asn Gln Tyr Leu Asn Tyr |      |
| 215 220 225                                                     |      |
| AGA AAT ATC GCT TTA GGC TTG TTT ATC TTT TCT ATC GGT TTG TTT AAA | 776  |
| Arg Asn Ile Ala Leu Gly Leu Phe Ile Phe Ser Ile Gly Leu Phe Lys |      |
| 230 235 240                                                     |      |
| AAG GTC GTG ATT GCA GAT AAT ACC GCT CAT TTT GCT GAT TTT GGA TTT | 824  |
| Lys Val Val Ile Ala Asp Asn Thr Ala His Phe Ala Asp Phe Gly Phe |      |
| 245 250 255                                                     |      |
| GAT AAG GCG ACT AGC TTA AGT TTT ATT CAA GCA TGG ATG ACT TCT TTA | 872  |
| Asp Lys Ala Thr Ser Leu Ser Phe Ile Gln Ala Trp Met Thr Ser Leu |      |
| 260 265 270                                                     |      |
| TCT TAT TCG TTC CAG CTG TAT TTT GAT TTT AGC GGT TAT TGC GAT ATG | 920  |
| Ser Tyr Ser Phe Gln Leu Tyr Phe Asp Phe Ser Gly Tyr Cys Asp Met |      |
| 275 280 285 290                                                 |      |
| GCT ATA GGC ATT GGC CTC TTT TTT AAC ATC AAA CTC CCT ATC AAT TTT | 968  |
| Ala Ile Gly Ile Gly Leu Phe Phe Asn Ile Lys Leu Pro Ile Asn Phe |      |
| 295 300 305                                                     |      |
| AAT AGC CCC TAT AAG GCT TTG AAT ATC CAA GAT TTT TGG AGG AGG TGG | 1016 |
| Asn Ser Pro Tyr Lys Ala Leu Asn Ile Gln Asp Phe Trp Arg Arg Trp |      |
| 310 315 320                                                     |      |
| CAT ATC ACT TTG AGC CGC TTC TTA AAA GAG TAT TTG TAT ATC CCT TTA | 1064 |
| His Ile Thr Leu Ser Arg Phe Leu Lys Glu Tyr Leu Tyr Ile Pro Leu |      |
| 325 330 335                                                     |      |
| GGG GGT AAT AGG GTG AAA GAA TTA ATC GTG TAT AGG AAT TTA ATT TTA | 1112 |
| Gly Gly Asn Arg Val Lys Glu Leu Ile Val Tyr Arg Asn Leu Ile Leu |      |

| 340                                                               | 345 | 350 |      |
|-------------------------------------------------------------------|-----|-----|------|
| GTG TTT TTG ATT GGG GGG TTT TGG CAT GGG GCT GGT TGG ACT TTT ATC   |     |     | 1160 |
| Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr Phe Ile   |     |     |      |
| 355                                                               | 360 | 365 | 370  |
| ATT TGG GGG CTA TTG CAT GGG ATT GCT TTG AGC GTT CAT AGA GCG TAT   |     |     | 1208 |
| Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg Ala Tyr   |     |     |      |
|                                                                   | 375 | 380 | 385  |
| TCT CAT GCC ACT AGA AAA TTC CAT TTC ACT ATG CCA AAG ATT TTA GCA   |     |     | 1256 |
| Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile Leu Ala   |     |     |      |
|                                                                   | 390 | 395 | 400  |
| TGG CTC ATC ACT TTT AAT TTT ATC AAT CTC GCA TGG GTG TTT TTT AGA   |     |     | 1304 |
| Trp Leu Ile Thr Phe Asn Phe Ile Asn Leu Ala Trp Val Phe Phe Arg   |     |     |      |
|                                                                   | 405 | 410 | 415  |
| GCC AAA AAT TTA GAA AGC GCT TTG AAG GTT TTA AAG GGG ATG GTT GGT   |     |     | 1352 |
| Ala Lys Asn Leu Glu Ser Ala Leu Lys Val Leu Lys Gly Met Val Gly   |     |     |      |
|                                                                   | 420 | 425 | 430  |
| TTG AAT GGT GTT TCG CTT TGT CAT CTT TCA AAA GAG GCA TCA GAG TTT   |     |     | 1400 |
| Leu Asn Gly Val Ser Leu Cys His Leu Ser Lys Glu Ala Ser Glu Phe   |     |     |      |
|                                                                   | 435 | 440 | 445  |
| TTA AAT CGT GTC AAT GAT AAC ATG ATC ATG CAC ACC ATA ATG TAT GCA   |     |     | 1448 |
| Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met Tyr Ala   |     |     |      |
|                                                                   | 455 | 460 | 465  |
| TCC CCC ACA TTT AAA ATG TGT GTT TTG ATG ATA ATC ATC TCT TTT TGT   |     |     | 1496 |
| Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser Phe Cys   |     |     |      |
|                                                                   | 470 | 475 | 480  |
| TTA AAA AAT AGT TCC CAT TTA TAC CAA TCC AAT CAA ATG GAT TGG ATT   |     |     | 1544 |
| Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp Trp Ile   |     |     |      |
|                                                                   | 485 | 490 | 495  |
| AAA ACA ACA AGC GCT TGT TTG TTG CTC TCT ATA GGT TTT TTA TTT ATT   |     |     | 1592 |
| Lys Thr Thr Ser Ala Cys Leu Leu Leu Ser Ile Gly Phe Leu Phe Ile   |     |     |      |
|                                                                   | 500 | 505 | 510  |
| TTT GCC AGT TCT CAA TCG GTA TTT TTG TAT TTT AAT TTT TAGGACACTG CT |     |     | 1643 |
| Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe               |     |     |      |
|                                                                   | 515 | 520 | 525  |
| ATGGAATTTT ATAAAAACA AACTTTAATC ATTGTTTCTT T                      |     |     | 1684 |

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 527 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ala | Ser | Ile | Ile | Ser | Ile | Leu | Arg | Val | Phe | Val | Leu | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Thr | Pro | Leu | Phe | Ile | Phe | Ala | Phe | Leu | Pro | Val | Gly | Phe | Leu | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Phe | Ile | Leu | Gln | Ala | Tyr | Ala | Lys | Asn | Pro | Leu | Phe | Pro | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Leu | Val | Leu | Ala | Ser | Leu | Phe | Phe | Tyr | Ala | Phe | Trp | Asn | Val | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Leu | Pro | Leu | Leu | Val | Gly | Ser | Ile | Val | Phe | Asn | Tyr | Phe | Val | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Lys | Ile | His | Gln | Thr | Gln | Pro | Asn | Ala | Tyr | Lys | Arg | Leu | Trp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Leu | Gly | Leu | Ile | Ala | Asn | Val | Ser | Leu | Leu | Gly | Phe | Phe | Lys | Tyr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Asp | Phe | Phe | Leu | Thr | Asn | Phe | Asn | Leu | Ile | Trp | Lys | Ser | His | Phe |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Thr | Leu | His | Leu | Ile | Leu | Pro | Leu | Ala | Ile | Ser | Phe | Phe | Thr | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Gln | Gln | Ile | Ala | Tyr | Leu | Met | Asp | Thr | Tyr | Lys | Gln | Asn | Gln | Ile | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Pro | Lys | Met | Arg | Glu | Arg | Val | Ser | Glu | Asn | Ala | Pro | Ile | Leu | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Pro | Pro | Thr | Ser | Phe | Phe | Ser | Leu | Ser | His | Phe | Leu | Asp | Tyr | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Phe | Val | Ser | Phe | Phe | Pro | Gln | Leu | Ile | Ala | Gly | Pro | Ile | Val | His |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Ser | Glu | Met | Met | Pro | Gln | Phe | Lys | Asp | Lys | Asn | Asn | Gln | Tyr | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Tyr | Arg | Asn | Ile | Ala | Leu | Gly | Leu | Phe | Ile | Phe | Ser | Ile | Gly | Leu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Phe | Lys | Lys | Val | Val | Ile | Ala | Asp | Asn | Thr | Ala | His | Phe | Ala | Asp | Phe |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Phe | Asp | Lys | Ala | Thr | Ser | Leu | Ser | Phe | Ile | Gln | Ala | Trp | Met | Thr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Leu | Ser | Tyr | Ser | Phe | Gln | Leu | Tyr | Phe | Asp | Phe | Ser | Gly | Tyr | Cys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Met | Ala | Ile | Gly | Ile | Gly | Leu | Phe | Phe | Asn | Ile | Lys | Leu | Pro | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Phe | Asn | Ser | Pro | Tyr | Lys | Ala | Leu | Asn | Ile | Gln | Asp | Phe | Trp | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Trp | His | Ile | Thr | Leu | Ser | Arg | Phe | Leu | Lys | Glu | Tyr | Leu | Tyr | Ile |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Leu | Gly | Gly | Asn | Arg | Val | Lys | Glu | Leu | Ile | Val | Tyr | Arg | Asn | Leu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Leu | Val | Phe | Leu | Ile | Gly | Gly | Phe | Trp | His | Gly | Ala | Gly | Trp | Thr |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Ile | Ile | Trp | Gly | Leu | Leu | His | Gly | Ile | Ala | Leu | Ser | Val | His | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Tyr | Ser | His | Ala | Thr | Arg | Lys | Phe | His | Phe | Thr | Met | Pro | Lys | Ile |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Ala | Trp | Leu | Ile | Thr | Phe | Asn | Phe | Ile | Asn | Leu | Ala | Trp | Val | Phe |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | Arg | Ala | Lys | Asn | Leu | Glu | Ser | Ala | Leu | Lys | Val | Leu | Lys | Gly | Met |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Val | Gly | Leu | Asn | Gly | Val | Ser | Leu | Cys | His | Leu | Ser | Lys | Glu | Ala | Ser |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |

Glu Phe Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met  
 450 455 460  
 Tyr Ala Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser  
 465 470 475 480  
 Phe Cys Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp  
 485 490 495  
 Trp Ile Lys Thr Thr Ser Ala Cys Leu Leu Ser Ile Gly Phe Leu  
 500 505 510  
 Phe Ile Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe  
 515 520 525

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...3920
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAGTCGCAC CCTTTGTGCA AAAATCGTTT TACAAGAAGA AAGGAAAAAA ATG GAA  | 56  |
| Met Glu                                                         |     |
| 1                                                               |     |
| ATA CAA CAA ACA CAC CGC AAA ATC AAT CGC CCT TTG GTT TCT CTC GCT | 104 |
| Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser Leu Ala |     |
| 5 10 15                                                         |     |
| TTA GTA GGA GCG TTA GTC AGC ATC ACA CCG CAA CAA AGT CAT GCC GCC | 152 |
| Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His Ala Ala |     |
| 20 25 30                                                        |     |
| TTT TTC ACA ACC GTG ATC ATT CCA GCC ATT GTT GGG GGG ATT GCT ACA | 200 |
| Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile Ala Thr |     |
| 35 40 45 50                                                     |     |
| GGC GCT GCT GTA GGA ACG GTC TCA GGG CTT CTT GGC TGG GGG CTA AAA | 248 |
| Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly Leu Lys |     |
| 55 60 65                                                        |     |
| CAA GCC GAA GAA GCC AAT AAA ACC CCA GAT AAA CCC GAT AAA GTT TGG | 296 |
| Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys Val Trp |     |
| 70 75 80                                                        |     |
| CGC ATT CAA GCA GGA AAA GGC TTT AAT GAA TTC CCT AAC AAG GAA TAC | 344 |
| Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys Glu Tyr |     |
| 85 90 95                                                        |     |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GAC TTA TAC AGA TCC CTA CTA TCT AGT AAG ATT GAT GGA GGC TGG GAT | 392  |
| Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly Trp Asp |      |
| 100 105 110                                                     |      |
| TGG GGG AAT GCC GCT ACG CAT TAT TGG GTC AAA GGC GGG CAA TGG AAC | 440  |
| Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln Trp Asn |      |
| 115 120 125 130                                                 |      |
| AAG CTT GAA GTG GAT ATG AAA GAC GCT GTA GGG ACT TAT AAT CTC TCA | 488  |
| Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn Leu Ser |      |
| 135 140 145                                                     |      |
| GGG CTA AGA AAC TTT ACT GGT GGG GAT TTA GAT GTC AAT ATG CAA AAA | 536  |
| Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met Gln Lys |      |
| 150 155 160                                                     |      |
| GCC ACT TTG CGC TTG GGC CAA TTC AAT GGC AAT TCT TTC ACA AGC TAT | 584  |
| Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr |      |
| 165 170 175                                                     |      |
| AAG GAT AGC GCT GAT CGC ACC ACG AGA GTG GAT TTC AAC GCT AAA AAT | 632  |
| Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn |      |
| 180 185 190                                                     |      |
| ATC TTA ATT GAT AAT TTT TTA GAA ATC AAT AAT CGT GTG GGT TCT GGA | 680  |
| Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly |      |
| 195 200 205 210                                                 |      |
| GCC GGG AGG AAA GCC AGC TCT ACG GTT TTA ACT TTG CAA GCT TCA GAA | 728  |
| Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu |      |
| 215 220 225                                                     |      |
| GGG ATT ACT AGC AGT AAA AAT GCG GAA ATT TCT CTT TAT GAT GGC GCC | 776  |
| Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala |      |
| 230 235 240                                                     |      |
| ACG CTC AAT TTG GCT TCA AAC AGC GTT AAA TTA ATG GGT AAT GTG TGG | 824  |
| Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp |      |
| 245 250 255                                                     |      |
| ATG GGC CGT TTG CAA TAT GTG GGA GCG TAT TTG GCC CCT TCA TAC AGC | 872  |
| Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser |      |
| 260 265 270                                                     |      |
| ACG ATA AAC ACT TCA AAA GTG ACA GGG GAA GTG AAT TTT AAC CAT CTC | 920  |
| Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu |      |
| 275 280 285 290                                                 |      |
| ACT GTG GGC GAT CAC AAC GCC GCT CAA GCA GGC ATT ATC GCT AGT AAC | 968  |
| Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn |      |
| 295 300 305                                                     |      |
| AAG ACT CAT ATT GGC ACA CTG GAT TTG TGG CAA AGC GCG GGA CTA AAC | 1016 |
| Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn |      |
| 310 315 320                                                     |      |
| ATT ATC GCC CCT CCA GAA GGC GGT TAT AAG GAT AAA CCT AAG GAT AAA | 1064 |
| Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys |      |















1. *Author* (last name, first name, middle initial) 2. *Title* (of the article) 3. *Journal* (name of the journal) 4. *Volume* (number of the volume) 5. *Issue* (number of the issue) 6. *Page* (number of the page) 7. *Year* (year of publication) 8. *DOI* (Digital Object Identifier) 9. *URL* (Uniform Resource Locator) 10. *Accession Number* (number assigned to the article) 11. *Keywords* (terms used to describe the article) 12. *Abstract* (summary of the article) 13. *Introduction* (beginning of the article) 14. *Methods* (description of the research methods) 15. *Results* (findings of the study) 16. *Discussion* (interpretation of the results) 17. *Conclusion* (summary of the findings) 18. *References* (list of sources cited) 19. *Appendix* (additional information) 20. *Footnote* (additional information) 21. *Page Number* (number of the page) 22. *Page Range* (range of pages) 23. *Page Count* (total number of pages) 24. *Page Size* (dimensions of the page) 25. *Page Orientation* (vertical or horizontal) 26. *Page Color* (background color) 27. *Page Font* (typeface) 28. *Page Size* (dimensions of the page) 29. *Page Orientation* (vertical or horizontal) 30. *Page Color* (background color) 31. *Page Font* (typeface) 32. *Page Size* (dimensions of the page) 33. *Page Orientation* (vertical or horizontal) 34. *Page Color* (background color) 35. *Page Font* (typeface) 36. *Page Size* (dimensions of the page) 37. *Page Orientation* (vertical or horizontal) 38. *Page Color* (background color) 39. *Page Font* (typeface) 40. *Page Size* (dimensions of the page) 41. *Page Orientation* (vertical or horizontal) 42. *Page Color* (background color) 43. *Page Font* (typeface) 44. *Page Size* (dimensions of the page) 45. *Page Orientation* (vertical or horizontal) 46. *Page Color* (background color) 47. *Page Font* (typeface) 48. *Page Size* (dimensions of the page) 49. *Page Orientation* (vertical or horizontal) 50. *Page Color* (background color) 51. *Page Font* (typeface) 52. *Page Size* (dimensions of the page) 53. *Page Orientation* (vertical or horizontal) 54. *Page Color* (background color) 55. *Page Font* (typeface) 56. *Page Size* (dimensions of the page) 57. *Page Orientation* (vertical or horizontal) 58. *Page Color* (background color) 59. *Page Font* (typeface) 60. *Page Size* (dimensions of the page) 61. *Page Orientation* (vertical or horizontal) 62. *Page Color* (background color) 63. *Page Font* (typeface) 64. *Page Size* (dimensions of the page) 65. *Page Orientation* (vertical or horizontal) 66. *Page Color* (background color) 67. *Page Font* (typeface) 68. *Page Size* (dimensions of the page) 69. *Page Orientation* (vertical or horizontal) 70. *Page Color* (background color) 71. *Page Font* (typeface) 72. *Page Size* (dimensions of the page) 73. *Page Orientation* (vertical or horizontal) 74. *Page Color* (background color) 75. *Page Font* (typeface) 76. *Page Size* (dimensions of the page) 77. *Page Orientation* (vertical or horizontal) 78. *Page Color* (background color) 79. *Page Font* (typeface) 80. *Page Size* (dimensions of the page) 81. *Page Orientation* (vertical or horizontal) 82. *Page Color* (background color) 83. *Page Font* (typeface) 84. *Page Size* (dimensions of the page) 85. *Page Orientation* (vertical or horizontal) 86. *Page Color* (background color) 87. *Page Font* (typeface) 88. *Page Size* (dimensions of the page) 89. *Page Orientation* (vertical or horizontal) 90. *Page Color* (background color) 91. *Page Font* (typeface) 92. *Page Size* (dimensions of the page) 93. *Page Orientation* (vertical or horizontal) 94. *Page Color* (background color) 95. *Page Font* (typeface) 96. *Page Size* (dimensions of the page) 97. *Page Orientation* (vertical or horizontal) 98. *Page Color* (background color) 99. *Page Font* (typeface) 100. *Page Size* (dimensions of the page)

|     |      |      |      |      |      |      |     |      |      |     |      |      |      |      |     |  |  |
|-----|------|------|------|------|------|------|-----|------|------|-----|------|------|------|------|-----|--|--|
|     |      |      |      | 725  |      |      |     |      | 730  |     |      |      |      | 735  |     |  |  |
| Ile | Gly  | Tyr  | Gly  | Asn  | Val  | Ser  | Leu | Gly  | Thr  | Asn | Ser  | Ile  | Ser  | Asn  | Val |  |  |
|     |      |      | 740  |      |      |      |     | 745  |      |     |      |      |      | 750  |     |  |  |
| Asn | Leu  | Ile  | Glu  | Gln  | Phe  | Lys  | Glu | Arg  | Leu  | Ala | Leu  | Tyr  | Asn  | Asn  | Asn |  |  |
|     |      | 755  |      |      |      |      | 760 |      |      |     |      | 765  |      |      |     |  |  |
| Asn | Arg  | Met  | Asp  | Ile  | Cys  | Val  | Val | Arg  | Asn  | Thr | Asp  | Asp  | Ile  | Lys  | Ala |  |  |
|     | 770  |      |      |      | 775  |      |     |      |      |     | 780  |      |      |      |     |  |  |
| Cys | Gly  | Thr  | Ala  | Ile  | Gly  | Asn  | Gln | Ser  | Met  | Val | Asn  | Asn  | Pro  | Asp  | Asn |  |  |
| 785 |      |      |      |      | 790  |      |     |      |      | 795 |      |      |      |      | 800 |  |  |
| Tyr | Lys  | Tyr  | Leu  | Ile  | Gly  | Lys  | Ala | Trp  | Lys  | Asn | Ile  | Gly  | Ile  | Ser  | Lys |  |  |
|     |      |      | 805  |      |      |      |     | 810  |      |     |      |      |      | 815  |     |  |  |
| Thr | Ala  | Asn  | Gly  | Ser  | Lys  | Ile  | Ser | Val  | Tyr  | Tyr | Leu  | Gly  | Asn  | Ser  | Thr |  |  |
|     |      |      | 820  |      |      |      |     | 825  |      |     |      |      |      | 830  |     |  |  |
| Pro | Thr  | Glu  | Lys  | Gly  | Gly  | Asn  | Thr | Thr  | Asn  | Leu | Pro  | Thr  | Asn  | Thr  | Thr |  |  |
|     |      | 835  |      |      |      |      | 840 |      |      |     |      |      | 845  |      |     |  |  |
| Ser | Asn  | Val  | Arg  | Ser  | Ala  | Asn  | Asn | Ala  | Leu  | Ala | Gln  | Asn  | Ala  | Pro  | Phe |  |  |
|     | 850  |      |      |      |      | 855  |     |      |      |     | 860  |      |      |      |     |  |  |
| Ala | Gln  | Pro  | Ser  | Ala  | Thr  | Pro  | Asn | Leu  | Val  | Ala | Ile  | Asn  | Gln  | His  | Asp |  |  |
| 865 |      |      |      |      | 870  |      |     |      |      | 875 |      |      |      |      | 880 |  |  |
| Phe | Gly  | Thr  | Ile  | Glu  | Ser  | Val  | Phe | Glu  | Leu  | Ala | Asn  | Arg  | Ser  | Lys  | Asp |  |  |
|     |      |      | 885  |      |      |      |     | 890  |      |     |      |      |      | 895  |     |  |  |
| Ile | Asp  | Thr  | Leu  | Tyr  | Ala  | Asn  | Ser | Gly  | Ala  | Gln | Gly  | Arg  | Asp  | Leu  | Leu |  |  |
|     |      | 900  |      |      |      |      |     | 905  |      |     |      |      | 910  |      |     |  |  |
| Gln | Thr  | Leu  | Leu  | Ile  | Asp  | Ser  | His | Asp  | Ala  | Gly | Tyr  | Ala  | Arg  | Gln  | Met |  |  |
|     |      | 915  |      |      |      |      | 920 |      |      |     |      |      | 925  |      |     |  |  |
| Ile | Asp  | Asn  | Thr  | Ser  | Thr  | Gly  | Glu | Ile  | Thr  | Lys | Gln  | Leu  | Asn  | Ala  | Ala |  |  |
|     | 930  |      |      |      |      | 935  |     |      |      |     | 940  |      |      |      |     |  |  |
| Thr | Thr  | Thr  | Leu  | Asn  | Asn  | Ile  | Ala | Ser  | Leu  | Glu | His  | Lys  | Thr  | Ser  | Ser |  |  |
| 945 |      |      |      | 950  |      |      |     |      | 955  |     |      |      |      |      | 960 |  |  |
| Leu | Gln  | Thr  | Leu  | Ser  | Leu  | Ser  | Asn | Ala  | Met  | Ile | Leu  | Asn  | Ser  | Arg  | Leu |  |  |
|     |      |      | 965  |      |      |      |     | 970  |      |     |      |      |      | 975  |     |  |  |
| Val | Asn  | Leu  | Ser  | Arg  | Arg  | His  | Thr | Asn  | Asn  | Ile | Asp  | Ser  | Phe  | Ala  | Gln |  |  |
|     |      | 980  |      |      |      |      |     | 985  |      |     |      |      | 990  |      |     |  |  |
| Arg | Leu  | Gln  | Ala  | Leu  | Lys  | Asp  | Gln | Lys  | Phe  | Ala | Ser  | Leu  | Glu  | Ser  | Ala |  |  |
|     |      | 995  |      |      |      | 1000 |     |      |      |     |      | 1005 |      |      |     |  |  |
| Ala | Glu  | Val  | Leu  | Tyr  | Gln  | Phe  | Ala | Pro  | Lys  | Tyr | Glu  | Lys  | Pro  | Thr  | Asn |  |  |
|     | 1010 |      |      |      | 1015 |      |     |      |      |     | 1020 |      |      |      |     |  |  |
| Val | Trp  | Ala  | Asn  | Ala  | Ile  | Gly  | Gly | Thr  | Ser  | Leu | Asn  | Asn  | Gly  | Gly  | Asn |  |  |
| 025 |      |      |      | 1030 |      |      |     |      | 1035 |     |      |      |      | 1040 |     |  |  |
| Ala | Ser  | Leu  | Tyr  | Gly  | Thr  | Ser  | Ala | Gly  | Val  | Asp | Ala  | Tyr  | Leu  | Asn  | Gly |  |  |
|     |      |      | 1045 |      |      |      |     | 1050 |      |     |      |      | 1055 |      |     |  |  |
| Glu | Val  | Glu  | Ala  | Ile  | Val  | Gly  | Gly | Phe  | Gly  | Ser | Tyr  | Gly  | Tyr  | Ser  | Ser |  |  |
|     |      | 1060 |      |      |      | 1065 |     |      |      |     |      | 1070 |      |      |     |  |  |
| Phe | Asn  | Asn  | Gln  | Ala  | Asn  | Ser  | Leu | Asn  | Ser  | Gly | Ala  | Asn  | Asn  | Thr  | Asn |  |  |
|     | 1075 |      |      |      |      | 1080 |     |      |      |     | 1085 |      |      |      |     |  |  |
| Phe | Gly  | Val  | Tyr  | Ser  | Arg  | Ile  | Phe | Ala  | Asn  | Gln | His  | Glu  | Phe  | Asp  | Phe |  |  |
|     | 1090 |      |      |      | 1095 |      |     |      |      |     | 1100 |      |      |      |     |  |  |
| Glu | Ala  | Gln  | Gly  | Ala  | Leu  | Gly  | Ser | Asp  | Gln  | Ser | Ser  | Leu  | Asn  | Phe  | Lys |  |  |
| 105 |      |      |      | 1110 |      |      |     |      | 1115 |     |      |      |      | 1120 |     |  |  |
| Ser | Ala  | Leu  | Leu  | Arg  | Asp  | Leu  | Asn | Gln  | Ser  | Tyr | Asn  | Tyr  | Leu  | Ala  | Tyr |  |  |
|     |      |      | 1125 |      |      |      |     | 1130 |      |     |      |      | 1135 |      |     |  |  |
| Ser | Ala  | Ala  | Thr  | Arg  | Ala  | Ser  | Tyr | Gly  | Tyr  | Asp | Phe  | Ala  | Phe  | Phe  | Arg |  |  |
|     | 1140 |      |      |      |      | 1145 |     |      |      |     |      | 1150 |      |      |     |  |  |
| Asn | Ala  | Leu  | Val  | Leu  | Lys  | Pro  | Ser | Val  | Gly  | Val | Ser  | Tyr  | Asn  | His  | Leu |  |  |
|     | 1155 |      |      |      |      | 1160 |     |      |      |     | 1165 |      |      |      |     |  |  |
| Gly | Ser  | Thr  | Asn  | Phe  | Lys  | Ser  | Asn | Ser  | Asn  | Gln | Val  | Ala  | Leu  | Lys  | Asn |  |  |
|     | 1170 |      |      |      | 1175 |      |     |      | 1180 |     |      |      |      |      |     |  |  |
| Gly | Ser  | Ser  | Ser  | Gln  | His  | Leu  | Phe | Asn  | Ala  | Ser | Ala  | Asn  | Val  | Glu  | Ala |  |  |

185                      1190                      1195                      1200  
 Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met Asn Ala Gly Val  
                          1205                      1210                      1215  
 Leu Gln Glu Phe Ala Asn Phe Gly Ser Ser Asn Ala Val Ser Leu Asn  
                          1220                      1225                      1230  
 Thr Phe Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg  
                          1235                      1240                      1245  
 Val Met Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu Asn  
                          1250                      1255                      1260  
 Leu Gly Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly His Phe  
 265                      1270                      1275                      1280  
 Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe  
                          1285                      1290

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...1284
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTAGTAGAAA TTGAAGCGAT AGCCATTAAG TAATTTATTA AAGGGACTAT CAGC ATG | 57  |
| Met                                                             |     |
| 1                                                               |     |
| AAA AAA GAG GTC GTG GTC ATA GGC GGT GGG ATT GTA GGG CTT TCT TGT | 105 |
| Lys Lys Glu Val Val Val Ile Gly Gly Gly Ile Val Gly Leu Ser Cys |     |
| 5 10 15                                                         |     |
| GCG TAT TCT ATG CAC AAG TTA GGC CAT AAG GTC TGC GTG ATA GAA AAA | 153 |
| Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu Lys |     |
| 20 25 30                                                        |     |
| AAC GAT GGC GCA AAC GGC ACT TCT TTT GGG AAT GCT GGG CTT ATT TCT | 201 |
| Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile Ser |     |
| 35 40 45                                                        |     |
| GCG TTT AAA AAA GCC CCA CTC TCA TGC CCT GGT GTG GTG TTA GAC ACC | 249 |
| Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp Thr |     |
| 50 55 60 65                                                     |     |
| CTG AAG CTC ATG CTC AAA AAC CAA GCC CCT TTA AAA TTC CAT TTC GGG | 297 |
| Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe Gly |     |
| 70 75 80                                                        |     |
| CTT AAT TTA AAG CTC TAT CAA TGG ATT TTA AAA TTT GTA AAA AGC GCG | 345 |





AAC ATG AAA AAG AAT TTA GCC GCT TTC ACG CAG CCT TTT GAA ATG AAA 1065  
Asn Met Lys Lys Asn Leu Ala Ala Phe Thr Gln Pro Phe Glu Met Lys  
325 330 335  
GAC GCC ATA GAG TGG TGC GGT TTC AGA CCC TTA ACC CCT AAT GAT ATT 1113  
Asp Ala Ile Glu Trp Cys Gly Phe Arg Pro Leu Thr Pro Asn Asp Ile  
340 345 350  
CCT TAT TTG GGC TAT GAC AAA CGC TAT AAA AAC TTA ATC CAT GCG ACA 1161  
Pro Tyr Leu Gly Tyr Asp Lys Arg Tyr Lys Asn Leu Ile His Ala Thr  
355 360 365  
GGG CTA GGG TGG CTT GGC ATC ACT TTT GGC CCA GCC ATT GGT AAA ATC 1209  
Gly Leu Gly Trp Leu Gly Ile Thr Phe Gly Pro Ala Ile Gly Lys Ile  
370 375 380 385  
ATC GCC AAT TTG AGC CAA GAC GGA GCG AAT GAA AAA AAT GCC GAT ATT 1257  
Ile Ala Asn Leu Ser Gln Asp Gly Ala Asn Glu Lys Asn Ala Asp Ile  
390 395 400  
ATG CTT TTT TCT GCA TTT TTT AGG GAT TAAGGAATTT CTTTTTTAAA CCCTAGT 1311  
Met Leu Phe Ser Ala Phe Phe Arg Asp  
405 410  
TTATTAAGGA GTTTTTTATGG AAAC 1335

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Lys Lys Glu Val Val Ile Gly Gly Gly Ile Val Gly Leu Ser  
1 5 10 15  
Cys Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu  
20 25 30  
Lys Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile  
35 40 45  
Ser Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp  
50 55 60  
Thr Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe  
65 70 75 80  
Gly Leu Asn Leu Lys Leu Tyr Gln Trp Ile Leu Lys Phe Val Lys Ser  
85 90 95  
Ala Asn Ala Lys Ser Thr His Arg Thr Met Ala Leu Phe Glu Arg Tyr  
100 105 110  
Gly Trp Leu Ser Ile Asp Met Tyr His Gln Met Leu Lys Asp Gly Met  
115 120 125  
Asp Phe Trp Tyr Lys Glu Asp Gly Leu Leu Met Ile Tyr Thr Leu Glu  
130 135 140  
Glu Ser Phe Glu Lys Lys Leu Lys Thr Cys Asp Asn Ser Gly Ala Tyr





|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAT TCC ATA CGC TAT AAC AAA TAT TTG CCC GTA GGC TCT CAC CAT TTA | 824  |
| Asn Ser Ile Arg Tyr Asn Lys Tyr Leu Pro Val Gly Ser His His Leu |      |
| 245 250 255                                                     |      |
| ACC ACG GAT TTA TCG CAC ATG CTC AAC ACC CCA TTC CCT TAC GCT GAA | 872  |
| Thr Thr Asp Leu Ser His Met Leu Asn Thr Pro Phe Pro Tyr Ala Glu |      |
| 260 265 270                                                     |      |
| GAA GTT AAG ATC AAA TAC GGG GAT CTT TCT TTT GAA GGC GGC GAA GAA | 920  |
| Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly Glu Glu |      |
| 275 280 285 290                                                 |      |
| ACG CCC TCT CAA AAT GTC CAA ATC CCT ACC ACC GGC TCG GAT GGC CAT | 968  |
| Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Gly Ser Asp Gly His     |      |
| 295 300 305                                                     |      |
| GAA AGC CAT ATT GTG CCG CTT AGT GAA ATC CAA ACT ATC ATG AGA GAA | 1016 |
| Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met Arg Glu |      |
| 310 315 320                                                     |      |
| AGG GCT TTA GAA ACT TTT AAA ATC ATC CAC AGG AGC ATT CAA GAT AGC | 1064 |
| Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln Asp Ser |      |
| 325 330 335                                                     |      |
| GGC TTA GAA GAG CAT TTG GGC GGA GGC GTT GTG TTA ACC GGT GGC ATG | 1112 |
| Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly Gly Met |      |
| 340 345 350                                                     |      |
| GCT TTA ATG AAA GGG ATC AAA GAA TTA GCC AGA ACC CAT TTC ACT AAT | 1160 |
| Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe Thr Asn |      |
| 355 360 365 370                                                 |      |
| TAC CCG GTG CGT TTG GCA GCC CCT GTG GAA AAA TAC AAT ATC ATG GGC | 1208 |
| Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile Met Gly |      |
| 375 380 385                                                     |      |
| ATG TTT GAA GAT TTG AAA GAC CCT CGC TTT TCA GTC GTA GTT GGC TTG | 1256 |
| Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val Gly Leu |      |
| 390 395 400                                                     |      |
| ATT TTA TAC AAA GCA GGG GGG CAT ACC AAT TAT GAA AGA GAC TCT AAA | 1304 |
| Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp Ser Lys |      |
| 405 410 415                                                     |      |
| GGG GTT ATC CGC TAC CAT GAA AGC GAT GAT TAC ACA AGA ACA GCC CAT | 1352 |
| Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr Ala His |      |
| 420 425 430                                                     |      |
| CAA TCA AGC CCT ACC CCC CAT ATC CAT TCA TCG CCC ACA GAA AGG AAT | 1400 |
| Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu Arg Asn |      |
| 435 440 445 450                                                 |      |
| TTG AGC GAT TTA AAA GCC CCT AGT GCT CCT TTA AAC ACC GCT AAA AAC | 1448 |
| Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala Lys Asn |      |
| 455 460 465                                                     |      |
| GAT GAC TTT TTA CCT ATA AAA CCC ACC GAA CAA AAA GGT TTT TTT AAA | 1496 |
| Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys |      |

AGT TTC CTT GAT AAG ATT TCT AAA TTC TTT TAAGATACAG CCATTTCTTT ATG 1549  
 Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe  
 485 490

CGATAAAAAC GCCTTGATGG TTATCAAAAG 1579

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | His | Lys | Glu | Ile | Val | Ile | Gly | Val | Asp | Leu | Gly | Ser | Arg | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Cys | Ala | Ile | Val | Ala | Glu | Phe | Lys | Glu | Gly | Ile | Leu | Arg | Ile | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Thr | Ala | His | Gln | Asp | Ser | Lys | Glu | Ile | Asn | Ser | Lys | Ala | Ile | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Gly | Arg | Ile | Asn | Ser | Leu | Ala | His | Ala | Ser | Asn | Ala | Ile | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Ile | Asn | Ser | Ala | Lys | Met | Ala | Gly | Leu | Asn | Ala | Asp | Glu | Asp |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Asn | Asn | Pro | Met | Pro | His | Phe | Gly | Glu | Tyr | His | Pro | Lys | Thr | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ile | Val | Ser | Phe | Ser | Gly | Ala | Tyr | Thr | Glu | Ser | Ile | Arg | Asp | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Thr | Gly | Val | Ala | Ser | Thr | Lys | Asp | Asn | Val | Val | Thr | Ile | Asp | Glu | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Arg | Ala | Ile | Asn | Ser | Ala | Cys | Ala | Lys | Ala | Gly | Leu | Asp | Asn | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Lys | His | Ile | Leu | His | Ala | Leu | Pro | Tyr | Arg | Phe | Thr | Leu | Asp | Lys | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Val | Asn | Asp | Pro | Leu | Gly | Met | Ser | Gly | Thr | Arg | Leu | Glu | Val | Phe |
|     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |     |
| Ile | His | Ile | Val | Tyr | Thr | Glu | Lys | Asn | Asn | Ile | Glu | Asn | Leu | Glu | Lys |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Ile | Met | Ile | Gln | Ser | Gly | Val | Glu | Ile | Glu | Asn | Ile | Val | Ile | Asn | Ser |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Tyr | Ala | Ala | Ser | Ile | Ala | Thr | Leu | Ser | Asn | Asp | Glu | Arg | Glu | Leu | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Val | Ala | Cys | Val | Asp | Met | Gly | Gly | Glu | Thr | Cys | Asn | Leu | Thr | Ile | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Gly | Asn | Ser | Ile | Arg | Tyr | Asn | Lys | Tyr | Leu | Pro | Val | Gly | Ser | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| His | Leu | Thr | Thr | Asp | Leu | Ser | His | Met | Leu | Asn | Thr | Pro | Phe | Pro | Tyr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Glu | Glu | Val | Lys | Ile | Lys | Tyr | Gly | Asp | Leu | Ser | Phe | Glu | Gly | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Glu | Thr | Pro | Ser | Gln | Asn | Val | Gln | Ile | Pro | Thr | Thr | Gly | Ser | Asp |

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 290                                                             |     | 295 |     | 300 |
| Gly His Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met |     |     |     |     |
| 305                                                             |     | 310 |     | 315 |
| Arg Glu Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln |     |     |     |     |
|                                                                 | 325 |     | 330 | 335 |
| Asp Ser Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly |     |     |     |     |
|                                                                 | 340 |     | 345 | 350 |
| Gly Met Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe |     |     |     |     |
|                                                                 | 355 |     | 360 | 365 |
| Thr Asn Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile |     |     |     |     |
|                                                                 | 370 |     | 375 | 380 |
| Met Gly Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val |     |     |     |     |
| 385                                                             |     | 390 |     | 395 |
| Gly Leu Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp |     |     |     |     |
|                                                                 | 405 |     | 410 | 415 |
| Ser Lys Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr |     |     |     |     |
|                                                                 | 420 |     | 425 | 430 |
| Ala His Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu |     |     |     |     |
|                                                                 | 435 |     | 440 | 445 |
| Arg Asn Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala |     |     |     |     |
|                                                                 | 450 |     | 455 | 460 |
| Lys Asn Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe |     |     |     |     |
| 465                                                             |     | 470 |     | 475 |
| Phe Lys Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe                 |     |     |     | 480 |
|                                                                 | 485 |     | 490 |     |

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1934
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGCGCTTGAA ATTTTGTAGCC ATTTATGACA CGAATTTAGA CGAATTTTAC ATG ATA | 56  |
| Met Ile                                                         |     |
| 1                                                               |     |
| AGA GTG GCA GGG CTT AAA CAA CTC TAT GAG CAT AAA ATC GCC TCT AAA | 104 |
| Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala Ser Lys |     |
| 5 10 15                                                         |     |
| GGC ATT GAT GGC GCA AGC CCT GAA GAA CAA TTA GAA AAA ATC AAG CAT | 152 |
| Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile Lys His |     |
| 20 25 30                                                        |     |
| TAT TTA GCG CAT GAA ATT GAA GAA AGG GAG TTA GAA TTC CAA AAA ATC | 200 |





|                                                                 |      |
|-----------------------------------------------------------------|------|
| CCT CAT TTC AAT GAA AAC GAT CTT TTC AAA TCT ATA GAA AAA CAG GAT | 920  |
| Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys Gln Asp |      |
| 275 280 285 290                                                 |      |
| CTG TTG CTG TTT CAT CCT TAT GAA AGT TTT GAG CCT GTG ATT GAT TTA | 968  |
| Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile Asp Leu |      |
| 295 300 305                                                     |      |
| ATA GAG CAA GCC GCT AGC GAT CCA GCC ACC CTT TCT ATC AAA ATG ACG | 1016 |
| Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys Met Thr |      |
| 310 315 320                                                     |      |
| CTT TAT CGT GTG GGC AAG CAT TCC CCC ATT GTC AAA GCT TTG ATT GAA | 1064 |
| Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu Ile Glu |      |
| 325 330 335                                                     |      |
| GCG GCG AGC AAG ATT CAA GTG AGC GTT TTA GTG GAA TTA AAA GCG CGC | 1112 |
| Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys Ala Arg |      |
| 340 345 350                                                     |      |
| TTT GAT GAA GAG AGC AAT CTG CAC TGG GCA AAA GCT TTA GAA AGG GCG | 1160 |
| Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu Arg Ala |      |
| 355 360 365 370                                                 |      |
| GGC GCG TTA GTC GTT TAT GGC GTT TTC AAA CTC AAA GTG CAT GCT AAA | 1208 |
| Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His Ala Lys |      |
| 375 380 385                                                     |      |
| ATG CTA TTG ATC ACT AAA AAA ACA GAC AAC CAA TTA CGC CAT TTC ACC | 1256 |
| Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His Phe Thr |      |
| 390 395 400                                                     |      |
| CAT TTA AGC ACG GGC AAT TAC AAC CCT TTG AGC GCT AAA GTC TAT ACC | 1304 |
| His Leu Ser Thr Gly Asn Tyr Asn Pro Leu Ser Ala Lys Val Tyr Thr |      |
| 405 410 415                                                     |      |
| GAT GTG AGT TTT TTT AGC GCT AAA AAT GAA ATC GCT AAC GAC ATT ATC | 1352 |
| Asp Val Ser Phe Phe Ser Ala Lys Asn Glu Ile Ala Asn Asp Ile Ile |      |
| 420 425 430                                                     |      |
| AAG CTT TTC CAT TCC TTG CTC ACT AGC AGC GCG ACT AAT AGC GCA TTA | 1400 |
| Lys Leu Phe His Ser Leu Leu Thr Ser Ser Ala Thr Asn Ser Ala Leu |      |
| 435 440 445 450                                                 |      |
| GAA ACG CTT TTT ATG GCA CCC AAA CAA ATC AAG CCT AAA ATC ATT GAA | 1448 |
| Glu Thr Leu Phe Met Ala Pro Lys Gln Ile Lys Pro Lys Ile Ile Glu |      |
| 455 460 465                                                     |      |
| CTC ATT CAA AAT GAA ATG AAT CAC CAA CAA GAA GGC TAT ATC ATT TTA | 1496 |
| Leu Ile Gln Asn Glu Met Asn His Gln Gln Glu Gly Tyr Ile Ile Leu |      |
| 470 475 480                                                     |      |
| AAA GCC AAC GCC CTA GTG GAT AGC GAA ATC ATT GAA TGG CTC TAT CAA | 1544 |
| Lys Ala Asn Ala Leu Val Asp Ser Glu Ile Ile Glu Trp Leu Tyr Gln |      |
| 485 490 495                                                     |      |
| GCC TCT CAA AAA GGG GTT AAA ATT GAT CTC ATT ATT AGA GGG ATT TGC | 1592 |
| Ala Ser Gln Lys Gly Val Lys Ile Asp Leu Ile Ile Arg Gly Ile Cys |      |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Glu | Gln | Leu | Tyr | Ala | Leu | Val | Leu | Pro | Phe | Lys | Leu | Asp | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Thr | Phe | Pro | Pro | Leu | Ala | Asn | Leu | Thr | Phe | Ala | Leu | Phe | Ala | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Lys | Asp | Lys | Glu | Thr | Gln | Ile | Ile | Ser | Tyr | Ala | Leu | Ile | Lys | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Pro |
| Ser | Phe | Ile | Phe | Arg | Phe | Val | Glu | Leu | Glu | Lys | Gly | Leu | Phe | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     | Leu |
| Ala | Glu | Glu | Ile | Val | Glu | Ala | His | Leu | Glu | Glu | Leu | Phe | Leu | Glu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Ile | Leu | Asp | Cys | Met | Ala | Phe | Arg | Val | Thr | Cys | Asp | Ala | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Ala | Ile | Thr | Glu | Asp | Glu | Ala | His | Asp | Tyr | Ala | Asp | Leu | Met | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Lys |
| Ser | Leu | Arg | Lys | Arg | Asn | Gln | Gly | Glu | Ile | Val | Arg | Leu | Gln | Thr |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     | Gln |
| Lys | Gly | Ser | Gln | Glu | Leu | Leu | Lys | Thr | Leu | Leu | Ala | Ser | Leu | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     | Ser |
| Phe | Gln | Thr | His | Ser | Tyr | Lys | Lys | His | Lys | Leu | Thr | Gly | Met | His |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Tyr | Lys | Ser | Ala | Ile | Met | Leu | Asn | Leu | Gly | Asp | Leu | Trp | Glu | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |
| Asn | His | Ser | Asp | Phe | Lys | Ala | Leu | Lys | Ser | Pro | Asn | Phe | Thr | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 | Lys |
| Ile | His | Pro | His | Phe | Asn | Glu | Asn | Asp | Leu | Phe | Lys | Ser | Ile | Glu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     | Lys |
| Gln | Asp | Leu | Leu | Leu | Phe | His | Pro | Tyr | Glu | Ser | Phe | Glu | Pro | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     | Ile |
| Asp | Leu | Ile | Glu | Gln | Ala | Ala | Ser | Asp | Pro | Ala | Thr | Leu | Ser | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | Lys |
| Met | Thr | Leu | Tyr | Arg | Val | Gly | Lys | His | Ser | Pro | Ile | Val | Lys | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |
| Ile | Glu | Ala | Ala | Ser | Lys | Ile | Gln | Val | Ser | Val | Leu | Val | Glu | Leu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 | Lys |
| Ala | Arg | Phe | Asp | Glu | Glu | Ser | Asn | Leu | His | Trp | Ala | Lys | Ala | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     | Glu |
| Arg | Ala | Gly | Ala | Leu | Val | Val | Tyr | Gly | Val | Phe | Lys | Leu | Lys | Val |
|     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     | His |
| Ala | Lys | Met | Leu | Leu | Ile | Thr | Lys | Lys | Thr | Asp | Asn | Gln | Leu | Arg |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |
| Phe | Thr | His | Leu | Ser | Thr | Gly | Asn | Tyr | Asn | Pro | Leu | Ser | Ala | Lys |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |
| Tyr | Thr | Asp | Val | Ser | Phe | Phe | Ser | Ala | Lys | Asn | Glu | Ile | Ala | Asn |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 | Asp |
| Ile | Ile | Lys | Leu | Phe | His | Ser | Leu | Leu | Thr | Ser | Ser | Ala | Thr | Asn |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     | Ser |
| Ala | Leu | Glu | Thr | Leu | Phe | Met | Ala | Pro | Lys | Gln | Ile | Lys | Pro | Lys |
|     | 450 |     |     |     |     | 455 |     |     |     | 460 |     |     |     | Ile |
| Ile | Glu | Leu | Ile | Gln | Asn | Glu | Met | Asn | His | Gln | Gln | Glu | Gly | Tyr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |
| Ile | Leu | Lys | Ala | Asn | Ala | Leu | Val | Asp | Ser | Glu | Ile | Ile | Glu | Trp |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     | 495 |
| Tyr | Gln | Ala | Ser | Gln | Lys | Gly | Val | Lys | Ile | Asp | Leu | Ile | Ile | Arg |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 | Gly |
| Ile | Cys | Cys | Leu | Lys | Pro | Gln | Val | Lys | Gly | Leu | Ser | Glu | Asn | Ile |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     | Arg |
| Val | Tyr | Ser | Ile | Val | Gly | Lys | Tyr | Leu | Glu | His | Ala | Arg | Ile | Tyr |

530 535 540  
Phe Lys His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg  
545 550 555 560  
Asn Leu Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys  
565 570 575  
Ile Ala His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr  
580 585 590  
Leu Lys Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser  
595 600 605  
Asn Pro Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala  
610 615 620  
Leu Lys Thr Phe  
625

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...563
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TATAATATAG ATTTTATTTT AGCTAAAAAT GGCATGGGTT TTAGCAAGGA ATG GGC 56  
Met Gly  
1

TTG AAA AAT CTC TCA ACA CTT CTG GTG TTT TTA TTC TTT TGT TTA GGG 104  
Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys Leu Gly  
5 10 15

TGT GTG AGC AAT TTT AAT GAA GAC ACT TAC ACG CTA GAC TTA GTT TTA 152  
Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu Val Leu  
20 25 30

GAA AAA AAG ATC CAA GCC AGC AGG AAA GGT GAA ATC ACC CAA GAT AAT 200  
Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln Asp Asn  
35 40 45 50

GTG CCT ATC ATC ACG GCT ATC GCT ACG CAT TTA AAC GAT GTG GAT AGC 248  
Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val Asp Ser  
55 60 65

GGC ACT TAC TAT GAC CAT GAG TAT TTT TTA GTG GAG ATT TTC ACG CAA 296  
Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe Thr Gln  
70 75 80

AAT AAC GAC TGG ATA GAT GAT GGC TAT ATT TCT TAT GAA CTT TTT GGC 344

Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu Phe Gly  
85 90 95

ACA AAA CCT ATA GGC TCA GAG CCT TTA TGG GTG CGA GAA ATC ACA AAA 392  
Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile Thr Lys  
100 105 110

GAT GAA TTT GAT GGC ATT TTA GAA ACC ACG AAC AGG TGG AGC AGA GCT 440  
Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser Arg Ala  
115 120 125 130

TTT TTG CTC GCT TTT AAC AAA TTG GAT TAT TTA GCG GTT CAA GAA GCC 488  
Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln Glu Ala  
135 140 145

AAA CTA GAG CTT GAT GCC TAT AGT TTG GGC AAG ATT GTT TTT AAT TTC 536  
Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe Asn Phe  
150 155 160

GCT TAT CAA GTC CCC CTA CCT CAA TTT TAATGCGCTT AGATTACGCC TTATTCA 590  
Ala Tyr Gln Val Pro Leu Pro Gln Phe  
165 170

GTCAGCATTT AGTAAATAGC AGAGAA 616

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Gly Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys  
1 5 10 15

Leu Gly Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu  
20 25 30

Val Leu Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln  
35 40 45

Asp Asn Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val  
50 55 60

Asp Ser Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe  
65 70 75 80

Thr Gln Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu  
85 90 95

Phe Gly Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile  
100 105 110

Thr Lys Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser  
115 120 125

Arg Ala Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln  
130 135 140

Glu Ala Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe  
145 150 155 160

Asn Phe Ala Tyr Gln Val Pro Leu Pro Gln Phe  
165 170

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 966...2291
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
ATTGTGAATT AGGAGTGAGC GTGAATAGTA ATGGCAATAA AGACAAACAA CAGCAGAATG 60
TAAGCAGTGG GATTTCTCAA ATCTCATTA AAAAGGTGGC AACTTTTGAT GAAAATGGGG 120
CGAGTTTTGA GAATTTAAAT TCTATCAACT TTATTTATGG GGCTAATGGG AGCGGTAAGA 180
CAACCACTTC TAGTTTTTTA AAAAATCTAG CTGAAAATGG GATTGAAGAC AAGTTTGCTA 240
ATAGTAAAT AGCATGGTAT AACAAATGAGA GTTTAAAGAT TGAAGTTTAT AACAAGCAAT 300
TTAAAGAAGA GCAATTGAGA AACTCTCAAG TTAAAGGCAT TTTTACGCTC GGTAAAAAAA 360
CGAACGAGAA TTTAGAAAAA ATTGAAAGCA AGAAAGAATC AATAAACAAA GAGAATGAAA 420
AGAAAATAAA AAATGAAGCA AGCTTGCAAG TTTTAACACA AAAAAAGGAA AAGGAAGAAA 480
AGGATTTTGC TGATAGGTGT TGGGAAAAAC TTTATAAGAA AAATGAAGAG GATTTTAAAG 540
AAACGCTAGA AGGCTTTAAG CGTAAAGAGA AGTTTAAAGA AAAAATCCTT AAGGAATTTG 600
AAAACGATAA ATACAATCAA AGCGAAATAG TAGGGTTAGA AAAATTAAAG GAAAAAATTG 660
AGATTGTTTT TGGTGAAAAC CAAACAGAAT TGGCACTATT GGAATGCAAT TTAACAGATT 720
TTGATTTTAT TGAAAATCAT TCTATTTGGG AACAAAAAAT TGTAGGGAGT GGTGATGCAG 780
CCATTGCAGA TTTAATAAAA AGATTAAGCA ATGAAGATTG GGTAGCTCAA GGTAGAGAAT 840
ATATAAAAGA TAATAGTATA TGCCCTTTCT GTCAAAAAGA AACCATTACC GAAGAATTTA 900
AAAAACAAC AGAATCTTAT TTTGATACAA GTTATCAAGA ATCTATTGAA ACGATCAAGG 960
AAAAG ATG GAA GAC TAC GCA AGC AGA ACC GCT GGA GCA CTG GAG CGA CTT 1010
Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu
 1 5 10 15

GAT AAG ATT GTT GAA ACA GAA CAG AAG AAT CAA CAA ACT AAA TTG GAC 1058
Asp Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp
 20 25 30

ACA GAA AAT TTG AAA ATA ATT ATT GAA ACT TTG AGA AGT AAA ATC AAT 1106
Thr Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn
 35 40 45

GGG AAT CAG CAA AAG ATG CTT GAT AAA AGT AAA GAA ATG AGC AGA AAT 1154
Gly Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn
 50 55 60

TTT AAG CTT GAT AGC ACT AAA AAC GAG ATA GAC GCA ATT AAA GAT TTG 1202
Phe Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu
 65 70 75
```

|                                                                 |      |
|-----------------------------------------------------------------|------|
| ATT AAA AAG GCT AAT GAG CAA ATA GCC AAT TAT AAT GAG ATG ATA AAG | 1250 |
| Ile Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys |      |
| 80 85 90 95                                                     |      |
| GAT ATT GAA AAA CAG AAA AAG AGT TGT AAG GAA CAA ACT TGG AAA TTT | 1298 |
| Asp Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe |      |
| 100 105 110                                                     |      |
| CTA GTC AAT GAA TTT AAA AGT GAT ATA CAA GAA TAT AAT AAA AAG TAT | 1346 |
| Leu Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr |      |
| 115 120 125                                                     |      |
| TGC GGT TTG GAG AAA GGA ATA AAC AAT TTA GAG AAA GCA ATT AGT GAA | 1394 |
| Cys Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu |      |
| 130 135 140                                                     |      |
| AAT CAA GAA GAG GTA AAG AAA TTA GAA AAT GAA ATT AAG GAA TTA GAA | 1442 |
| Asn Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu |      |
| 145 150 155                                                     |      |
| AAA ACT ATG GTA AGC ATA AAG CCC ATT GTC AAT GAA ATC AAT ACG CTT | 1490 |
| Lys Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu |      |
| 160 165 170 175                                                 |      |
| TTA AAA GGG TAT GGA TTC GCG AAT TTT AGT TTG GCA TGC ACT GAA GAT | 1538 |
| Leu Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp |      |
| 180 185 190                                                     |      |
| GAA AAA TTT TAT CGT ATT CAA AGA GAA GAT GGT CAA TTA GTA GGA GAA | 1586 |
| Glu Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu |      |
| 195 200 205                                                     |      |
| ACA CTG AGC GAG GGT GAA GTT ACT TTC ATC ACT TTC TTA TAT TAT TAT | 1634 |
| Thr Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr |      |
| 210 215 220                                                     |      |
| CAT TTA GCA AAA GGC TCT TTA GAA GAG AAC GAT ATA TCA AAA AAT AAG | 1682 |
| His Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys |      |
| 225 230 235                                                     |      |
| GTT TTA GTG ATT GAT GAC CCC ATT TCA AGT TTG GAT AGC AAT ATA TTG | 1730 |
| Val Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu |      |
| 240 245 250 255                                                 |      |
| TTT ATA GTG AGT GTT TTA GTT AAA GAT CTT ATG AAA GAA GCC ATG GAA | 1778 |
| Phe Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu |      |
| 260 265 270                                                     |      |
| GAA AAA ACA AAC ATC AAG CAA GTT ATT ATA CTA ACC CAC AAC ACA TAT | 1826 |
| Glu Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr |      |
| 275 280 285                                                     |      |
| TTT TAC AAG GAA ATT ACA TTA GAA TGT GAT TTA AAA CGC TAT CAA GGG | 1874 |
| Phe Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly |      |
| 290 295 300                                                     |      |
| AAA TAT TCT TTT TGG ATA ATT AAA AAG GAT AAT AAT GTT TCA AAA ATT | 1922 |
| Lys Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile |      |







(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 51...3740  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTATGTGGGC TACAACATAG GCTTTTGATT AAACAAAATA AGGGAAAAAT ATG ATA  | 56  |
| Met Ile                                                         |     |
| 1                                                               |     |
| AAA AAA GCT AGA AAA TTC ATA CCA TTC TTT TTA ATT GGC TCC CTC TTA | 104 |
| Lys Lys Ala Arg Lys Phe Ile Pro Phe Phe Leu Ile Gly Ser Leu Leu |     |
| 5 10 15                                                         |     |
| GCT GAA GAC AAT GGC TGG TAT ATG TCT GTA GGC TAT CAA ATC GGT GGC | 152 |
| Ala Glu Asp Asn Gly Trp Tyr Met Ser Val Gly Tyr Gln Ile Gly Gly |     |
| 20 25 30                                                        |     |
| ACG CAA CAA TTC ATC AAT AAC AAA CAA CTT TTA GAA AAT CAA AAT ATC | 200 |
| Thr Gln Gln Phe Ile Asn Asn Lys Gln Leu Leu Glu Asn Gln Asn Ile |     |
| 35 40 45 50                                                     |     |
| ATC AAC AGC GTA ACC CAA AGC GCG ATC AAC ATT GCA GGG CCT ACT ACC | 248 |
| Ile Asn Ser Val Thr Gln Ser Ala Ile Asn Ile Ala Gly Pro Thr Thr |     |
| 55 60 65                                                        |     |
| GGC CTT ATC ACT TTA AGC TCT CAA ACC GTC ATT GAC GCT TTA GGC TAT | 296 |
| Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu Gly Tyr |     |
| 70 75 80                                                        |     |
| GGC GTG AGT AAC ACT GTT GGC AAC CAA TTA GAG GGC ATT TCT AAT ATC | 344 |
| Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser Asn Ile |     |
| 85 90 95                                                        |     |
| TTG AAT CAA ATT GGC AAA AGA AAA GAC TTT TAT TCT AGC CGT CAA ATC | 392 |
| Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg Gln Ile |     |
| 100 105 110                                                     |     |
| TCT AGC ATT TCC CAA CAA ATC ATA GGG CTT AAA GGA AGC TCT GAT CCC | 440 |
| Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser Asp Pro |     |
| 115 120 125 130                                                 |     |
| TTA AAA GCC CAT TCT TCA CAG ATC ACA GCC AAA CTC CTT TCC AAC ACC | 488 |
| Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser Asn Thr |     |
| 135 140 145                                                     |     |
| CAA AGC GCG TTT GAT CAG GGC ATC GCG CTA AGC ACT AAC ATC ATT AGC | 536 |
| Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile Ile Ser |     |
| 150 155 160                                                     |     |
| TCT ATC AAT AGC CTA AAC CCT AGC AAC AAC ACC CAA GAG GTT AAA AAA | 584 |
| Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val Lys Lys |     |
| 165 170 175                                                     |     |
| CAG CTC CAA AAC ACC GCG CAA TCC ATG ACA GAA TTG TTG CAA CAA ATT | 632 |
| Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln Gln Ile |     |

| 180                                                                                                                                                   | 185 | 190 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| GAA CAC AGC ATC ACT AAA ACC ACT AGC ACC ACT TAC GCG CAA TCC TTA<br>Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln Ser Leu<br>195 200 205 210 |     |     | 680  |
| CTC TCC AAT CTA ACC GAT GCG GTG AAT GCC TCT AGC AAT AAT ACC GCT<br>Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn Thr Ala<br>215 220 225     |     |     | 728  |
| TAT GTG AGC GCT CTT GTT AAC GCT TTA AAC ACT TTA GGG GTA GGG GTT<br>Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val Gly Val<br>230 235 240     |     |     | 776  |
| TTC CCC ACC ACA ACC ACA ACG CAT GTG GTG TTA AAC CCA CCG GGA CAA<br>Phe Pro Thr Thr Thr Thr Thr His Val Val Leu Asn Pro Pro Gly Gln<br>245 250 255     |     |     | 824  |
| GTC GTA TTC TAT CCA ACC AAT TCC ATT TTA GGC TCT ACT TCT TCA AAC<br>Val Val Phe Tyr Pro Thr Asn Ser Ile Leu Gly Ser Thr Ser Ser Asn<br>260 265 270     |     |     | 872  |
| AGC AAT AAC CAA CAA CAA TAC AAC AAC ACC CTT TTA ATG AAC ACC TTA<br>Ser Asn Asn Gln Gln Gln Tyr Asn Asn Thr Leu Leu Met Asn Thr Leu<br>275 280 285 290 |     |     | 920  |
| CAA GGG ACA TTA AGC GCT AAT ACT CAA AAT AAC CCC AAT GGT TGC GCC<br>Gln Gly Thr Leu Ser Ala Asn Thr Gln Asn Asn Pro Asn Gly Cys Ala<br>295 300 305     |     |     | 968  |
| AAT CAA GTC CAG TGT TTG GAG CAA TTC ATC CAA AAT TTA GCC CCT TTA<br>Asn Gln Val Gln Cys Leu Glu Gln Phe Ile Gln Asn Leu Ala Pro Leu<br>310 315 320     |     |     | 1016 |
| GCC GCA ACC CCC ACT TCA AAC AAC CAG GCC AAC CAG CAA GTC CAA GCC<br>Ala Ala Thr Pro Thr Ser Asn Asn Gln Ala Asn Gln Gln Val Gln Ala<br>325 330 335     |     |     | 1064 |
| ATC GCT CAA AAG CTT CAA AGC GTT GCT ATC AAC ACT TTA GAC AAC AAT<br>Ile Ala Gln Lys Leu Gln Ser Val Ala Ile Asn Thr Leu Asp Asn Asn<br>340 345 350     |     |     | 1112 |
| GCG ATC AAC AAC ACC ACC TAT AAT TTA AAC AAT TTG CAC AAC GCT TTG<br>Ala Ile Asn Asn Thr Thr Tyr Asn Leu Asn Asn Leu His Asn Ala Leu<br>355 360 365 370 |     |     | 1160 |
| AAT TTC CAA GCC TAT GAA AGC ACG ATA GAA CAA TAC AAT AAC GCT TTA<br>Asn Phe Gln Ala Tyr Glu Ser Thr Ile Glu Gln Tyr Asn Asn Ala Leu<br>375 380 385     |     |     | 1208 |
| AAA CAA ATT TCT TGG ATC AGT TTT ACT GAG CCT AAA AAC TTA CTC AAA<br>Lys Gln Ile Ser Trp Ile Ser Phe Thr Glu Pro Lys Asn Leu Leu Lys<br>390 395 400     |     |     | 1256 |
| AAC ACT TCC AAT AAC TAC CAA ATC GGC ACC GTT ACC AAC GCT CAA GGG<br>Asn Thr Ser Asn Asn Tyr Gln Ile Gly Thr Val Thr Asn Ala Gln Gly<br>405 410 415     |     |     | 1304 |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CAA AAT ATC AGC GCC TAT GAT TGC ATG ACT GCT ACC GGA AGC CTT TCT | 1352 |
| Gln Asn Ile Ser Ala Tyr Asp Cys Met Thr Ala Thr Gly Ser Leu Ser |      |
| 420 425 430                                                     |      |
| AGC AAT GCT TCT AGC GGG ATT TCA TGC TCA GCC ACA AGC TCC ACA AGT | 1400 |
| Ser Asn Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser Thr Ser |      |
| 435 440 445 450                                                 |      |
| TCC ACA AAT AGC TTT GAC AAT TCT TTA GTC GCT ACC TCC AAA GTC CAA | 1448 |
| Ser Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys Val Gln |      |
| 455 460 465                                                     |      |
| ACC ATC AAC GGC AAA GAG CAG ATC GGC GTG AAT TCT TTT AAC CTT GTC | 1496 |
| Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn Leu Val |      |
| 470 475 480                                                     |      |
| TCT CAA GTG TGG AGC GTT TAT AAT TCT TTA AAA ACT TCA GAA GAA AAT | 1544 |
| Ser Gln Val Trp Ser Val Tyr Asn Ser Leu Lys Thr Ser Glu Glu Asn |      |
| 485 490 495                                                     |      |
| TTG CAA AAA AAC GCC AAT ATT TTA TGC GCT AAT GGG ACG CAA TCT GGG | 1592 |
| Leu Gln Lys Asn Ala Asn Ile Leu Cys Ala Asn Gly Thr Gln Ser Gly |      |
| 500 505 510                                                     |      |
| ACA AGC TCA TGC AAT AGC TCT TCA GGG GGT TTG AGC ATC AGC GGG AAC | 1640 |
| Thr Ser Ser Cys Asn Ser Ser Ser Gly Gly Leu Ser Ile Ser Gly Asn |      |
| 515 520 525 530                                                 |      |
| GCC CAA TTG CAA AAT ATT TTA AGC CCT ACT AGT GGG ACT ACC ACT AAT | 1688 |
| Ala Gln Leu Gln Asn Ile Leu Ser Pro Thr Ser Gly Thr Thr Thr Asn |      |
| 535 540 545                                                     |      |
| ACT CAA GCT AAA AGC AAC GCT CCC AAA CTA AAA GCG ATG GTG GTG GTG | 1736 |
| Thr Gln Ala Lys Ser Asn Ala Pro Lys Leu Lys Ala Met Val Val Val |      |
| 550 555 560                                                     |      |
| AAT AAT GAA GAA GAA GCT AAA ACG GCC AAT TTA GCC CAA AGC AGC GGG | 1784 |
| Asn Asn Glu Glu Glu Ala Lys Thr Ala Asn Leu Ala Gln Ser Ser Gly |      |
| 565 570 575                                                     |      |
| ACA ACC ACA CAA TCT CCT AAC AGC ACG GTG ATG GGA GCT TTA AAC ACC | 1832 |
| Thr Thr Thr Gln Ser Pro Asn Ser Thr Val Met Gly Ala Leu Asn Thr |      |
| 580 585 590                                                     |      |
| GTG TTG CAA AAT GTC AGC AAT TTC CAA CAA AGC ATT CAA AAC GCT TTT | 1880 |
| Val Leu Gln Asn Val Ser Asn Phe Gln Gln Ser Ile Gln Asn Ala Phe |      |
| 595 600 605 610                                                 |      |
| CAA AAC CAA GAA AGT AAT ATC CAA GCT TGG GCG AAT GCG ATT TAT AAC | 1928 |
| Gln Asn Gln Glu Ser Asn Ile Gln Ala Trp Ala Asn Ala Ile Tyr Asn |      |
| 615 620 625                                                     |      |
| ACT AAT GGG AGT CAG TCG CAA GAG ATG ACA CCT AAC AAT AAC CAA GAT | 1976 |
| Thr Asn Gly Ser Gln Ser Gln Glu Met Thr Pro Asn Asn Asn Gln Asp |      |
| 630 635 640                                                     |      |
| TTA CGC ATC CAA TTG AGG GCG AAT TTT TAC CAG CTC ATC AAT ACC ATT | 2024 |
| Leu Arg Ile Gln Leu Arg Ala Asn Phe Tyr Gln Leu Ile Asn Thr Ile |      |

| 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| AAC | CAG | CAA | GTG | CCT | ACA | GAC | ATG | AAT | GCT | TTA | ATT | AAT | CAA | AGC | CAA | 2072 |  |
| Asn | Gln | Gln | Val | Pro | Thr | Asp | Met | Asn | Ala | Leu | Ile | Asn | Gln | Ser | Gln |      |  |
| 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |     |     |     |      |  |
| CAA | ACC | CAA | CAA | ACA | AGC | GGA | TCA | GCA | AGC | AAT | AAT | AAC | GCA | TGC | GCG | 2120 |  |
| Gln | Thr | Gln | Gln | Thr | Ser | Gly | Ser | Ala | Ser | Asn | Asn | Asn | Ala | Cys | Ala |      |  |
| 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |     | 690 |      |  |
| AGT | GGA | ATG | AGT | GGG | AGT | AAT | GGT | AAC | TGG | TGC | TAT | CAG | CAA | TGG | TCC | 2168 |  |
| Ser | Gly | Met | Ser | Gly | Ser | Asn | Gly | Asn | Trp | Cys | Tyr | Gln | Gln | Trp | Ser |      |  |
|     |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     | 705 |      |  |
| GAT | TCT | AAG | GCT | TAT | TAC | AGC | GGG | TTG | CAA | AGC | GCT | TTA | GGG | TAT | CAA | 2216 |  |
| Asp | Ser | Lys | Ala | Tyr | Tyr | Ser | Gly | Leu | Gln | Ser | Ala | Leu | Gly | Tyr | Gln |      |  |
| 710 |     |     |     |     | 715 |     |     |     |     | 720 |     |     |     |     |     |      |  |
| ACG | CAA | GCG | ACA | ACT | CAA | AGC | GGG | AGC | AAT | GGT | GGG | AAC | AGC | ATC | ACC | 2264 |  |
| Thr | Gln | Ala | Thr | Thr | Gln | Ser | Gly | Ser | Asn | Gly | Gly | Asn | Ser | Ile | Thr |      |  |
| 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |     |     |     |     |      |  |
| TAC | AAT | GTC | CAA | CAA | ATC | ACG | CTC | ACT | AGT | AAT | GGT | TTG | CTC | AAC | CAA | 2312 |  |
| Tyr | Asn | Val | Gln | Gln | Ile | Thr | Leu | Thr | Ser | Asn | Gly | Leu | Leu | Asn | Gln |      |  |
| 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |     |     |     |      |  |
| ATC | ATC | ACA | AAT | CTT | AAG | AGC | GTT | AAT | GGA | GGC | AAT | GGC | GCG | AGT | GGT | 2360 |  |
| Ile | Ile | Thr | Asn | Leu | Lys | Ser | Val | Asn | Gly | Gly | Asn | Gly | Ala | Ser | Gly |      |  |
| 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |     | 770 |      |  |
| ACA | GGC | AGT | GGG | AAT | GGC | ACC | AGT | CAA | ATC | AAC | ACA | GCC | TAC | CAG | ATG | 2408 |  |
| Thr | Gly | Ser | Gly | Asn | Gly | Thr | Ser | Gln | Ile | Asn | Thr | Ala | Tyr | Gln | Met |      |  |
| 775 |     |     |     |     | 780 |     |     |     |     | 785 |     |     |     |     |     |      |  |
| CTC | ACA | GAC | GCC | AGC | GAT | GGG | AAA | TTA | GGG | ACT | TAT | AGT | AGT | AGT | AGT | 2456 |  |
| Leu | Thr | Asp | Ala | Ser | Asp | Gly | Lys | Leu | Gly | Thr | Tyr | Ser | Ser | Ser | Ser |      |  |
| 790 |     |     |     |     | 795 |     |     |     |     | 800 |     |     |     |     |     |      |  |
| GGC | AGT | AAT | AAC | GGC | TAT | ACG | CCA | TGC | AAT | AGC | ACC | AAT | GGG | AGC | AAT | 2504 |  |
| Gly | Ser | Asn | Asn | Gly | Tyr | Thr | Pro | Cys | Asn | Ser | Thr | Asn | Gly | Ser | Asn |      |  |
| 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |     |     |     |     |      |  |
| AAA | ACG | AGT | GGG | AAC | AAT | TGT | TAT | GAA | CCC | AAC | AAA | CAA | CAA | AAC | GCC | 2552 |  |
| Lys | Thr | Ser | Gly | Asn | Asn | Cys | Tyr | Glu | Pro | Asn | Lys | Gln | Gln | Asn | Ala |      |  |
| 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |     |     |     |      |  |
| ACC | ACC | GCA | ACC | GCC | ACA | ACC | GAC | AGC | AAT | TTA | CAA | AAA | GTC | TAT | AAT | 2600 |  |
| Thr | Thr | Ala | Thr | Ala | Thr | Thr | Asp | Ser | Asn | Leu | Gln | Lys | Val | Tyr | Asn |      |  |
| 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |     | 850 |      |  |
| GAC | GCC | CAA | AAA | ATA | GCC | AAC | ATT | ATC | GCC | AGC | TCT | GGG | AAC | AAT | AAA | 2648 |  |
| Asp | Ala | Gln | Lys | Ile | Ala | Asn | Ile | Ile | Ala | Ser | Ser | Gly | Asn | Asn | Lys |      |  |
| 855 |     |     |     |     | 860 |     |     |     |     | 865 |     |     |     |     |     |      |  |
| GGC | GTT | GAA | AAC | GGC | TTA | AAA | CAA | TTC | TTT | GAA | GCG | TTA | AAA | AAT | AAT | 2696 |  |
| Gly | Val | Glu | Asn | Gly | Leu | Lys | Gln | Phe | Phe | Glu | Ala | Leu | Lys | Asn | Asn |      |  |
| 870 |     |     |     |     | 875 |     |     |     |     | 880 |     |     |     |     |     |      |  |



| 1110                                                              | 1115 | 1120 |      |
|-------------------------------------------------------------------|------|------|------|
| AAT TTT GGG CTA TTT GCT GGG GTC CAA CTG GGC GGC GCA ACC TGG CTT   |      |      | 3464 |
| Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr Trp Leu   |      |      |      |
| 1125                                                              | 1130 | 1135 |      |
| AGC TCC TTA AGG CAA CAA ATC ATT GAC AAC TGG GGG AGT GCT AAT GAC   |      |      | 3512 |
| Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala Asn Asp   |      |      |      |
| 1140                                                              | 1145 | 1150 |      |
| ATC CAT TCA ACG AAT TTT CAA GTG GCG CTG AAT TTT GGG GTG CGC ACC   |      |      | 3560 |
| Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val Arg Thr   |      |      |      |
| 1155                                                              | 1160 | 1165 | 1170 |
| AAC TTC GCG GAG TTT AAG CGT TTT GCT AAG AAA TTC CAC AAT CAA GGG   |      |      | 3608 |
| Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn Gln Gly   |      |      |      |
| 1175                                                              | 1180 | 1185 |      |
| GTC ATC AGC CAA AAG AGC GTG GAA TTT GGG ATC AAA GTG CCT CTC ATC   |      |      | 3656 |
| Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro Leu Ile   |      |      |      |
| 1190                                                              | 1195 | 1200 |      |
| AAT CAA GCG TAT TTG AAT AGC GCT GGA GCT GAT GTG AGT TAC AGG AGG   |      |      | 3704 |
| Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr Arg Arg   |      |      |      |
| 1205                                                              | 1210 | 1215 |      |
| CTT TAT ACT TTT TAT ATC AAT TAC ATC ATG GGG TTT TAAAAAAGGG TGTGTC |      |      | 3756 |
| Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe                   |      |      |      |
| 1220                                                              | 1225 | 1230 |      |
| ATGGAAATCT TACAATTCAT CGGCTATGGG AATATGG                          |      |      | 3793 |

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Lys | Lys | Ala | Arg | Lys | Phe | Ile | Pro | Phe | Phe | Leu | Ile | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Glu | Asp | Asn | Gly | Trp | Tyr | Met | Ser | Val | Gly | Tyr | Gln | Ile |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Thr | Gln | Gln | Phe | Ile | Asn | Asn | Lys | Gln | Leu | Leu | Glu | Asn | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ile | Ile | Asn | Ser | Val | Thr | Gln | Ser | Ala | Ile | Asn | Ile | Ala | Gly | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Gly | Leu | Ile | Thr | Leu | Ser | Ser | Gln | Thr | Val | Ile | Asp | Ala | Leu |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Tyr | Gly | Val | Ser | Asn | Thr | Val | Gly | Asn | Gln | Leu | Glu | Gly | Ile | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Ile | Leu | Asn | Gln | Ile | Gly | Lys | Arg | Lys | Asp | Phe | Tyr | Ser | Ser | Arg |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Ser | 100 | Ser | Ile | Ser | Gln | Gln | 105 | Ile | Ile | Gly | Leu | Lys | 110 | Gly | Ser | Ser |
| Asp | Pro | Leu | 115 | Lys | Ala | His | Ser | Ser | 120 | Gln | Ile | Thr | Ala | Lys | 125 | Leu | Leu | Ser |
| Asn | Thr | Gln | 130 | Ser | Ala | Phe | Asp | Gln | 135 | Gly | Ile | Ala | Leu | Ser | 140 | Thr | Asn | Ile |
| Ile | Ser | Ser | 145 | Ile | Asn | Ser | Leu | Asn | 150 | Pro | Ser | Asn | Asn | Thr | 155 | Gln | Glu | Val |
| Lys | Lys | Gln | 165 | Leu | Gln | Asn | Thr | Ala | 170 | Gln | Ser | Met | Thr | Glu | 175 | Leu | Leu | Gln |
| Gln | Ile | Glu | 180 | His | Ser | Ile | Thr | Lys | 185 | Thr | Thr | Ser | Thr | Thr | 190 | Tyr | Ala | Gln |
| Ser | Leu | Leu | 195 | Ser | Asn | Leu | Thr | Asp | 200 | Ala | Val | Asn | Ala | Ser | 205 | Ser | Asn | Asn |
| Thr | Ala | Tyr | 210 | Val | Ser | Ala | Leu | Val | 215 | Asn | Ala | Leu | Asn | Thr | 220 | Leu | Gly | Val |
| Gly | Val | Phe | 225 | Pro | Thr | Thr | Thr | Thr | 230 | His | Val | Val | Leu | Asn | 235 | Pro | Pro |     |
| Gly | Gln | Val | 245 | Val | Phe | Tyr | Pro | Thr | 250 | Asn | Ser | Ile | Leu | Gly | 255 | Ser | Thr | Ser |
| Ser | Asn | Ser | 260 | Asn | Asn | Gln | Gln | Gln | 265 | Tyr | Asn | Asn | Thr | Leu | 270 | Leu | Met | Asn |
| Thr | Leu | Gln | 275 | Gly | Thr | Leu | Ser | Ala | 280 | Asn | Thr | Gln | Asn | Asn | 285 | Pro | Asn | Gly |
| Cys | Ala | Asn | 290 | Gln | Val | Gln | Cys | Leu | 295 | Glu | Gln | Phe | Ile | Gln | 300 | Asn | Leu | Ala |
| Pro | Leu | Ala | 305 | Ala | Thr | Pro | Thr | Ser | 310 | Asn | Asn | Gln | Ala | Asn | 315 | Gln | Gln | Val |
| Gln | Ala | Ile | 325 | Ala | Gln | Lys | Leu | Gln | 330 | Ser | Val | Ala | Ile | Asn | 335 | Thr | Leu | Asp |
| Asn | Asn | Ala | 340 | Ile | Asn | Asn | Thr | Thr | 345 | Tyr | Asn | Leu | Asn | Asn | 350 | Leu | His | Asn |
| Ala | Leu | Asn | 355 | Phe | Gln | Ala | Tyr | Glu | 360 | Ser | Thr | Ile | Glu | Gln | 365 | Tyr | Asn | Asn |
| Ala | Leu | Lys | 370 | Gln | Ile | Ser | Trp | Ile | 375 | Ser | Phe | Thr | Glu | Pro | 380 | Lys | Asn | Leu |
| Leu | Lys | Asn | 385 | Thr | Ser | Asn | Asn | Tyr | 390 | Gln | Ile | Gly | Thr | Val | 395 | Thr | Asn | Ala |
| Gln | Gly | Gln | 405 | Asn | Ile | Ser | Ala | Tyr | 410 | Asp | Cys | Met | Thr | Ala | 415 | Thr | Gly | Ser |
| Leu | Ser | Ser | 420 | Asn | Ala | Ser | Ser | Gly | 425 | Ile | Ser | Cys | Ser | Ala | 430 | Thr | Ser | Ser |
| Thr | Ser | Ser | 435 | Thr | Asn | Ser | Phe | Asp | 440 | Asn | Ser | Leu | Val | Ala | 445 | Thr | Ser | Lys |
| Val | Gln | Thr | 450 | Ile | Asn | Gly | Lys | Glu | 455 | Gln | Ile | Gly | Val | Asn | 460 | Ser | Phe | Asn |
| Leu | Val | Ser | 465 | Gln | Val | Trp | Ser | Val | 470 | Tyr | Asn | Ser | Leu | Lys | 475 | Thr | Ser | Glu |
| Glu | Asn | Leu | 485 | Lys | Asn | Ala | Asn | Ile | 490 | Leu | Cys | Ala | Asn | Gly | 495 | Thr | Gln |     |
| Ser | Gly | Thr | 500 | Ser | Ser | Cys | Asn | Ser | 505 | Ser | Ser | Gly | Gly | Leu | 510 | Ser | Ile | Ser |
| Gly | Asn | Ala | 515 | Gln | Leu | Gln | Asn | Ile | 520 | Leu | Ser | Pro | Thr | Ser | 525 | Gly | Thr | Thr |
| Thr | Asn | Thr | 530 | Gln | Ala | Lys | Ser | Asn | 535 | Ala | Pro | Lys | Leu | Lys | 540 | Ala | Met | Val |
| Val | Val | Asn | 545 | Asn | Glu | Glu | Glu | Ala | 550 | Lys | Thr | Ala | Asn | Leu | 555 | Ala | Gln | Ser |





025                      1030                      1035                      1040  
 Ser Gln Tyr Ala Ala Lys Ser Thr Gln His Gly Met Ser Asn Gly  
                          1045                      1050                      1055  
 Leu Gly Val Gly Leu Gly Tyr Lys Tyr Phe Phe Gly Lys Ala Arg Lys  
                          1060                      1065                      1070  
 Leu Gly Leu Arg His Tyr Phe Phe Phe Asp Tyr Gly Phe Ser Glu Ile  
                          1075                      1080                      1085  
 Gly Leu Ala Asn Gln Ser Val Lys Ala Asn Ile Phe Ala Tyr Gly Val  
                          1090                      1095                      1100  
 Gly Thr Asp Phe Leu Trp Asn Leu Phe Arg Arg Thr Tyr Asn Thr Lys  
 105                      1110                      1115                      1120  
 Ala Leu Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr  
                          1125                      1130                      1135  
 Trp Leu Ser Ser Leu Arg Gln Gln Ile Asp Asn Trp Gly Ser Ala  
                          1140                      1145                      1150  
 Asn Asp Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val  
                          1155                      1160                      1165  
 Arg Thr Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn  
                          1170                      1175                      1180  
 Gln Gly Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro  
 185                      1190                      1195                      1200  
 Leu Ile Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr  
                          1205                      1210                      1215  
 Arg Arg Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe  
                          1220                      1225                      1230

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1226
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

|                                                                            |             |     |
|----------------------------------------------------------------------------|-------------|-----|
| TAAGGATAAA ATCAAGCGAT TAGCCCGAAT TTTAAGAGAG TATTAAG                        | ATG AAT AAA | 56  |
|                                                                            | Met Asn Lys |     |
|                                                                            | 1           |     |
| AAA GCG TAT TTT GGG GAG TTT GGA GGG AGT TTT GTT TCG GAG TTG TTA            |             | 104 |
| Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu            |             |     |
| 5                      10                      15                          |             |     |
| GTG CCT GCA TTA AGA GAA TTA GAA CAG GCG TTT GAT GCG TGT TTG AAA            |             | 152 |
| Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys            |             |     |
| 20                      25                      30                      35 |             |     |
| GAT GAA AAA TTC CAA AAA GAA TAT TTT CGT CTT TTA AAG GAT TTT GTG            |             | 200 |



ATT TTG CAT GGG AAT AAA ACC TAT CTT TTA CAA GAT GAT GAA GGC CAG 920  
 Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp Glu Gly Gln  
 280 285 290

ATT GCA GAA AGC CAT AGC ATT AGC GCC GGG CTT GAT TAT CCA GGA GTG 968  
 Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val  
 295 300 305

GGG CCA GAA CAC AGC TAT TTA AAA GAA AGT GGG CGT GCG GTT TAT GAA 1016  
 Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala Val Tyr Glu  
 310 315 320

AGC GCA AGC GAT GCT GAA GCG CTA GAA GCC TTC AAG TTG TTG TGC CAA 1064  
 Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln  
 325 330 335

AAA GAA GGC ATT ATC CCA GCG CTA GAA AGC TCA CAC GCC TTA GCG TAT 1112  
 Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr  
 340 345 350 355

GCC TTA AAG CTC GCT CAA AAA TGC GAA GAA GAA AGC ATC ATC GTA GTG 1160  
 Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val  
 360 365 370

AAT TTA AGC GGC AGA GGG GAT AAG GAT TTA AGC ACC GTT TAT AAC GCT 1208  
 Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala  
 375 380 385

TTA AAA GGA GGT TTA AAA TGAGGTATCA AAACATGTTT GAAACCTTAA AAA 1259  
 Leu Lys Gly Leu Lys  
 390

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Asn Lys Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser  
 1 5 10 15  
 Glu Leu Leu Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala  
 20 25 30  
 Cys Leu Lys Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys  
 35 40 45  
 Asp Phe Val Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val  
 50 55 60  
 Ser Asn Pro Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His  
 65 70 75 80  
 Gly Gly Ala His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala  
 85 90 95

Lys Lys Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln  
 100 105 110  
 His Gly Val Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys  
 115 120 125  
 Val Val Phe Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val  
 130 135 140  
 Phe Arg Met His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly  
 145 150 155 160  
 Ser Ala Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala  
 165 170 175  
 Ser Ser Tyr Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro  
 180 185 190  
 His Pro Tyr Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp  
 195 200 205  
 Glu Val Lys Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr  
 210 215 220  
 Val Ile Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser  
 225 230 235 240  
 Ala Phe Leu Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala  
 245 250 255  
 Gly Leu Gly Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly  
 260 265 270  
 Arg Val Gly Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp  
 275 280 285  
 Glu Gly Gln Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr  
 290 295 300  
 Pro Gly Val Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala  
 305 310 315 320  
 Val Tyr Glu Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu  
 325 330 335  
 Leu Cys Gln Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala  
 340 345 350  
 Leu Ala Tyr Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile  
 355 360 365  
 Ile Val Val Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val  
 370 375 380  
 Tyr Asn Ala Leu Lys Gly Gly Leu Lys  
 385 390

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 197...547
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGGTGATGCA AAACCAAAAC AAGCGCATCA TGAATTACAT TCCTATTAAG TTGAATTTAA 60  
 GTGGGGTGAT CCCCCCTATT TTCGCTTCAG CTTTGCTCGT GTTCCCTTCT ACGATTTTGC 120  
 AGCAAGCCAC AAGCAACAAA ACCTTGCAAG CGGTTGCGNA TTTTAAAGC CCGCAAGGTA 180  
 TCGGTATAAT ATTTTG ATG TTC TTG CTC ATC ATC TTT TTT GCT TAC TTT TAT 232  
                   Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr  
                   1                  5                  10

TCT TCT ATT GTG TTC AAT TCT AAG GAT ATT GCG GAT AAT TTG AGG CGT 280  
 Ser Ser Ile Val Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg  
           15                  20                  25

AAT GGC GGG TAT ATT CCA GGG CTT AGG CCT GGA GAG GGG ACT TCA TCG 328  
 Asn Gly Gly Tyr Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser  
           30                  35                  40

TTT TTA AAT TCT GTA GCG AGT AAG CTC ACT TTG TGG GGT TCA TTG TAT 376  
 Phe Leu Asn Ser Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr  
           45                  50                  55                  60

TTA GCG CTC ATT TCT ACC GTG CCT TGG ATT TTG GTT AAG GCT ATG GGC 424  
 Leu Ala Leu Ile Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly  
                   65                  70                  75

GTG CCT TTT TAC TTT GGA GGC ACA GCG GTG CTG ATT GTG GTT CAA GTC 472  
 Val Pro Phe Tyr Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val  
                   80                  85                  90

GCT ATT GAC ACC ATG AAA AAG ATT GAA GCG CAA ATT TAT ATG AGC AAG 520  
 Ala Ile Asp Thr Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys  
           95                  100                  105

TAT AAA ACT TTA AGC GCG GTA GGC TTT TAATGGCAAT CTCTATTAAA AGCCCAA 574  
 Tyr Lys Thr Leu Ser Ala Val Gly Phe  
           110                  115

AAGAAATCAA AGCTCTAAGA AAAGCCG 601

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr Ser Ser Ile Val  
 1                  5                  10                  15  
 Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg Asn Gly Gly Tyr  
           20                  25                  30  
 Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser Phe Leu Asn Ser  
           35                  40                  45  
 Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr Leu Ala Leu Ile  
           50                  55                  60

Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly Val Pro Phe Tyr  
65 70 75 80  
Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val Ala Ile Asp Thr  
85 90 95  
Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys Tyr Lys Thr Leu  
100 105 110  
Ser Ala Val Gly Phe  
115

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...675
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAAAACAGGA TAACGCATGA AACATGTGAG TAGGGATTTT GATACCGGTT GGGTTGCGTA 60  
TCA ATG ACT CTA GGC ATT GAT GAA GCG GGT AGG GGG TGT TTG GCC GGT 108  
Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly  
1 5 10 15  
TCG CTT TTT GTG GCT GGG GTG GCG TGT AAT GAA AAA ACA GCC TTA GAA 156  
Ser Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu  
20 25 30  
TTT CTA AAA ATG GGT TTA AAA GAC AGC AAG AAG CTC AGC CTA AAA AAG 204  
Phe Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys  
35 40 45  
CGC TTT TTC TTA GAA TAT AAG ATC AAA ACG CAT GGT GAG GTG GGG TTT 252  
Arg Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe  
50 55 60  
TTC GTG GTT AAA AAA AGC GCA AAT GAA ATT GAT AGC TTG GGC TTA GGG 300  
Phe Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly  
65 70 75  
GCG TGT TTG AAA CTC GCT GTG CAA GAA ATT TTA GAA AAT GGT TGC TCT 348  
Ala Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser  
80 85 90 95  
TTA GTT GAT GAA ATA AAA ATA GAC GGC AAC ACG GCG TTT GGC TTG AAC 396  
Leu Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn  
100 105 110  
AAA CGC TAC CCC CAT ATA CAA ACC ATC ATC AAG GGC GAT GAA ACA ATC 444

Lys Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile  
115 120 125

GCT CAA ATC GCT ATG GCG TCT GTT TTG GCG AAA GCT TTT AAG GAC AGA 492  
Ala Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg  
130 135 140

GAA ATG CTA GAG TTG CAC GCT TTG TTT AAG GAA TAC GGC TGG GAT AAG 540  
Glu Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys  
145 150 155

AAT TGC GGG TAT GGG ACT AAA CAA CAT ATA GAA GCG ATC ATT AAG CTA 588  
Asn Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu  
160 165 170 175

GGG GCT ACG CCT TTT CAT CGG CAT AGC TTC ACG CTT AAA AAC CGC ATC 636  
Gly Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile  
180 185 190

TTA AAT CCC AAA CTC TTA GAG GTG GAA CAA CGC CTT ATT TAAAAGGGCG CT 687  
Leu Asn Pro Lys Leu Leu Glu Val Glu Gln Arg Leu Ile  
195 200

GAGATGGGTA GCGCTCGCTG AAGAAAGGTC GATGCGTT 725

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly Ser  
1 5 10 15

Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu Phe  
20 25 30

Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys Arg  
35 40 45

Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe Phe  
50 55 60

Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly Ala  
65 70 75 80

Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser Leu  
85 90 95

Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn Lys  
100 105 110

Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile Ala  
115 120 125

Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg Glu  
130 135 140

Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys Asn  
145 150 155 160



Cys Gly Tyr Gly Thr Lys Gln His Ile Glu Ala Ile Ile Lys Leu Gly  
165 170 175  
Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile Leu  
180 185 190  
Asn Pro Lys Leu Leu Glu Val Glu Gln Arg Leu Ile  
195 200

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2821 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...2769
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| GATTAATCAG TGGAAGAATA CAAAGACACC CTAAACTTAA ACACAACCAC CTTTCTCT ATG | 60  |
| Met                                                                 |     |
| 1                                                                   |     |
| AAG GGG AAT TTG AGC GTT AAT GAG CCT AAA ACT TAC GCC AAA TGG CAA     | 108 |
| Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp Gln     |     |
| 5 10 15                                                             |     |
| GAG CAA CAA GCG TTT AAA CGC ATG CAA GCT AGG AAA GAC AAC CAT GGG     | 156 |
| Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His Gly     |     |
| 20 25 30                                                            |     |
| GAT TTC ACT TTG CAT GAC GGG CCG CCT TAT GCG AAC GGG CAT TTG CAT     | 204 |
| Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu His     |     |
| 35 40 45                                                            |     |
| TTG GGG CAT GCC TTA AAT AAA ATT TTA AAA GAC ATT GTC GTT AAA AGA     | 252 |
| Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys Arg     |     |
| 50 55 60 65                                                         |     |
| GAA TAT TTT AAG GGG AAG AAA ATC TAT TAC ACG CCC GGT TGG GAT TGC     | 300 |
| Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp Cys     |     |
| 70 75 80                                                            |     |
| CAT GGT TTG CCC ATT GAG CAG CAA ATT TTA GAG CGA TTA GAA AAA GAA     | 348 |
| His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys Glu     |     |
| 85 90 95                                                            |     |
| AAA ACA AGC CTA GAA AAC CCC ACG CTG TTT AGA GAA AAG TGC CGA GAT     | 396 |
| Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg Asp     |     |
| 100 105 110                                                         |     |
| CAT GCG AAG AAA TTT TTA GAA ATC CAA AAG AAT GAA TTT TTG CAA TTG     | 444 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| His | Ala | Lys | Lys | Phe | Leu | Glu | Ile | Gln | Lys | Asn | Glu | Phe | Leu | Gln | Leu |      |
| 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |      |
| GGT | GTT | TTG | GGG | GAT | TTT | GAA | GAT | CCT | TAT | AAA | ACC | ATG | GAT | TTT | AAA | 492  |
| Gly | Val | Leu | Gly | Asp | Phe | Glu | Asp | Pro | Tyr | Lys | Thr | Met | Asp | Phe | Lys |      |
| 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |      |
| TTT | GAA | GCG | AGC | ATT | TAT | AGA | GCC | TTA | GTG | GAA | GTG | GCT | AAA | AAA | GGG | 540  |
| Phe | Glu | Ala | Ser | Ile | Tyr | Arg | Ala | Leu | Val | Glu | Val | Ala | Lys | Lys | Gly |      |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |      |
| CTT | TTG | AAA | GAG | CGC | CAC | AAG | CCT | ATT | TAT | TGG | AGT | TAT | GCA | TGC | GAG | 588  |
| Leu | Leu | Lys | Glu | Arg | His | Lys | Pro | Ile | Tyr | Trp | Ser | Tyr | Ala | Cys | Glu |      |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |      |
| AGC | GCT | TTA | GCG | GAA | GCT | GAA | GTG | GAA | TAC | AAA | ATG | AAA | AAA | TCG | CCC | 636  |
| Ser | Ala | Leu | Ala | Glu | Ala | Glu | Val | Glu | Tyr | Lys | Met | Lys | Lys | Ser | Pro |      |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |      |
| TCC | ATT | TTC | GTG | GCG | TTT | GGT | TTG | AAA | AAG | GAG | AGT | TTA | GAA | AAA | TTA | 684  |
| Ser | Ile | Phe | Val | Ala | Phe | Gly | Leu | Lys | Lys | Glu | Ser | Leu | Glu | Lys | Leu |      |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |      |
| AAA | GTC | AAA | AAA | GCG | AGC | TTG | GTG | ATT | TGG | ACG | ACC | ACG | CCT | TGG | ACT | 732  |
| Lys | Val | Lys | Lys | Ala | Ser | Leu | Val | Ile | Trp | Thr | Thr | Thr | Pro | Trp | Thr |      |
| 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |      |
| TTG | TAT | GCG | AAT | GTA | GCG | ATC | GCT | TTG | AAA | AAA | GAC | GCT | GTT | TAT | GCG | 780  |
| Leu | Tyr | Ala | Asn | Val | Ala | Ile | Ala | Leu | Lys | Lys | Asp | Ala | Val | Tyr | Ala |      |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |      |
| CTC | ACC | CAA | AAA | GGC | TAT | TTA | GTC | GCT | AAA | GCC | TTG | CAT | GAA | AAA | TTA | 828  |
| Leu | Thr | Gln | Lys | Gly | Tyr | Leu | Val | Ala | Lys | Ala | Leu | His | Glu | Lys | Leu |      |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |      |
| GCC | GCT | TTA | GGG | GTG | GTG | GAT | AAT | GAG | ATC | ACA | CAT | GAA | TTC | AAT | TCC | 876  |
| Ala | Ala | Leu | Gly | Val | Val | Asp | Asn | Glu | Ile | Thr | His | Glu | Phe | Asn | Ser |      |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |      |
| AAT | GAT | TTA | GAA | TAT | TTA | GTG | GCT | ACA | AAC | CCG | CTC | AAT | CAA | AGG | GAT | 924  |
| Asn | Asp | Leu | Glu | Tyr | Leu | Val | Ala | Thr | Asn | Pro | Leu | Asn | Gln | Arg | Asp |      |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |      |
| TCG | CTG | GTG | GCT | TTA | GGA | GAG | CAT | GTC | GGT | TTA | GAA | GAT | GGC | ACA | GGA | 972  |
| Ser | Leu | Val | Ala | Leu | Gly | Glu | His | Val | Gly | Leu | Glu | Asp | Gly | Thr | Gly |      |
| 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     | 305 |      |
| GCC | GTG | CAT | ACC | GCA | CCT | GGG | CAT | GGT | GAA | GAG | GAC | TAT | TAT | TTA | GGC | 1020 |
| Ala | Val | His | Thr | Ala | Pro | Gly | His | Gly | Glu | Glu | Asp | Tyr | Tyr | Leu | Gly |      |
|     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |      |
| TTA | AGA | TAT | AAT | TTA | GAA | GTG | TTA | ATG | TCT | GTA | GAT | GAG | AAA | GGT | TGC | 1068 |
| Leu | Arg | Tyr | Asn | Leu | Glu | Val | Leu | Met | Ser | Val | Asp | Glu | Lys | Gly | Cys |      |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |      |
| TAT | GAT | GAG | GGC | ATT | ATC | CAT | AAC | CAA | CTA | TTA | GAT | GAA | AGC | TAT | CTG | 1116 |
| Tyr | Asp | Glu | Gly | Ile | Ile | His | Asn | Gln | Leu | Leu | Asp | Glu | Ser | Tyr | Leu |      |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GGC | GAG | CAT | GTT | TTT | AAG | GCT | CAA | AAA | CGC | ATT | ATA | GAG | CAA | TTG | GGC | 1164 |
| Gly | Glu | His | Val | Phe | Lys | Ala | Gln | Lys | Arg | Ile | Ile | Glu | Gln | Leu | Gly |      |
| 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |      |
| GAT | TCT | TTA | TTG | CTA | GAG | CAA | GAG | ATT | GAG | CAT | TCT | TAT | CCG | CAT | TGC | 1212 |
| Asp | Ser | Leu | Leu | Leu | Glu | Gln | Glu | Ile | Glu | His | Ser | Tyr | Pro | His | Cys |      |
| 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     | 385 |      |
| TGG | AGG | ACG | CAC | AAG | CCT | GTG | ATT | TAC | AGA | GCG | ACT | ACG | CAA | TGG | TTT | 1260 |
| Trp | Arg | Thr | His | Lys | Pro | Val | Ile | Tyr | Arg | Ala | Thr | Thr | Gln | Trp | Phe |      |
|     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |      |
| ATT | TTA | ATG | GAT | GAG | CCT | TTT | ATC | CAA | AAT | GAT | GGC | TCT | CAA | AAA | ACC | 1308 |
| Ile | Leu | Met | Asp | Glu | Pro | Phe | Ile | Gln | Asn | Asp | Gly | Ser | Gln | Lys | Thr |      |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |      |
| TTA | AGA | GAA | GTG | GCT | TTA | GAT | GCG | ATT | GAA | AAG | GTG | GAA | TTT | GTG | CCA | 1356 |
| Leu | Arg | Glu | Val | Ala | Leu | Asp | Ala | Ile | Glu | Lys | Val | Glu | Phe | Val | Pro |      |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |      |
| AGC | AGC | GGG | AAA | AAC | CGC | CTA | AAA | ACC | ATG | ATA | GAA | AAC | CGC | CCT | GAT | 1404 |
| Ser | Ser | Gly | Lys | Asn | Arg | Leu | Lys | Thr | Met | Ile | Glu | Asn | Arg | Pro | Asp |      |
|     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |      |
| TGG | TGC | TTG | AGC | CGG | CAA | AGA | AAA | TGG | GGC | GTG | CCA | CTG | GCC | TTT | TTC | 1452 |
| Trp | Cys | Leu | Ser | Arg | Gln | Arg | Lys | Trp | Gly | Val | Pro | Leu | Ala | Phe | Phe |      |
| 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |      |
| ATA | GAC | AAA | CGC | ACG | AAT | AAG | CCT | TGT | TTT | GAA | AGC | GAA | GTT | TTA | GAG | 1500 |
| Ile | Asp | Lys | Arg | Thr | Asn | Lys | Pro | Cys | Phe | Glu | Ser | Glu | Val | Leu | Glu |      |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |     |      |
| CAT | GTG | GCC | AAT | CTT | TTT | GAG | AAA | AAA | GGC | TGT | GAT | GTG | TGG | TGG | GAG | 1548 |
| His | Val | Ala | Asn | Leu | Phe | Glu | Lys | Lys | Gly | Cys | Asp | Val | Trp | Trp | Glu |      |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |     |      |
| TAT | AGC | GTG | AAA | GAT | TTA | TTG | CCC | CCT | AGC | TAT | CAA | GAG | GAC | GCC | AAG | 1596 |
| Tyr | Ser | Val | Lys | Asp | Leu | Leu | Pro | Pro | Ser | Tyr | Gln | Glu | Asp | Ala | Lys |      |
|     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |     |      |
| CAT | TAT | GAG | AAA | ATC | ATG | CAC | ATT | TTA | GAC | GTG | TGG | TTT | GAT | AGT | GGT | 1644 |
| His | Tyr | Glu | Lys | Ile | Met | His | Ile | Leu | Asp | Val | Trp | Phe | Asp | Ser | Gly |      |
|     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |     |      |
| AGC | ACC | TTT | AAG | GCG | GTT | TTA | GAA | GAC | TAT | CAT | GGA | GAA | AAA | GGG | CAA | 1692 |
| Ser | Thr | Phe | Lys | Ala | Val | Leu | Glu | Asp | Tyr | His | Gly | Glu | Lys | Gly | Gln |      |
| 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     | 545 |     |      |
| AGC | CCT | AGC | GAT | GTG | ATC | TTA | GAA | GGG | AGC | GAT | CAG | CAT | AGG | GGG | TGG | 1740 |
| Ser | Pro | Ser | Asp | Val | Ile | Leu | Glu | Gly | Ser | Asp | Gln | His | Arg | Gly | Trp |      |
|     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |     |      |
| TTT | CAA | AGC | TCG | CTT | CTA | ATC | GGT | TGT | GTT | TTA | AAC | AAC | CAA | GCC | CCT | 1788 |
| Phe | Gln | Ser | Ser | Leu | Leu | Ile | Gly | Cys | Val | Leu | Asn | Asn | Gln | Ala | Pro |      |
|     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |     |      |
| TTT | AAA | AAG | GTC | ATT | ACG | CAT | GGC | TTT | ATC | GTA | GAT | GAA | AAG | GGC | GAA | 1836 |
| Phe | Lys | Lys | Val | Ile | Thr | His | Gly | Phe | Ile | Val | Asp | Glu | Lys | Gly | Glu |      |







|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 610                                                             | 615 | 620 |
| Asp Tyr Gln Asn Asp Leu Arg Val Ser Gln Thr Phe Phe Thr Gln Thr |     |     |
| 625                                                             | 630 | 635 |
| Glu Gln His Tyr Lys Lys Phe Arg Asn Thr Leu Lys Phe Leu Leu Ala |     | 640 |
|                                                                 | 645 | 650 |
| Asn Phe Ser Asp Met Asp Leu Lys Asn Leu Glu Arg Pro His Asn Phe |     | 655 |
|                                                                 | 660 | 665 |
| Ser Pro Leu Asp His Phe Met Leu Glu Thr Leu Glu Thr Ile Ser Ala |     | 670 |
|                                                                 | 675 | 680 |
| Gly Val Asn Ser Ala Phe Glu Glu His Asp Phe Val Lys Gly Leu Asn |     | 685 |
|                                                                 | 690 | 695 |
| Ile Leu Met Ala Phe Val Thr Asn Glu Leu Ser Gly Ile Tyr Leu Asp |     | 700 |
| 705                                                             | 710 | 715 |
| Ala Cys Lys Asp Ser Leu Tyr Cys Asp Ser Lys Asn Asn Glu Lys Arg |     | 720 |
|                                                                 | 725 | 730 |
| Gln Ala Ile Gln Met Val Leu Leu Ala Thr Ala Ser Lys Leu Cys Tyr |     | 735 |
|                                                                 | 740 | 745 |
| Phe Leu Ala Pro Ile Leu Thr His Thr Ile Glu Glu Val Leu Glu His |     | 750 |
|                                                                 | 755 | 760 |
| Ser Gln Ala Leu Arg Ile Phe Leu Gln Ala Lys Asp Val Phe Asp Leu |     | 765 |
|                                                                 | 770 | 775 |
| Lys Asp Ile Ser Val Ser Glu Lys Leu His Leu Lys Glu Phe Lys Lys |     | 780 |
| 785                                                             | 790 | 795 |
| Pro Glu Asn Phe Glu Ala Val Leu Ala Leu Arg Ser Ala Phe Asn Glu |     | 800 |
|                                                                 | 805 | 810 |
| Glu Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu |     | 815 |
|                                                                 | 820 | 825 |
| Cys Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu |     | 830 |
|                                                                 | 835 | 840 |
| Glu Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser |     | 845 |
|                                                                 | 850 | 855 |
| Glu Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro |     | 860 |
| 865                                                             | 870 | 875 |
| Arg Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg |     | 880 |
|                                                                 | 885 | 890 |
| Cys Glu Gln Val Leu Lys Glu Arg                                 |     | 895 |
|                                                                 | 900 |     |

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...288
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TGTAGAATGA AATCCTAGCC AGTGAGCTAG AATTTAAATT TTTAATCAAA GGAGTCATCA

60

TGGCACACC ATG AAG AAC AAC ACG GCG GGC ACC ACC ACC ACC ATC ACC ACA 111  
Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr  
1 5 10

CAC ACC ACC ACC ACT ATC ATG GCG GTG AAC ACC ACC ATC ACC ACC ACA 159  
His Thr Thr Thr Thr Ile Met Ala Val Asn Thr Thr Thr Thr Thr Thr  
15 20 25 30

GCT CTC ATC ATG AAG AAG GTT GTT GCA GCA CTA GCG ACA GTC ATC ATC 207  
Ala Leu Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile  
35 40 45

AAG AAG AAG GTT GCT GCC ACG GGC ATC ACG AGT AAT ATC GGT GTG GCT 255  
Lys Lys Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala  
50 55 60

AGG GGC AAC TTG ACT AGG GTT GTC TCT GGC TTT TGACTTTAAA ATACAATCAT 308  
Arg Gly Asn Leu Thr Arg Val Val Ser Gly Phe  
65 70

TCCATTCTAA CCCATTCTGA TCAAACCCGT T 339

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr His Thr  
1 5 10 15  
Thr Thr Thr Ile Met Ala Val Asn Thr Thr Thr Thr Thr Thr Ala Leu  
20 25 30  
Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile Lys Lys  
35 40 45  
Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala Arg Gly  
50 55 60  
Asn Leu Thr Arg Val Val Ser Gly Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence



(D) OTHER INFORMATION:

|                                                           |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |            |    |
|-----------------------------------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|----|
| GTTTTTCTACT TATGATTTTGG TGGAAGAATA TTGCAAAATTA AAGGAAATGC |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   | ATG<br>Met<br>1   | CTT<br>Leu | 56 |
| GAA<br>Glu                                                | AAA<br>Lys        | GTG<br>Val<br>5   | TTT<br>Phe        | CAA<br>Gln        | GAA<br>Glu        | ATT<br>Ile        | ACC<br>Thr<br>10  | AAT<br>Asn        | AAA<br>Lys        | AGA<br>Arg        | AAG<br>Lys        | TTT<br>Phe<br>15  | TTT<br>Phe        | GCA<br>Ala        | AGT<br>Ser        | 104        |    |
| TCT<br>Ser                                                | AGC<br>Ser<br>20  | ACA<br>Thr        | GGG<br>Gly        | GAG<br>Glu        | CAG<br>Gln        | TTT<br>Phe<br>25  | GAA<br>Glu        | AAC<br>Asn        | CAA<br>Gln        | TTT<br>Phe<br>30  | AGG<br>Arg        | AAT<br>Asn        | GAA<br>Glu        | TTA<br>Leu        | AAA<br>Lys        | 152        |    |
| AAA<br>Lys<br>35                                          | CAC<br>His        | TTT<br>Phe        | AGC<br>Ser        | GAA<br>Glu        | ATC<br>Ile<br>40  | AAT<br>Asn        | GGC<br>Gly        | GAT<br>Asp        | TTA<br>Leu        | ACA<br>Thr<br>45  | GAA<br>Glu        | GAA<br>Glu        | TTA<br>Leu        | AGC<br>Ser<br>50  | CAT<br>His        | 200        |    |
| ATT<br>Ile                                                | GAA<br>Glu        | GAA<br>Glu        | AAG<br>Lys        | CCT<br>Pro<br>55  | AAT<br>Asn        | AAA<br>Lys        | GAA<br>Glu        | ATC<br>Ile        | AAA<br>Lys<br>60  | ACC<br>Thr        | ACT<br>Thr        | TTT<br>Phe        | AAC<br>Asn        | CAA<br>Gln<br>65  | CTC<br>Leu        | 248        |    |
| AAA<br>Lys                                                | AAG<br>Lys        | CAA<br>Gln<br>70  | GTT<br>Val        | TTA<br>Leu        | GAA<br>Glu        | AAA<br>Lys        | AAT<br>Asn        | CAC<br>His<br>75  | CCG<br>Pro        | CAC<br>His        | ACC<br>Thr        | CTT<br>Leu<br>80  | AAA<br>Lys        | AAC<br>Asn        | CCT<br>Pro        | 296        |    |
| TTT<br>Phe                                                | TCA<br>Ser        | AAC<br>Asn<br>85  | CTT<br>Leu        | ACA<br>Thr        | AGC<br>Ser        | CAT<br>His        | TTT<br>Phe<br>90  | TTA<br>Leu        | TAC<br>Tyr        | CAG<br>Gln        | CCT<br>Pro        | TTT<br>Phe<br>95  | GGC<br>Gly        | TCA<br>Ser        | CAA<br>Gln        | 344        |    |
| AAT<br>Asn                                                | TAC<br>Tyr<br>100 | CCT<br>Pro        | GAT<br>Asp        | TTT<br>Phe        | TTG<br>Leu        | GTT<br>Val<br>105 | TTT<br>Phe        | ATT<br>Ile        | TTT<br>Phe        | GAC<br>Asp        | TAT<br>Tyr<br>110 | GTG<br>Val        | GTG<br>Val        | GGG<br>Gly        | ATT<br>Ile        | 392        |    |
| GAA<br>Glu<br>115                                         | ATC<br>Ile        | AAG<br>Lys        | TTT<br>Phe        | TCT<br>Ser        | AAA<br>Lys<br>120 | AAC<br>Asn        | GAT<br>Asp        | AAG<br>Lys        | GGT<br>Gly        | GAA<br>Glu<br>125 | AAA<br>Lys        | AAT<br>Asn        | CTT<br>Leu        | CAA<br>Gln        | ACA<br>Thr<br>130 | 440        |    |
| TCT<br>Ser                                                | CGC<br>Arg        | CCC<br>Pro        | ATG<br>Met        | TGG<br>Trp<br>135 | AAT<br>Asn        | TCA<br>Ser        | AAC<br>Asn        | CTG<br>Leu        | CCT<br>Pro<br>140 | AAA<br>Lys        | CCC<br>Pro        | AAT<br>Asn        | GCG<br>Ala        | ATT<br>Ile<br>145 | TAT<br>Tyr        | 488        |    |
| GTG<br>Val                                                | TAT<br>Tyr        | GGA<br>Gly        | GTC<br>Val<br>150 | GCT<br>Ala        | AAT<br>Asn        | GCA<br>Ala        | AAC<br>Asn        | ATC<br>Ile<br>155 | ACT<br>Thr        | TTT<br>Phe        | TTT<br>Phe        | AAA<br>Lys        | GGC<br>Gly<br>160 | TCA<br>Ser        | GAT<br>Asp        | 536        |    |
| ATT<br>Ile                                                | TTG<br>Leu        | AGT<br>Ser<br>165 | TAT<br>Tyr        | GAA<br>Glu        | ACC<br>Thr        | AGA<br>Arg        | GAG<br>Glu<br>170 | GTC<br>Val        | TTG<br>Leu        | CTC<br>Leu        | AAG<br>Lys        | TAT<br>Tyr<br>175 | TTT<br>Phe        | GAT<br>Asp        | ATT<br>Ile        | 584        |    |
| TTA<br>Leu                                                | GAT<br>Asp<br>180 | AAA<br>Lys        | GAT<br>Asp        | GAA<br>Glu        | AGA<br>Arg        | AGT<br>Ser<br>185 | TTG<br>Leu        | AAA<br>Lys        | AAC<br>Asn        | GCC<br>Ala        | TTA<br>Leu<br>190 | AAG<br>Lys        | GAT<br>Asp        | TTA<br>Leu        | GAA<br>Glu        | 632        |    |

AAC CCT TTT GGG TTT GCC CCC TAC ATC AGA AAA GCT TAT GAG CAT AAA 680  
 Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu His Lys  
 195 200 205 210

AGG AAT TTT CTA ACC ACC ACC AGA TTG AAA GCT TCT TTT CGC CCA ACC 728  
 Arg Asn Phe Leu Thr Thr Arg Leu Lys Ala Ser Phe Arg Pro Thr  
 215 220 225

ACA TTT TAAGAGAGCG GAATGTCTTG GAATTTTGA AAACGCTCAC TCATTAGCGT AT 786  
 Thr Phe

T 787

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Leu Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe  
 1 5 10 15  
 Ala Ser Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu  
 20 25 30  
 Leu Lys Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu  
 35 40 45  
 Ser His Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn  
 50 55 60  
 Gln Leu Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys  
 65 70 75 80  
 Asn Pro Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly  
 85 90 95  
 Ser Gln Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val  
 100 105 110  
 Gly Ile Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu  
 115 120 125  
 Gln Thr Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala  
 130 135 140  
 Ile Tyr Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly  
 145 150 155 160  
 Ser Asp Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe  
 165 170 175  
 Asp Ile Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp  
 180 185 190  
 Leu Glu Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu  
 195 200 205  
 His Lys Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg  
 210 215 220  
 Pro Thr Thr Phe  
 225

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...493
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
CCAAACCCTT TTGAAACACT TGCTCACTAA CCCATTATAA GCCGCAAAAA CC ATG CTC 58
 Met Leu
 1

TCT TTA AAA CAA GAT TCC TTT TTT TTC TTA TGT TTA GGA ATC CTG GGG 106
Ser Leu Lys Gln Asp Ser Phe Phe Phe Leu Cys Leu Gly Ile Leu Gly
 5 10 15

TTT TAT TTT TAT AGC CTT TTG AGG GAT TTA ATG CCT TTT TTA CCC CCA 154
Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu Pro Pro
 20 25 30

ATG ATT GGG TTT TTA TTC TTG TTT TAT GCG AAA AAA TAC GAT CAT TTT 202
Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp His Phe
 35 40 45 50

TTA CCC AGT TTG AGC GTG TTT GGT TGT TTG TTT TGG TTT GAG AGC ATG 250
Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu Ser Met
 55 60 65

CAT TTA AAG ACT TTA GGC GTT TTA GCT TTA TTG TTT TTA ATC TAC CAT 298
His Leu Lys Thr Leu Gly Val Leu Ala Leu Leu Phe Leu Ile Tyr His
 70 75 80

CAA ATC GCC TAT AAA AAC TCT TTA AAG CTT TTT AAT GAC GGC TTT TTA 346
Gln Ile Ala Tyr Lys Asn Ser Leu Lys Leu Phe Asn Asp Gly Phe Leu
 85 90 95

TTC AAA ACT TTG CAT GTT TTT TTG GTT TAT TAC CTT TAT TTA TCG CGC 394
Phe Lys Thr Leu His Val Phe Leu Val Tyr Tyr Leu Tyr Leu Ser Arg
 100 105 110

TTT TTT TCG ATG TCT TTG AGT TTG AAA ATA CTC GGC TTT CTC GCT CTT 442
Phe Phe Ser Met Ser Leu Ser Leu Lys Ile Leu Gly Phe Leu Ala Leu
 115 120 125 130

TTT GCT TTA ATA GAA AGC GCT TTG TGG GGT TTG TAT GAA AAA TCT TCG 490
Phe Ala Leu Ile Glu Ser Ala Leu Trp Gly Leu Tyr Glu Lys Ser Ser
 135 140 145
```

CTA TAAGCTTTTG CTCTTTGTTT TTATAGGGTT TTGGGGGTTA CTAGCCT  
Leu

540

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Leu | Lys | Gln | Asp | Ser | Phe | Phe | Phe | Leu | Cys | Leu | Gly | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gly | Phe | Tyr | Phe | Tyr | Ser | Leu | Leu | Arg | Asp | Leu | Met | Pro | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Met | Ile | Gly | Phe | Leu | Phe | Leu | Phe | Tyr | Ala | Lys | Lys | Tyr | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Phe | Leu | Pro | Ser | Leu | Ser | Val | Phe | Gly | Cys | Leu | Phe | Trp | Phe | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Met | His | Leu | Lys | Thr | Leu | Gly | Val | Leu | Ala | Leu | Leu | Phe | Leu | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Tyr | His | Gln | Ile | Ala | Tyr | Lys | Asn | Ser | Leu | Lys | Leu | Phe | Asn | Asp | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Leu | Phe | Lys | Thr | Leu | His | Val | Phe | Leu | Val | Tyr | Tyr | Leu | Tyr | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Phe | Phe | Ser | Met | Ser | Leu | Ser | Leu | Lys | Ile | Leu | Gly | Phe | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Leu | Phe | Ala | Leu | Ile | Glu | Ser | Ala | Leu | Trp | Gly | Leu | Tyr | Glu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1835
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CACTAAAGTC AATCCAAGCG CAAGTTGGAT GAAAAAATAA GAAGGAAGTT ATG AAA  
Met Lys

56

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAG | TCA | TTC | AAA | AAA | TTA | GGC | TTT | GTC | TCT | TTA | GCG | GCT | AGT | GGC | GTG | 104 |
| Lys | Ser | Phe | Lys | Lys | Leu | Gly | Phe | Val | Ser | Leu | Ala | Ala | Ser | Gly | Val |     |
|     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     |
| CTT | TTA | GGG | AGC | ATG | AAC | GCT | ACC | GAT | TTA | GAA | ACC | TAC | GCA | GCA | TTG | 152 |
| Leu | Leu | Gly | Ser | Met | Asn | Ala | Thr | Asp | Leu | Glu | Thr | Tyr | Ala | Ala | Leu |     |
|     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |
| CAA | AAA | TCA | TCG | CAT | GTT | TTT | GGT | AAT | TAT | GCT | GAA | AAG | GAT | AAG | GAT | 200 |
| Gln | Lys | Ser | Ser | His | Val | Phe | Gly | Asn | Tyr | Ala | Glu | Lys | Asp | Lys | Asp |     |
| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |
| AGT | AAA | TTA | ACA | AGC | GAT | TCA | CCA | ACG | CAA | CAA | CAA | GAT | CAA | AAA | GTA | 248 |
| Ser | Lys | Leu | Thr | Ser | Asp | Ser | Pro | Thr | Gln | Gln | Gln | Asp | Gln | Lys | Val |     |
|     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     | 65  |     |
| GCC | CAA | AAC | ACC | GCT | TCA | AAC | GAC | AGC | CAA | GAA | GCG | ACA | ACA | CTT | GAA | 296 |
| Ala | Gln | Asn | Thr | Ala | Ser | Asn | Asp | Ser | Gln | Glu | Ala | Thr | Thr | Leu | Glu |     |
|     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |
| AAC | ACC | GCT | TCT | ACT | GAC | AAC | ACA | ACC | GCC | ACA | ACT | GAT | GAA | ACT | TAT | 344 |
| Asn | Thr | Ala | Ser | Thr | Asp | Asn | Thr | Thr | Ala | Thr | Thr | Asp | Glu | Thr | Tyr |     |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |
| ACA | AAA | AGC | ACT | GAC | ACT | ACT | GTA | GCT | GGT | GCG | GCT | CAA | AAA | GTA | GAA | 392 |
| Thr | Lys | Ser | Thr | Asp | Thr | Thr | Val | Ala | Gly | Ala | Ala | Gln | Lys | Val | Glu |     |
|     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |
| ACC | GAT | AAC | ACA | GCC | GTT | CAA | AGC | GCT | GAA | CAA | ACT | TTA | AAA | ACA | GAT | 440 |
| Thr | Asp | Asn | Thr | Ala | Val | Gln | Ser | Ala | Glu | Gln | Thr | Leu | Lys | Thr | Asp |     |
| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |
| GTA | GCT | AAA | GTT | CAA | GCT | GAT | GCT | AGT | GCT | AAA | GAT | TTT | GAT | GAA | ACC | 488 |
| Val | Ala | Lys | Val | Gln | Ala | Asp | Ala | Ser | Ala | Lys | Asp | Phe | Asp | Glu | Thr |     |
|     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |
| ACT | TTT | CAA | GCC | GAT | CAA | GCA | GCA | GAG | CAA | ACC | GCT | GAA | AAA | GCT | TTA | 536 |
| Thr | Phe | Gln | Ala | Asp | Gln | Ala | Ala | Glu | Gln | Thr | Ala | Glu | Lys | Ala | Leu |     |
|     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |
| CAA | CAG | GCT | GAG | AGC | AAA | CTC | AAC | ACC | GAT | CAA | CAG | ACT | TTA | AAC | ACA | 584 |
| Gln | Gln | Ala | Glu | Ser | Lys | Leu | Asn | Thr | Asp | Gln | Gln | Thr | Leu | Asn | Thr |     |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     |
| GCG | TTA | CAA | GAT | CAG | ACG | AAA | ACA | CCA | ACC | CCA | TCA | ACC | CCA | CCA | ACT | 632 |
| Ala | Leu | Gln | Asp | Gln | Thr | Lys | Thr | Pro | Thr | Pro | Ser | Thr | Pro | Pro | Thr |     |
|     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |     |
| AAA | GAG | GAA | CCA | AAA | CAC | ACC | GCT | TCA | AGC | GGC | ACA | CCA | CCA | GCT | CCA | 680 |
| Lys | Glu | Glu | Pro | Lys | His | Thr | Ala | Ser | Ser | Gly | Thr | Pro | Pro | Ala | Pro |     |
| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |
| GAA | AGC | CCA | CCA | GCT | AAA | AAA | GAT | GAA | ACA | AGT | GGC | ACA | CCA | AGT | GCT | 728 |
| Glu | Ser | Pro | Pro | Ala | Lys | Lys | Asp | Glu | Thr | Ser | Gly | Thr | Pro | Ser | Ala |     |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |



| 455 |            |            |            |            |            |     |     |     |     | 460 |     |     |     |     | 465 |      |  |  |  |  |
|-----|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|--|
| CAA | GTG        | AAT        | AAC        | TTC        | ACT        | TAT | GGC | GTG | GGC | TTT | GAT | GTG | CTC | TAT | AAC | 1496 |  |  |  |  |
| Gln | Val        | Asn        | Asn        | Phe        | Thr        | Tyr | Gly | Val | Gly | Phe | Asp | Val | Leu | Tyr | Asn |      |  |  |  |  |
|     |            |            | 470        |            |            |     |     | 475 |     |     |     |     | 480 |     |     |      |  |  |  |  |
| TTC | TAT        | GAA        | AGC        | AAA        | GAG        | GGC | TAT | AAC | ACA | GCA | GGG | TTG | TTC | TTA | GGC | 1544 |  |  |  |  |
| Phe | Tyr        | Glu        | Ser        | Lys        | Glu        | Gly | Tyr | Asn | Thr | Ala | Gly | Leu | Phe | Leu | Gly |      |  |  |  |  |
|     |            | 485        |            |            |            |     | 490 |     |     |     |     | 495 |     |     |     |      |  |  |  |  |
| TTT | GGG        | TTA        | GGA        | GGG        | GAT        | TCG | TTT | ATC | GTT | CAA | GGA | GAG | AGC | TAC | TTG | 1592 |  |  |  |  |
| Phe | Gly        | Leu        | Gly        | Gly        | Asp        | Ser | Phe | Ile | Val | Gln | Gly | Glu | Ser | Tyr | Leu |      |  |  |  |  |
|     | 500        |            |            |            |            | 505 |     |     |     |     | 510 |     |     |     |     |      |  |  |  |  |
| AAA | TCT        | CAA        | ATG        | CAC        | ATT        | TGC | AAC | AAC | ACC | GCC | GGC | TGT | TCA | GCG | AGC | 1640 |  |  |  |  |
| Lys | Ser        | Gln        | Met        | His        | Ile        | Cys | Asn | Asn | Thr | Ala | Gly | Cys | Ser | Ala | Ser |      |  |  |  |  |
| 515 |            |            |            |            | 520        |     |     |     |     | 525 |     |     |     |     | 530 |      |  |  |  |  |
| ATG | AAC        | ACA        | AGC        | TAC        | TTC        | CAA | ATG | CCT | GTT | GAA | TTT | GGT | TTT | AGG | AGC | 1688 |  |  |  |  |
| Met | Asn        | Thr        | Ser        | Tyr        | Phe        | Gln | Met | Pro | Val | Glu | Phe | Gly | Phe | Arg | Ser |      |  |  |  |  |
|     |            |            |            | 535        |            |     |     |     | 540 |     |     |     |     | 545 |     |      |  |  |  |  |
| AAT | TTC        | TCT        | AAA        | CAC        | AGC        | GGG | ATT | GAA | GTG | GGC | TTT | AAA | TTG | CCT | TTA | 1736 |  |  |  |  |
| Asn | Phe        | Ser        | Lys        | His        | Ser        | Gly | Ile | Glu | Val | Gly | Phe | Lys | Leu | Pro | Leu |      |  |  |  |  |
|     |            |            | 550        |            |            |     | 555 |     |     |     |     |     | 560 |     |     |      |  |  |  |  |
| TTC | ACC        | AAC        | CAA        | TTC        | TAT        | AAA | GAA | AGG | GGC | GTA | GAT | GGA | TCG | GTA | GAT | 1784 |  |  |  |  |
| Phe | Thr        | Asn        | Gln        | Phe        | Tyr        | Lys | Glu | Arg | Gly | Val | Asp | Gly | Ser | Val | Asp |      |  |  |  |  |
|     |            |            | 565        |            |            |     | 570 |     |     |     |     | 575 |     |     |     |      |  |  |  |  |
| GTG | TTC        | TAT        | AAA        | AGG        | AAT        | TTC | TCT | ATT | TAT | TTT | AAC | TAC | ATG | ATC | AAC | 1832 |  |  |  |  |
| Val | Phe        | Tyr        | Lys        | Arg        | Asn        | Phe | Ser | Ile | Tyr | Phe | Asn | Tyr | Met | Ile | Asn |      |  |  |  |  |
|     | 580        |            |            |            |            | 585 |     |     |     |     | 590 |     |     |     |     |      |  |  |  |  |
| TTC | TAAGCCTTTC | TATTCTTTCC | AATAGAGGGT | TTTCTCTCTG | TTGGTTTCTT | TTT |     |     |     |     |     |     |     |     |     | 1888 |  |  |  |  |
| Phe |            |            |            |            |            |     |     |     |     |     |     |     |     |     |     |      |  |  |  |  |
| 595 |            |            |            |            |            |     |     |     |     |     |     |     |     |     |     |      |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ser | Phe | Lys | Lys | Leu | Gly | Phe | Val | Ser | Leu | Ala | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Leu | Leu | Gly | Ser | Met | Asn | Ala | Thr | Asp | Leu | Glu | Thr | Tyr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Gln | Lys | Ser | Ser | His | Val | Phe | Gly | Asn | Tyr | Ala | Glu | Lys | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Asp | Ser | Lys | Leu | Thr | Ser | Asp | Ser | Pro | Thr | Gln | Gln | Gln | Asp | Gln |





[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

227

|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAC GCA AAA GCT TTC AAT GAC GCA CTC ATT AAG AGC ATG GAT ATT GAG | 393  |
| Asn Ala Lys Ala Phe Asn Asp Ala Leu Ile Lys Ser Met Asp Ile Glu |      |
| 105 110 115                                                     |      |
| CAT TAC CCT AGC GTT AAG ATT AGG GCT GTT GTA GCG CGA GAT AGC GAT | 441  |
| His Tyr Pro Ser Val Lys Ile Arg Ala Val Val Ala Arg Asp Ser Asp |      |
| 120 125 130                                                     |      |
| GTG AGG GCT GTG CCT ACT AAC AAA CCT TAT TAT CTT TCT CAA AAA GGC | 489  |
| Val Arg Ala Val Pro Thr Asn Lys Pro Tyr Tyr Leu Ser Gln Lys Gly |      |
| 135 140 145                                                     |      |
| TAT CCT TTT GAT AGG TAT CAA AAT TCG CTG ATT TTT CAA GGC ACG CCG | 537  |
| Tyr Pro Phe Asp Arg Tyr Gln Asn Ser Leu Ile Phe Gln Gly Thr Pro |      |
| 150 155 160                                                     |      |
| GTT TTA ATC ACG CAT TTT AAT CTA GAT AAA ACT TAT GCC CAC ATT CAA | 585  |
| Val Leu Ile Thr His Phe Asn Leu Asp Lys Thr Tyr Ala His Ile Gln |      |
| 165 170 175 180                                                 |      |
| AGC AGT TTT GTT TAT GGC TGG ATC AAA GTT AGC GAT TTA GTC TAC ATG | 633  |
| Ser Ser Phe Val Tyr Gly Trp Ile Lys Val Ser Asp Leu Val Tyr Met |      |
| 185 190 195                                                     |      |
| CAC GAT AAA GAC ATA GAG CTT TTA ACC CAT CTT AAA GAT TAT GTC ATG | 681  |
| His Asp Lys Asp Ile Glu Leu Leu Thr His Leu Lys Asp Tyr Val Met |      |
| 200 205 210                                                     |      |
| CCT ATA AAA GAT AAA ATC CCC CTT TAT ACA GAC TAT GGG GAT TTT TAC | 729  |
| Pro Ile Lys Asp Lys Ile Pro Leu Tyr Thr Asp Tyr Gly Asp Phe Tyr |      |
| 215 220 225                                                     |      |
| ACC AAC GCC AGA GTG GGC GAA TTG TTC GCT CTC ATC CCC CAA AGT CAA | 777  |
| Thr Asn Ala Arg Val Gly Glu Leu Phe Ala Leu Ile Pro Gln Ser Gln |      |
| 230 235 240                                                     |      |
| AAA ACA CCT CAA AAA CCC CAA AAA AAG GAA TTG AAA GCC TAT GGT TTT | 825  |
| Lys Thr Pro Gln Lys Pro Gln Lys Lys Glu Leu Lys Ala Tyr Gly Phe |      |
| 245 250 255 260                                                 |      |
| TTG AGA GAC GCT AAG GGT TAT GCA GCT TTA CAA AGC GTG ATC TTA GAA | 873  |
| Leu Arg Asp Ala Lys Gly Tyr Ala Ala Leu Gln Ser Val Ile Leu Glu |      |
| 265 270 275                                                     |      |
| GAA AAG GAT TTT TTT GTT TTC CCT AAG GCT TTT AAC AGC GAG AAC ATG | 921  |
| Glu Lys Asp Phe Phe Val Phe Pro Lys Ala Phe Asn Ser Glu Asn Met |      |
| 280 285 290                                                     |      |
| GCG TAT TTT ATA GAC ACC ATG TTA GGG CAA AAA TAC GGC TGG GGC GGG | 969  |
| Ala Tyr Phe Ile Asp Thr Met Leu Gly Gln Lys Tyr Gly Trp Gly Gly |      |
| 295 300 305                                                     |      |
| CTA TTG GGT AAT AGG GAT TGC TCG GCT TTC ACC AGA GAT AGT TTT GCT | 1017 |
| Leu Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg Asp Ser Phe Ala |      |
| 310 315 320                                                     |      |
| AAT TTT GGT ATT TTG CTC CCC AGA AAT TCC TAT GCG CAA AGC CGT TAT | 1065 |
| Asn Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala Gln Ser Arg Tyr |      |

|                                                                   |     |     |  |     |  |     |      |
|-------------------------------------------------------------------|-----|-----|--|-----|--|-----|------|
| 325                                                               |     | 330 |  | 335 |  | 340 |      |
| GCG AAC AAT TAT GTG GAT TTA AGC TCT ATG AAA GCC AAA GAA AAA GAA   |     |     |  |     |  |     | 1113 |
| Ala Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala Lys Glu Lys Glu   |     |     |  |     |  |     |      |
|                                                                   | 345 |     |  | 350 |  | 355 |      |
| GAC TAC ATC CTT AAA AAC GCC ACG CCT TTT GGA ACG CTC ATC TAT TTA   |     |     |  |     |  |     | 1161 |
| Asp Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr Leu Ile Tyr Leu   |     |     |  |     |  |     |      |
|                                                                   | 360 |     |  | 365 |  | 370 |      |
| AAA GGG CAT ATC ATG CTT TAT TTA GGC GCA CAC AAC CAT CAA GCG ATA   |     |     |  |     |  |     | 1209 |
| Lys Gly His Ile Met Leu Tyr Leu Gly Ala His Asn His Gln Ala Ile   |     |     |  |     |  |     |      |
|                                                                   | 375 |     |  | 380 |  | 385 |      |
| GTC GCT CAC AGC ATT TGG TCG GTG CAA ACC CAA AAG CAT TTT AAA ACC   |     |     |  |     |  |     | 1257 |
| Val Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys His Phe Lys Thr   |     |     |  |     |  |     |      |
|                                                                   | 390 |     |  | 395 |  | 400 |      |
| TTG AGC CAT AAA ATA GGA GGC GTG GTG ATC ACT TCG TTA TGG TTA GCT   |     |     |  |     |  |     | 1305 |
| Leu Ser His Lys Ile Gly Gly Val Val Ile Thr Ser Leu Trp Leu Ala   |     |     |  |     |  |     |      |
|                                                                   | 405 |     |  | 410 |  | 415 | 420  |
| GAA GAG CAT AAT GGG GCG TTT TCT AAA AAG AAA TTA TTG ATT GAT AGG   |     |     |  |     |  |     | 1353 |
| Glu Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu Leu Ile Asp Arg   |     |     |  |     |  |     |      |
|                                                                   | 425 |     |  | 430 |  | 435 |      |
| GTG CTT GGA ATG AGC GAT TTG AAA GAT TTT GTC AAT AAA ACT TCA AGC   |     |     |  |     |  |     | 1401 |
| Val Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn Lys Thr Ser Ser   |     |     |  |     |  |     |      |
|                                                                   | 440 |     |  | 445 |  | 450 |      |
| CCT TTA AAT GCG AAT TGATTTTCTT ATATTATGAT TACGATTTAT CAATTTAAAA C |     |     |  |     |  |     | 1457 |
| Pro Leu Asn Ala Asn                                               |     |     |  |     |  |     |      |
|                                                                   | 455 |     |  |     |  |     |      |
| ATTTGGAGAA AGA                                                    |     |     |  |     |  |     | 1470 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Tyr | Phe | Leu | Val | Val | Phe | Leu | Phe | Leu | Phe | Val | Gly | Cys | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Lys | Asp | Phe | Thr | Leu | Lys | Asp | Leu | Ser | Leu | Pro | Gln | Glu | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Tyr | Leu | Ala | Ser | Ser | Gln | Asn | Gly | Ser | Asn | Asn | Asn | Gln | Ser | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Pro | Gln | Ala | Leu | Arg | Glu | Asn | Leu | Lys | Glu | Ser | Tyr | Leu | Lys | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Trp | Tyr | Ser | Pro | Trp | Leu | Asp | Met | Lys | Val | Lys | Ser | Asn | Lys | Lys | Glu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  | Val | Phe | Trp | Ile | Leu | Lys | Glu | Met | Asn | Lys | Ser | Thr | Gly | Tyr | Gly | Glu |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Leu | Lys | Pro | Asn | Ala | Lys | Ala | Phe | Asn | Asp | Ala | Leu | Ile | Lys | Ser |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Met | Asp | Ile | Glu | His | Tyr | Pro | Ser | Val | Lys | Ile | Arg | Ala | Val | Val | Ala |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Arg | Asp | Ser | Asp | Val | Arg | Ala | Val | Pro | Thr | Asn | Lys | Pro | Tyr | Tyr | Leu |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Gln | Lys | Gly | Tyr | Pro | Phe | Asp | Arg | Tyr | Gln | Asn | Ser | Leu | Ile | Phe |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Gln | Gly | Thr | Pro | Val | Leu | Ile | Thr | His | Phe | Asn | Leu | Asp | Lys | Thr | Tyr |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | His | Ile | Gln | Ser | Ser | Phe | Val | Tyr | Gly | Trp | Ile | Lys | Val | Ser | Asp |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Leu | Val | Tyr | Met | His | Asp | Lys | Asp | Ile | Glu | Leu | Leu | Thr | His | Leu | Lys |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Asp | Tyr | Val | Met | Pro | Ile | Lys | Asp | Lys | Ile | Pro | Leu | Tyr | Thr | Asp | Tyr |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Gly | Asp | Phe | Tyr | Thr | Asn | Ala | Arg | Val | Gly | Glu | Leu | Phe | Ala | Leu | Ile |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Pro | Gln | Ser | Gln | Lys | Thr | Pro | Gln | Lys | Pro | Gln | Lys | Lys | Glu | Leu | Lys |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ala | Tyr | Gly | Phe | Leu | Arg | Asp | Ala | Lys | Gly | Tyr | Ala | Ala | Leu | Gln | Ser |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Val | Ile | Leu | Glu | Glu | Lys | Asp | Phe | Val | Phe | Pro | Lys | Ala | Phe | Asn |     |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Ser | Glu | Asn | Met | Ala | Tyr | Phe | Ile | Asp | Thr | Met | Leu | Gly | Gln | Lys | Tyr |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Gly | Trp | Gly | Gly | Leu | Leu | Gly | Asn | Arg | Asp | Cys | Ser | Ala | Phe | Thr | Arg |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Asp | Ser | Phe | Ala | Asn | Phe | Gly | Ile | Leu | Leu | Pro | Arg | Asn | Ser | Tyr | Ala |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Gln | Ser | Arg | Tyr | Ala | Asn | Asn | Tyr | Val | Asp | Leu | Ser | Ser | Met | Lys | Ala |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Lys | Glu | Lys | Glu | Asp | Tyr | Ile | Leu | Lys | Asn | Ala | Thr | Pro | Phe | Gly | Thr |     |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Leu | Ile | Tyr | Leu | Lys | Gly | His | Ile | Met | Leu | Tyr | Leu | Gly | Ala | His | Asn |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |
| His | Gln | Ala | Ile | Val | Ala | His | Ser | Ile | Trp | Ser | Val | Gln | Thr | Gln | Lys |     |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |
| His | Phe | Lys | Thr | Leu | Ser | His | Lys | Ile | Gly | Gly | Val | Val | Ile | Thr | Ser |     |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Leu | Trp | Leu | Ala | Glu | Glu | His | Asn | Gly | Ala | Phe | Ser | Lys | Lys | Lys | Leu |     |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |
| Leu | Ile | Asp | Arg | Val | Leu | Gly | Met | Ser | Asp | Leu | Lys | Asp | Phe | Val | Asn |     |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |
| Lys | Thr | Ser | Ser | Pro | Leu | Asn | Ala | Asn |     |     |     |     |     |     |     |     |
| 450 |     |     |     |     |     | 455 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 235 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...182  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```
CTTTTACTTT ATAATTATCG TTGGCATT TT AATATTCAAA GGAGCTTGAA ATG AGA 56
 Met Arg
 1

ATT TCT CTT TTA GCT GTA ATT TTA GCG TTA TTG TTT GTG GCT TGC CAC 104
Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala Cys His
 5 10 15

GAA ACT AAA AAA CAA ATC TTA CAA AAC GAA GCC GAT AGC ACC CCT TCA 152
Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr Pro Ser
 20 25 30

GAA AAA ACC ATT TGG CAA CCT GAA CAA AAA TAAAAATTGT AAAAATACTC AAA 205
Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
 35 40

GGCATT TTTT AAAATAAACG CAATAAAAAA 235
```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```
Met Arg Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala
 1 5 10 15
Cys His Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr
 20 25 30
Pro Ser Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
 35 40
```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |           |      |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------|------|------|
| Asp | Phe | Lys | Lys | Phe | Arg | Glu | Ile | Ala | Asp | Glu | Val | Gly | Ala | Leu       | Leu  |      |
| 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |           |      |      |
| TTA | GGC | GAT | ATA | GCC | CAT | GTG | GCA | GGG | CTT | GTG | GTA | ACC | GGT | GAG       | CAT  | 680  |
| Leu | Gly | Asp | Ile | Ala | His | Val | Ala | Gly | Leu | Val | Val | Thr | Gly | Glu       | His  |      |
| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |           | 210  |      |
| GCC | CAT | CCT | TTC | CCG | CAT | TGC | CAT | GTG | GTT | TCA | AGC | ACC | ACT | CAT       | AAG  | 728  |
| Ala | His | Pro | Phe | Pro | His | Cys | His | Val |     | Ser | Ser | Thr | Thr | His       | Lys  |      |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |           | 225  |      |
| ACC | TTA | AGA | GGG | CCT | AGA | GGG | GGG | ATT | ATT | TTA | ACT | AAT | GAT | GAA       | GAG  | 776  |
| Thr | Leu | Arg | Gly | Pro | Arg | Gly | Gly | Ile | Ile | Leu | Thr | Asn | Asp | Glu       | Glu  |      |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |           |      |      |
| ATA | GCG | GCT | AAG | ATT | GAC | AAA | GCG | ATT | TTT | CCA | GGA | ACT | CAA | GGC       | GGG  | 824  |
| Ile | Ala | Ala | Lys | Ile | Asp | Lys | Ala | Ile | Phe | Pro | Gly | Thr | Gln | Gly       | Gly  |      |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |           |      |      |
| CCT | TTG | ATG | CAT | GTG | ATT | GCT | GCT | AAA | GCG | GTG | GGT | TTT | AAA | GAG       | AAT  | 872  |
| Pro | Leu | Met | His | Val | Ile | Ala | Ala | Lys | Ala | Val | Gly | Phe | Lys | Glu       | Asn  |      |
|     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |           |      |      |
| CTA | AAA | CCA | GAA | TTT | AAA | GCT | TAT | GCA | CAA | TTA | GTG | AAA | TCT | AAC       | ATG  | 920  |
| Leu | Lys | Pro | Glu | Phe | Lys | Ala | Tyr | Ala | Gln | Leu | Val | Lys | Ser | Asn       | Met  |      |
| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |           | 290  |      |
| CAA | GTT | TTG | GCT | AAA | GCG | TTA | AAA | GAA | AAA | AAC | CAT | AAG | TTA | GTG       | AGT  | 968  |
| Gln | Val | Leu | Ala | Lys | Ala | Leu | Lys | Glu | Lys | Asn | His | Lys | Leu | Val       | Ser  |      |
|     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     | 305       |      |      |
| GGT | GGC | ACT | TCT | AAC | CAT | TTG | CTT | TTA | ATG | GAT | TTT | TTA | GAT | AAG       | CCT  | 1016 |
| Gly | Gly | Thr | Ser | Asn | His | Leu | Leu | Leu | Met | Asp | Phe | Leu | Asp | Lys       | Pro  |      |
|     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |           |      |      |
| TAT | AGC | GGG | AAA | GAC | GCT | GAT | ATT | GCA | TTA | GGG | AAT | GCC | GGA | ATC       | ACC  | 1064 |
| Tyr | Ser | Gly | Lys | Asp | Ala | Asp | Ile | Ala | Leu | Gly | Asn | Ala | Gly | Ile       | Thr  |      |
|     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |           |      |      |
| GTG | AAT | AAA | AAC | ACC | ATT | CCT | GGT | GAA | ACG | CGC | AGC | CCT | TTT | GTA       | ACG  | 1112 |
| Val | Asn | Lys | Asn | Thr | Ile | Pro | Gly | Glu | Thr | Arg | Ser | Pro | Phe | Val       | Thr  |      |
|     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |           |      |      |
| AGC | GGG | ATA | AGG | ATT | GGC | TCA | GCG | GCA | TTG | AGC | GCA | AGG | GGC | ATG       | GGA  | 1160 |
| Ser | Gly | Ile | Arg | Ile | Gly | Ser | Ala | Ala | Leu | Ser | Ala | Arg | Gly | Met       | Gly  |      |
| 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |           | 370  |      |
| GCT | AAG | GAA | TTT | GAA | ATC | ATA | GGG | AAT | AAA | ATA | TCA | GAT | ATT | TTG       | AAT  | 1208 |
| Ala | Lys | Glu | Phe | Glu | Ile | Ile | Gly | Asn | Lys | Ile | Ser | Asp | Ile | Leu       | Asn  |      |
|     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     | 385       |      |      |
| GAT | ATT | AAT | AAT | GTT | AGT | TTG | CAA | TTG | CAT | GTG | AAA | GAA | GAA | TTG       | AAA  | 1256 |
| Asp | Ile | Asn | Asn | Val | Ser | Leu | Gln | Leu | His | Val | Lys | Glu | Glu | Leu       | Lys  |      |
|     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |           |      |      |
| GCC | ATG | GTC | AAT | CAA | TTC | CCT | GTG | TAC | CAC | CAA | CCT | ATT | TTT | TAAGGGAGT | 1307 |      |
| Ala | Met | Val | Asn | Gln | Phe | Pro | Val | Tyr | His | Gln | Pro | Ile | Phe |           |      |      |
|     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |           |      |      |

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Tyr | Phe | Leu | Glu | Gln | Thr | Asp | Ser | Glu | Ile | Phe | Glu | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Glu | Glu | Tyr | Lys | Arg | Gln | Asn | Glu | His | Leu | Glu | Met | Ile | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Asn | Tyr | Thr | Phe | Ala | Ser | Val | Met | Glu | Ala | Met | Gly | Ser | Val | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Asn | Lys | Tyr | Ala | Glu | Gly | Tyr | Pro | Asn | Lys | Arg | Tyr | Tyr | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Glu | Val | Val | Asp | Lys | Ile | Glu | Ser | Leu | Ala | Ile | Glu | Arg | Ala | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Leu | Phe | Asn | Cys | Gln | Phe | Ala | Asn | Val | Gln | Ala | His | Ser | Gly | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ala | Asn | Asn | Ala | Val | Tyr | His | Ala | Leu | Leu | Lys | Pro | Tyr | Asp | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Leu | Gly | Met | Asp | Leu | Ser | Cys | Gly | Gly | His | Leu | Thr | His | Gly | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Val | Ser | Leu | Thr | Gly | Lys | His | Tyr | Gln | Ser | Phe | Ser | Tyr | Gly | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Leu | Asp | Gly | Tyr | Ile | Asp | Tyr | Glu | Glu | Ala | Leu | Lys | Ile | Ala | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Val | Lys | Pro | Glu | Ile | Ile | Val | Cys | Gly | Phe | Ser | Ala | Tyr | Pro | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ile | Asp | Phe | Lys | Lys | Phe | Arg | Glu | Ile | Ala | Asp | Glu | Val | Gly | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Leu | Gly | Asp | Ile | Ala | His | Val | Ala | Gly | Leu | Val | Val | Thr | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | His | Ala | His | Pro | Phe | Pro | His | Cys | His | Val | Val | Ser | Ser | Thr | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Lys | Thr | Leu | Arg | Gly | Pro | Arg | Gly | Gly | Ile | Ile | Leu | Thr | Asn | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Glu | Ile | Ala | Ala | Lys | Ile | Asp | Lys | Ala | Ile | Phe | Pro | Gly | Thr | Gln |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Gly | Pro | Leu | Met | His | Val | Ile | Ala | Ala | Lys | Ala | Val | Gly | Phe | Lys |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Asn | Leu | Lys | Pro | Glu | Phe | Lys | Ala | Tyr | Ala | Gln | Leu | Val | Lys | Ser |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Met | Gln | Val | Leu | Ala | Lys | Ala | Leu | Lys | Glu | Lys | Asn | His | Lys | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Ser | Gly | Gly | Thr | Ser | Asn | His | Leu | Leu | Leu | Met | Asp | Phe | Leu | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Pro | Tyr | Ser | Gly | Lys | Asp | Ala | Asp | Ile | Ala | Leu | Gly | Asn | Ala | Gly |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ile | Thr | Val | Asn | Lys | Asn | Thr | Ile | Pro | Gly | Glu | Thr | Arg | Ser | Pro | Phe |



$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) \delta(x-a) dx = f(a)$

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...1460  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

235

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Ala | Asn | Leu | Glu | Gln | Ser | Leu | Gly | Ile | Leu | Gly | Lys | Leu | Leu | Asp | Leu |      |  |
| 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |      |  |
| TCC | CAA | CAA | TAC | GCT | AGT | CAG | GGT | GTC | ATT | AAG | CCT | TTG | GTG | GTG | GAT | 440  |  |
| Ser | Gln | Gln | Tyr | Ala | Ser | Gln | Gly | Val | Ile | Lys | Pro | Leu | Val | Val | Asp | 130  |  |
| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |      |  |
| GTG | GGG | AAA | GAA | CAA | ATC | GGT | ATC | ACG | GAT | AGC | ATG | CTC | TTG | GTG | GCT | 488  |  |
| Val | Gly | Lys | Glu | Gln | Ile | Gly | Ile | Thr | Asp | Ser | Met | Leu | Leu | Val | Ala | 145  |  |
|     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |     |      |  |
| CAA | AAC | ATC | GTT | TTA | GCT | TTA | GGG | CAA | GTG | GAT | TTG | AGC | AAA | ATC | CAA | 536  |  |
| Gln | Asn | Ile | Val | Leu | Ala | Leu | Gly | Gln | Val | Asp | Leu | Ser | Lys | Ile | Gln | 160  |  |
|     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |     |      |  |
| CAA | AAC | AAT | AAC | GAA | CAG | CTA | TAC | GAA | AAT | ATT | ATG | AAA | GTC | ATG | CTT | 584  |  |
| Gln | Asn | Asn | Asn | Glu | Gln | Leu | Tyr | Glu | Asn | Ile | Met | Lys | Val | Met | Leu | 175  |  |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |     |      |  |
| TTA | GGC | GCG | GGC | GGG | ACT | AAT | GGG | GCG | TAT | AAT | GGC | GTG | AGT | GTG | GGC | 632  |  |
| Leu | Gly | Ala | Gly | Gly | Thr | Asn | Gly | Ala | Tyr | Asn | Gly | Val | Ser | Val | Gly | 190  |  |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     |     |     |     |      |  |
| GAC | ATT | GCC | ACG | GGC | ATG | CAA | AAT | TTT | TCT | TCG | CAA | ACG | GGC | TTG | ATA | 680  |  |
| Asp | Ile | Ala | Thr | Gly | Met | Gln | Asn | Phe | Ser | Ser | Gln | Thr | Gly | Leu | Ile | 210  |  |
| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |      |  |
| GGG | GCT | AAT | TCT | ACG | GTT | AGC | GAG | CTG | AAT | GCT | TTG | ATT | AAG | AGC | GGG | 728  |  |
| Gly | Ala | Asn | Ser | Thr | Val | Ser | Glu | Leu | Asn | Ala | Leu | Ile | Lys | Ser | Gly | 225  |  |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |     |      |  |
| ATT | TCT | TTG | GAT | CGT | GAG | ACT | TTG | GGG | TTA | GGG | AGT | TTT | ATT | GAA | AAA | 776  |  |
| Ile | Ser | Leu | Asp | Arg | Glu | Thr | Leu | Gly | Leu | Gly | Ser | Phe | Ile | Glu | Lys | 240  |  |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |     |     |      |  |
| AAT | ATC | TGT | AGC | GGT | GCA | TCG | TCT | TGT | TTT | AGT | GGG | AAT | CAG | CTT | ATC | 824  |  |
| Asn | Ile | Cys | Ser | Gly | Ala | Ser | Ser | Cys | Phe | Ser | Gly | Asn | Gln | Leu | Ile | 255  |  |
|     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |     |     |      |  |
| TAT | AAG | AAA | GGG | CTA | GAC | AGA | ACC | ATA | AAC | ATC | ATT | AAT | ACG | GTA | TTA | 872  |  |
| Tyr | Lys | Lys | Gly | Leu | Asp | Arg | Thr | Ile | Asn | Ile | Ile | Asn | Thr | Val | Leu | 270  |  |
|     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |     |     |      |  |
| GGT | CAG | TTT | GAA | TCT | TCG | GCT | AGT | TCT | CTT | TAT | AAG | ATT | TCT | TAT | ATC | 920  |  |
| Gly | Gln | Phe | Glu | Ser | Ser | Ala | Ser | Ser | Leu | Tyr | Lys | Ile | Ser | Tyr | Ile | 290  |  |
| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |     |      |  |
| CCT | AAC | CTC | TTT | TCG | CTC | AAG | GAT | TAC | CAG | TCA | GCG | AGC | ATG | AAC | GGC | 968  |  |
| Pro | Asn | Leu | Phe | Ser | Leu | Lys | Asp | Tyr | Gln | Ser | Ala | Ser | Met | Asn | Gly | 305  |  |
|     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |     |      |  |
| TTT | GGG | GCT | AAG | ATG | GGC | TAT | AAA | CAA | TTT | TTC | ACC | CAT | AAG | AAA | AAT | 1016 |  |
| Phe | Gly | Ala | Lys | Met | Gly | Tyr | Lys | Gln | Phe | Phe | Thr | His | Lys | Lys | Asn | 320  |  |
|     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |     |     |      |  |
| GTT | GGC | TTA | AGG | TAT | TAC | GGG | TTT | TTG | GAT | TAT | GGC | TAT | GCG | AAC | TTT | 1064 |  |
| Val | Gly | Leu | Arg | Tyr | Tyr | Gly | Phe | Leu | Asp | Tyr | Gly | Tyr | Ala | Asn | Phe | 335  |  |
|     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |     |     |      |  |

GGC GAT ACG AAT TTA AAA GTG GGG GCG AAT CTT GTT ACT TAT GGG GTA 1112  
 Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu Val Thr Tyr Gly Val  
 340 345 350

GGA ACG GAT TTT TTA TAC AAT GTG TAT GAA CGC TCT AGA AGG AGG GAA 1160  
 Gly Thr Asp Phe Leu Tyr Asn Val Tyr Glu Arg Ser Arg Arg Arg Glu  
 355 360 365 370

AGG ACT ACG ATC GGT CTT TTC TTT GGC GCT CAA ATT GCA GGG CAA ACT 1208  
 Arg Thr Thr Ile Gly Leu Phe Phe Gly Ala Gln Ile Ala Gly Gln Thr  
 375 380 385

TGG AGC ACT AAT GTA ACG AAC TTA TTG AGC GGG CAA AGG CCT GAT GTC 1256  
 Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly Gln Arg Pro Asp Val  
 390 395 400

AAG TCC AGT TCG TTC CAA TTC TTG TTT GAT TTG GGC GTG CGC ACC AAC 1304  
 Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu Gly Val Arg Thr Asn  
 405 410 415

TTT GCA AAA ACC AAT TTC AAT AAG CAC AGG CTA GAC CAA GGG ATA GAA 1352  
 Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu Asp Gln Gly Ile Glu  
 420 425 430

TTT GGG GTG AAA ATC CCT GTT ATC GCT CAT AAA TAT TTT GCA ACC CAA 1400  
 Phe Gly Val Lys Ile Pro Val Ile Ala His Lys Tyr Phe Ala Thr Gln  
 435 440 445 450

GGC TCA AGC GCG AGC TAT ATG AGG AAT TTT AGC TTC TAT GTG GGC TAT 1448  
 Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser Phe Tyr Val Gly Tyr  
 455 460 465

TCA GTC GGT TTT TAAGGAAGGC TCTTGATGAA AAATACCAAT ACAAAGAGA TAAAG 1505  
 Ser Val Gly Phe  
 470

AATACAAG 1513

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met Ser Leu Cys Arg Ala Glu Glu Asp Gly Ala Phe Phe Val Ile Asp  
 1 5 10 15  
 Tyr Gln Thr Ser Leu Ala Arg Gln Glu Leu Lys Asn Pro Gly Phe Thr  
 20 25 30  
 Gln Ala Gln Glu Leu Arg Gln Leu Ile Arg Asp Gly Ala Val Arg Leu  
 35 40 45  
 Gln Thr Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly Asn

|                     |                     |                             |     |    |
|---------------------|---------------------|-----------------------------|-----|----|
| 50                  |                     | 55                          |     | 60 |
| Lys Thr Ala Thr Leu | Leu Arg Glu Ser Leu | Lys Asn Asn Ala Gln Pro     |     |    |
| 65                  | 70                  | 75                          | 80  |    |
| Ser Gln Pro Asn Ala | Gln Pro Pro Gln Gln | Asn Gly Pro Ser Asn Gln     |     |    |
|                     | 85                  | 90                          | 95  |    |
| Ala Leu Ala Asn Leu | Glu Gln Ser Leu Gly | Ile Leu Gly Lys Leu Leu     |     |    |
|                     | 100                 | 105                         | 110 |    |
| Asp Leu Ser Gln Gln | Tyr Ala Ser Gln Gly | Val Ile Lys Pro Leu Val     |     |    |
|                     | 115                 | 120                         | 125 |    |
| Val Asp Val Gly Lys | Glu Gln Ile Gly Ile | Thr Asp Ser Met Leu Leu     |     |    |
|                     | 130                 | 135                         | 140 |    |
| Val Ala Gln Asn Ile | Val Leu Ala Leu Gly | Gln Val Asp Leu Ser Lys     |     |    |
|                     | 145                 | 150                         | 155 |    |
| Ile Gln Gln Asn Asn | Glu Gln Leu Tyr Glu | Asn Ile Met Lys Val         |     |    |
|                     | 165                 | 170                         | 175 |    |
| Met Leu Leu Gly Ala | Gly Gly Thr Asn Gly | Ala Tyr Asn Gly Val Ser     |     |    |
|                     | 180                 | 185                         | 190 |    |
| Val Gly Asp Ile Ala | Thr Gly Met Gln Asn | Phe Ser Ser Gln Thr Gly     |     |    |
|                     | 195                 | 200                         | 205 |    |
| Leu Ile Gly Ala Asn | Ser Thr Val Ser Glu | Leu Asn Ala Leu Ile Lys     |     |    |
|                     | 210                 | 215                         | 220 |    |
| Ser Gly Ile Ser Leu | Asp Arg Glu Thr Leu | Gly Leu Gly Ser Phe Ile     |     |    |
|                     | 225                 | 230                         | 235 |    |
| Glu Lys Asn Ile Cys | Ser Gly Ala Ser Ser | Cys Phe Ser Gly Asn Gln     |     |    |
|                     | 245                 | 250                         | 255 |    |
| Leu Ile Tyr Lys Lys | Gly Leu Asp Arg Thr | Ile Asn Ile Ile Asn Thr     |     |    |
|                     | 260                 | 265                         | 270 |    |
| Val Leu Gly Gln Phe | Glu Ser Ser Ala Ser | Ser Ser Leu Tyr Lys Ile Ser |     |    |
|                     | 275                 | 280                         | 285 |    |
| Tyr Ile Pro Asn Leu | Phe Ser Leu Lys Asp | Tyr Gln Ser Ala Ser Met     |     |    |
|                     | 290                 | 295                         | 300 |    |
| Asn Gly Phe Gly Ala | Lys Met Gly Tyr Lys | Gln Phe Phe Thr His Lys     |     |    |
|                     | 305                 | 310                         | 315 |    |
| Lys Asn Val Gly Leu | Arg Tyr Tyr Gly Phe | Leu Asp Tyr Gly Tyr Ala     |     |    |
|                     | 325                 | 330                         | 335 |    |
| Asn Phe Gly Asp Thr | Asn Leu Lys Val Gly | Ala Asn Leu Val Thr Tyr     |     |    |
|                     | 340                 | 345                         | 350 |    |
| Gly Val Gly Thr Asp | Phe Leu Tyr Asn Val | Tyr Glu Arg Ser Arg Arg     |     |    |
|                     | 355                 | 360                         | 365 |    |
| Arg Glu Arg Thr Thr | Ile Gly Leu Phe Phe | Gly Ala Gln Ile Ala Gly     |     |    |
|                     | 370                 | 375                         | 380 |    |
| Gln Thr Trp Ser Thr | Asn Val Thr Asn Leu | Leu Ser Gly Gln Arg Pro     |     |    |
|                     | 385                 | 390                         | 395 |    |
| Asp Val Lys Ser Ser | Ser Phe Gln Phe Leu | Phe Asp Leu Gly Val Arg     |     |    |
|                     | 405                 | 410                         | 415 |    |
| Thr Asn Phe Ala Lys | Thr Asn Phe Asn Lys | His Arg Leu Asp Gln Gly     |     |    |
|                     | 420                 | 425                         | 430 |    |
| Ile Glu Phe Gly Val | Lys Ile Pro Val Ile | Ala His Lys Tyr Phe Ala     |     |    |
|                     | 435                 | 440                         | 445 |    |
| Thr Gln Gly Ser Ser | Ala Ser Tyr Met Arg | Asn Phe Ser Phe Tyr Val     |     |    |
|                     | 450                 | 455                         | 460 |    |
| Gly Tyr Ser Val Gly | Phe                 |                             |     |    |
| 465                 | 470                 |                             |     |    |

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:



$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) \delta(x-a) dx = f(a)$

(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

```
(v) FRAGMENT TYPE: internal
```

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...458  
(D) OTHER INFORMATION:

|                                                                 |            |            |            |            |     |     |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|-----|-----|----|
| TTTTTGCACT                                                      | ATCGTTGTTT | GCGCTGTGGT | GTTTGGCACG | CTTGAAAAAA | ATG | CTC | 56 |
|                                                                 |            |            |            |            | Met | Leu |    |
|                                                                 |            |            |            |            | 1   |     |    |
| AAG AGT ACC ATC AAA GAA GAT TAT TTG ATG CTG ATG TCT AGA GAA GTG | 104        |            |            |            |     |     |    |
| Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg Glu Val |            |            |            |            |     |     |    |
| 5 10 15                                                         |            |            |            |            |     |     |    |

AGT GCT TTT GTG GGG ACT CTT TTC TTC ATT GGC TTG AGT TGC TAT GCG 152  
 Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys Tyr Ala  
 20 25 30

ATC TAT CAT GGC AAC ATG CCC GAT TAT TTG AGA CCG GCT TTG ATA GAC 200  
 Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu Ile Asp  
 35 40 45 50

ACT ATT AAG GCA GCG AGT GAT TCC ATC TAT TCC AGC TGC GAC TAC ATG 248  
 Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp Tyr Met  
 55 60 65

GAT TAT TTT TTG AAG GCT AGA AAG ATG TTA GAG GGG TTT GCT TGG TGG 296  
 Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala Trp Trp  
 70 75 80

AGC ATG TTC AAA GCG GAG AGC ATG GGC TTA AAT AAG GGG TTT ATG GTT 344  
 Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe Met Val  
 85 90 95

GCG GGC TGG GTA GCG TTT ATC ATC TAT AAC GCT CTT AGC GGG ATA GCC 392  
 Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly Ile Ala  
 100 105 110

ATC AGC AGG CTG AGC GCT CAA ATC ATT TAT TGG TTA TCA AAA TAT TTT 440  
 Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys Tyr Phe  
 115 120 125 130

AGG AGT GAG TAT GGA AAA TGATGTTAAA GAAGATCTAG AGCAAGCAAG ACCAAAGT 496  
 Arg Ser Glu Tyr Gly Lys  
 135

TAGAGCCAGA AAAGC 511

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met Leu Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg  
 1 5 10 15  
 Glu Val Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys  
 20 25 30  
 Tyr Ala Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu  
 35 40 45  
 Ile Asp Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp  
 50 55 60  
 Tyr Met Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala  
 65 70 75 80  
 Trp Trp Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe

Met Val Ala Gly Trp Val Ala Phe Ile Tyr Asn Ala Leu Ser Gly  
 100 105 110  
 Ile Ala Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys  
 115 120 125  
 Tyr Phe Arg Ser Glu Tyr Gly Lys  
 130 135

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...2150
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGTTACACA CTCTTTGAGA ACAAACGCC AAACCATTTA GGAAATTACC ATG CTA 56  
 Met Leu  
 1

AGA TTC GTT AGT AAA ACG ATT TGC TTG TCT TTA ATC GGC TTG TTC AAC 104  
 Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu Phe Asn  
 5 10 15

CCT TTA GAA GCC TTT CAA AAA CAC CAA AAA GAC GGC TTT TTT ATA GAA 152  
 Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe Ile Glu  
 20 25 30

GCT GGG TTT GAA ACT GGG TTA TTA GAA GGA ACG CAA ACT AAA GAA GAA 200  
 Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys Glu Glu  
 35 40 45 50

GTC ATA ACC ACC CAA AAA ATC TAT GAA AAC CCC CTA ACC CAC CCA CAA 248  
 Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His Pro Gln  
 55 60 65

ACT AAA GAA CAG CCT AAA GAA CAA AAT AAA AGC GAT ACG GCC ACC CCA 296  
 Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala Thr Pro  
 70 75 80

CAA AGC GCT TAC GGA AAA TAC TAC ATA CCC CAA AGC ACC ATT TTA AAA 344  
 Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile Leu Lys  
 85 90 95

AAT GCA ACG GCT TTA TTC ACC ACG GAC AAG ATA GAA AAT GGC TTA ACT 392  
 Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly Leu Thr  
 100 105 110



|                                                                 |      |
|-----------------------------------------------------------------|------|
| TTT TAT TCT CAA AAC CCT GTG TAT GCG AAT ATG GTT AAT GGG AGC GTA | 440  |
| Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly Ser Val |      |
| 115 120 125 130                                                 |      |
| ACC ATA CAA AAC TTT CTG CCT TAT AAT TTA AAC AAT GTT GAA CTG AGT | 488  |
| Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu Leu Ser |      |
| 135 140 145                                                     |      |
| TTT AAA GAC GCT CAA GGC AAG GTG GTC AAT TTA GGC GTG ATA GAG ACC | 536  |
| Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile Glu Thr |      |
| 150 155 160                                                     |      |
| ATC CCT AAA CAA TCT CAA ATT ACC TTG CCT GCA AGC TTG TTT AAT GAT | 584  |
| Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe Asn Asp |      |
| 165 170 175                                                     |      |
| TCA GAA TTT GAA CAA GCT GAT AGC TTT AAT TAC CAA CAA CTT CAA GCC | 632  |
| Ser Glu Phe Glu Gln Ala Asp Ser Phe Asn Tyr Gln Gln Leu Gln Ala |      |
| 180 185 190                                                     |      |
| ACT GCC ACA CAA TTT TCT GAC GCT AAC ACG CAA AGT TTG TTT CAA AAG | 680  |
| Thr Ala Thr Gln Phe Ser Asp Ala Asn Thr Gln Ser Leu Phe Gln Lys |      |
| 195 200 205 210                                                 |      |
| CTC AGC AAG ATC ACA ACC AAT GTA ACA ATG AGT TAT GAA AAC GCC GAT | 728  |
| Leu Ser Lys Ile Thr Thr Asn Val Thr Met Ser Tyr Glu Asn Ala Asp |      |
| 215 220 225                                                     |      |
| ACC AAC AAT TTT AAA GGT AAT TGC CAT GAT TGT GTG TCA GAT TTC ACC | 776  |
| Thr Asn Asn Phe Lys Gly Asn Cys His Asp Cys Val Ser Asp Phe Thr |      |
| 230 235 240                                                     |      |
| CCA CAA ACC GCA GAA GAA TTG ACC AAT TTA ATG CTA GAT ATG ATT GCG | 824  |
| Pro Gln Thr Ala Glu Glu Leu Thr Asn Leu Met Leu Asp Met Ile Ala |      |
| 245 250 255                                                     |      |
| GTG TTT GAC TCT AAA TCG TGG GAA GAA GCC GTT TTA AAC GCT CCT TTC | 872  |
| Val Phe Asp Ser Lys Ser Trp Glu Glu Ala Val Leu Asn Ala Pro Phe |      |
| 260 265 270                                                     |      |
| CAA TTT TCT AAC AGC TCA TCA GAG TGC GGC TCT GAC TTT CCT AAG TGC | 920  |
| Gln Phe Ser Asn Ser Ser Ser Glu Cys Gly Ser Asp Phe Pro Lys Cys |      |
| 275 280 285 290                                                 |      |
| GTG AAT CCT TTC AAT AAC GGG CGT GTC GCT CCC ATC TAT GAA AAA TAC | 968  |
| Val Asn Pro Phe Asn Asn Gly Arg Val Ala Pro Ile Tyr Glu Lys Tyr |      |
| 295 300 305                                                     |      |
| GTG CTA ACC CCA CAA TCC GTT ATA GAT GCG TTT AGA AGA ACG ATC AAT | 1016 |
| Val Leu Thr Pro Gln Ser Val Ile Asp Ala Phe Arg Arg Thr Ile Asn |      |
| 310 315 320                                                     |      |
| CTT GAA GTG AAT ATC CTA AAA TCA GGG TTT GTA GGG CTA GGG TAT GAA | 1064 |
| Leu Glu Val Asn Ile Leu Lys Ser Gly Phe Val Gly Leu Gly Tyr Glu |      |
| 325 330 335                                                     |      |
| CTT GAT GAT AAT GAT GGT AAT CTG GGG ATA GAA GCT TCT GCC TTA AAT | 1112 |
| Leu Asp Asp Asn Asp Gly Asn Leu Gly Ile Glu Ala Ser Ala Leu Asn |      |



ATC CAG CAA TTA AGC TAT GGT GGG GGA ATG GAT GTG TTG TTT GAT TTC 1832  
 Ile Gln Gln Leu Ser Tyr Gly Gly Gly Met Asp Val Leu Phe Asp Phe  
 580 585 590

ATC ACC ACT TAC GCT AAC AAA AAG CAA GAC AAC CCA ACT AAA AAA GTT 1880  
 Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys Lys Val  
 595 600 605 610

TTT GCT TCC TCT TTT GGG GTG TTT GGG GGG TTA AGG GGC TTA TAC AAT 1928  
 Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu Tyr Asn  
 615 620 625

AGC TAT TAT GTC TTC AAC CAA GTC AAA GGA AGC GGT AAT TTA GAT ATA 1976  
 Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu Asp Ile  
 630 635 640

GTT ACT GGG TTT AAT TAC CGC TAC AAG CAT TCT AAA TAT TCT GTA GGC 2024  
 Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser Val Gly  
 645 650 655

ATT AGC GTT CCT TTA ATC CAA AGC GGT ATT AAA ATC GCT TCT AAT AAT 2072  
 Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser Asn Asn  
 660 665 670

GGC ATC TAT GCG AAC TCC GTT GTT TTG AAT GAA GGG GGC AGT CAT TTT 2120  
 Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser His Phe  
 675 680 685 690

AAA GTG TTT TTT AAT TAC GGG TGG ATT TTT TAGGATTTAA AATCCCCAAT AAC 2173  
 Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe  
 695 700

CCCCTAAACT TGTGCGATAC TCGCTACAAA 2203

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Met Leu Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu  
 1 5 10 15  
 Phe Asn Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe  
 20 25 30  
 Ile Glu Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys  
 35 40 45  
 Glu Glu Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His  
 50 55 60  
 Pro Gln Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala  
 65 70 75 80  
 Thr Pro Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile

1

545 550 555 560  
 Leu Ala Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp  
 565 570 575  
 Glu Lys Ile Gln Gln Leu Ser Tyr Gly Gly Met Asp Val Leu Phe  
 580 585 590  
 Asp Phe Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys  
 595 600 605  
 Lys Val Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu  
 610 615 620  
 Tyr Asn Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu  
 625 630 635 640  
 Asp Ile Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser  
 645 650 655  
 Val Gly Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser  
 660 665 670  
 Asn Asn Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser  
 675 680 685  
 His Phe Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe  
 690 695 700

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TCGTTTGGGA AAAAGATATA GCCCATGCGC GTTTC AAGGG TAATGAAAGC ATG GTG | 56  |
| Met Val                                                         |     |
| 1                                                               |     |
| TAT GAA GAA AAT TTT GTG CAT GCC GGG TTT GTG CTT ATT GCG TGC AAT | 104 |
| Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala Cys Asn |     |
| 5 10 15                                                         |     |
| TAT GCG GCC TTG TGC GCG TTG AAT AAA AGA CAC AGC GTG GTG GTT TCT | 152 |
| Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val Val Ser |     |
| 20 25 30                                                        |     |
| AAT AAC ATC AAT TTT TAT GCC CCC CTA GAA TTG AAT CAA GAA GCA CTC | 200 |
| Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu Ala Leu |     |
| 35 40 45 50                                                     |     |
| ATT AAA GCG CAA GTG ATT CAA GAT GGC GTG AAA AAA GCT GAA ATA AAA | 248 |
| Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu Ile Lys |     |
| 55 60 65                                                        |     |

ATA GAG GCG TTT GTG TTA GAC ATT CAG GTT TTA GAG GGA ATG ATA GAA 296  
 Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met Ile Glu  
 70 75 80

ATT GTG GTG TTT GAT AAA AAG CCT TTT AAA TTC AAT TTT AAA GAA GAG T 345  
 Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys Glu Glu  
 85 90 95

AGTTAAATGG TTATTGTTTT AGTCGTGGAT AGTTTTAAAG ACACCAGTAA TG 397

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Val Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala  
 1 5 10 15  
 Cys Asn Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val  
 20 25 30  
 Val Ser Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu  
 35 40 45  
 Ala Leu Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu  
 50 55 60  
 Ile Lys Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met  
 65 70 75 80  
 Ile Glu Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys  
 85 90 95  
 Glu Glu

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1208
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATGATAGTAA GGAAATAAGA GTGGAATGCA AGAATCACCC TATTGAAAAG ATG GCA 56

Met Ala  
1

|                                                                                                                                    |     |
|------------------------------------------------------------------------------------------------------------------------------------|-----|
| GAA AAA TTA GAG GAA ACT AAT CCT GAA TGG TTT GAA AAA TGG AGG GAA<br>Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp Arg Glu | 104 |
| 5 10 15                                                                                                                            |     |
| AAA CAA TAC ACC CAA ACT GGC GAA TCT AAG CCA TCA AAA CGA ATC AAA<br>Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg Ile Lys | 152 |
| 20 25 30                                                                                                                           |     |
| GTT TTT AAA AAC TTT ACG GCA TTT GAT GAC AGA TTG TAT ACA ATT GAA<br>Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr Ile Glu | 200 |
| 35 40 45 50                                                                                                                        |     |
| TGT AAT TTA AAA AAT CTG GAT ACC CAT CAA AAA AAG TTT GAA ATT TGT<br>Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu Ile Cys | 248 |
| 55 60 65                                                                                                                           |     |
| GGG GCT CTG TAT GAC ATT TAT GAA CAA ATT TTT GAT GAA ACA CCA AGC<br>Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr Pro Ser | 296 |
| 70 75 80                                                                                                                           |     |
| TTG AAA GGG CGC GAT TTA GAA ACA TAC AAA GCA CAA GAT TTG TCA AAG<br>Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu Ser Lys | 344 |
| 85 90 95                                                                                                                           |     |
| AAA TTC ATG CAT TTA GGT TTT GAA CAG ATC TCA AAA GAT TTA AAC GAC<br>Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu Asn Asp | 392 |
| 100 105 110                                                                                                                        |     |
| TCT AGA TTG AAC GCT TTA TTG TGC TAT GAG GAA AAA GTC ATG CAA GCT<br>Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met Gln Ala | 440 |
| 115 120 125 130                                                                                                                    |     |
| TTG GCT AAA AAA TAC CCT AGT TTT TTA CAA GAT TTG CAT GAT ATA AAA<br>Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp Ile Lys | 488 |
| 135 140 145                                                                                                                        |     |
| AAA TAC AGG AAT AAA GAT AAA CAC GGC GAG AAA CCA CAA GAT GGG TCT<br>Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp Gly Ser | 536 |
| 150 155 160                                                                                                                        |     |
| TCT TTA ACG AGA GTG GAA TTA GAA AGA TAC AGA GAT GGA ATT TAT TTT<br>Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile Tyr Phe | 584 |
| 165 170 175                                                                                                                        |     |
| CTA GTA GAA AAT CTT TTA AAA AAC CCC TTG ATT AAA GAG AGA GAA AAT<br>Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg Glu Asn | 632 |
| 180 185 190                                                                                                                        |     |
| GCT CAA GAA GAA AAA CAT TAT AAG AAA AAT GCA GAG ATT GAC GAC CGA<br>Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp Asp Arg | 680 |
| 195 200 205 210                                                                                                                    |     |
| TCC CAG CTA TCA AAC TTA AAC GCA CCC AAA CCC TTA TTT GAA TGT TTT<br>Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu Cys Phe | 728 |
| 215 220 225                                                                                                                        |     |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GTA GGA GTT AAT CTG GCC AAA GCC AAA TAT TAT TCT AAA AAA GAA GAA   | 776  |
| Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys Glu Glu   |      |
| 230 235 240                                                       |      |
| AGA GAA AAA GAA AAG ATG ATC TTG AAT TTT TGT AAG ATA TTT GAA ATT   | 824  |
| Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe Glu Ile   |      |
| 245 250 255                                                       |      |
| ATT CTT TTT GAA GCT ATC CAA AAA CAA CCA AAG CCT GAT TTT AAA AAT   | 872  |
| Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe Lys Asn   |      |
| 260 265 270                                                       |      |
| AAA GAC GAG CTT TTA GGG GAT TAT CCT AAT CTT AAA AAT TTA GAT TCT   | 920  |
| Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu Asp Ser   |      |
| 275 280 285 290                                                   |      |
| TTA AGA GAA GTG AGG GAA GAC TTT TTG AAA AGA GCG TTT AAG AAT GAT   | 968  |
| Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys Asn Asp   |      |
| 295 300 305                                                       |      |
| GAA GCG AGT TTG GGA GCG TAT GTG TTA GTG TTG CTT AGC TGT AAG TAT   | 1016 |
| Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys Lys Tyr   |      |
| 310 315 320                                                       |      |
| TTT GAG AGC GTG TTT GAA AAA GTT CAA GAA TGG CTA GAT TTT ATC GCT   | 1064 |
| Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe Ile Ala   |      |
| 325 330 335                                                       |      |
| AGG CTT ATT GCT TTG AGA GGC CAT GTG CAC AAG ATA ACT AAA GAA CTT   | 1112 |
| Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys Glu Leu   |      |
| 340 345 350                                                       |      |
| GAA AGA TTA GAA GAA GAG GAT TTA GAA AAA TTG GAA AAA CAA GCA CTA   | 1160 |
| Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln Ala Leu   |      |
| 355 360 365 370                                                   |      |
| GAA TAT TTT AAT AAA ATA GCA AAT AAA ATA TAT CTA AAG GAG AAA CGA T | 1209 |
| Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu Lys Arg   |      |
| 375 380 385                                                       |      |
| GAGCGGAAT GAAGAATTGG AGCTAAGAGC CAGAGAAACT GAGTTGGATA AA          | 1261 |

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Lys | Leu | Glu | Glu | Thr | Asn | Pro | Glu | Trp | Phe | Glu | Lys | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | Lys | Gln | Tyr | Thr | Gln | Thr | Gly | Glu | Ser | Lys | Pro | Ser | Lys | Arg |





(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 51...359  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CATTTAATGC TAAGTCTAAT AAGATTGCCC TAGATAGACA TTACGCCAAA ATG TTT     | 56  |
| Met Phe                                                            |     |
| 1                                                                  |     |
| TTG CAA GTT GTA GCA AGA ACT CTA AGA AAG AAT GTC AAT ATA TTA GAA    | 104 |
| Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile Leu Glu    |     |
| 5 10 15                                                            |     |
| GAG CAA GGT TTT ATT GAA GTC ATT AAA GGA AAA CAA AGA TAC TTG TAT    | 152 |
| Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr    |     |
| 20 25 30                                                           |     |
| GTG TAT CTT AAA GAT TAC AGA GAA TTA GAG GGC TAT AAC TCC GTA GGA    | 200 |
| Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser Val Gly    |     |
| 35 40 45 50                                                        |     |
| GCT AAT CAA AAG AAC AAT ATC CCA TCG CCT TTT TTC TTA CAG ATT ATG    | 248 |
| Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln Ile Met    |     |
| 55 60 65                                                           |     |
| CGT TTC TTA GAA AAG TTT GCC AAA GAA ATT GAG AGA GTA AAA ATA ACA    | 296 |
| Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys Ile Thr    |     |
| 70 75 80                                                           |     |
| ACA AAG AAT GTG TTA TGC ATA TTC CTA GCC AAG AGC TTA TGC AAA GAG    | 344 |
| Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys Lys Glu    |     |
| 85 90 95                                                           |     |
| TTA ATA ATG TTG TTT TAA AATTCAC GCCTATTTCT AATCCTAATA CCACTTACAC T | 400 |
| Leu Ile Met Leu Phe                                                |     |
| 100                                                                |     |
| TTATCCTACA AG                                                      | 412 |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

|                                                                 |
|-----------------------------------------------------------------|
| Met Phe Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile |
| 1 5 10 15                                                       |
| Leu Glu Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr |

20 25 30  
 Leu Tyr Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser  
 35 40 45  
 Val Gly Ala Asn Gln Lys Asn Ile Pro Ser Pro Phe Phe Leu Gln  
 50 55 60  
 Ile Met Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys  
 65 70 75 80  
 Ile Thr Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys  
 85 90 95  
 Lys Glu Leu Ile Met Leu Phe  
 100

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1151
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

|                                                                 |            |            |            |            |         |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|---------|----|
| TTCTATTAAA                                                      | ATTAGTGTAT | GATTGAGATT | ATTTTGTATT | AGGATCAACC | ATG CAA | 56 |
|                                                                 |            |            |            |            | Met Gln |    |
|                                                                 |            |            |            |            | 1       |    |
| AAA GCC TTA TTA CAT TCA TCA TTC TTT TTA CCT TTA TTT TTA TCT TTT | 104        |            |            |            |         |    |
| Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu Phe Leu Ser Phe |            |            |            |            |         |    |
| 5 10 15                                                         |            |            |            |            |         |    |
| TGT ATC GCT GAA GAA AAT GGG GCG TAT GCG AGC GTG GGT TTT GAA TAT | 152        |            |            |            |         |    |
| Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe Glu Tyr |            |            |            |            |         |    |
| 20 25 30                                                        |            |            |            |            |         |    |
| TCC ATT AGT CAT GCC GTT GAA CAC AAT AAC CCC TTT TTA AAT CAA GAA | 200        |            |            |            |         |    |
| Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn Gln Glu |            |            |            |            |         |    |
| 35 40 45 50                                                     |            |            |            |            |         |    |
| CGC ATC CAA ATC ATT TCT AAC GCT CAA AAT AAA ATC TAT AAA CTC CAT | 248        |            |            |            |         |    |
| Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys Leu His |            |            |            |            |         |    |
| 55 60 65                                                        |            |            |            |            |         |    |
| CAA GTT AAA AAT GAA ATC ACA AGC ATG CCT AAA ACC TTT GCA TAT ATC | 296        |            |            |            |         |    |
| Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr Phe Ala Tyr Ile |            |            |            |            |         |    |
| 70 75 80                                                        |            |            |            |            |         |    |
| AAC AAC GCT TTA AAA AAC AAC TCC AAA TTA ACC CCC ACT GAA ATG CAA | 344        |            |            |            |         |    |
| Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro Thr Glu Met Gln |            |            |            |            |         |    |
| 85 90 95                                                        |            |            |            |            |         |    |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GCC GAA CAA TAC TAC CTC CAA TCC ACC TTT CAA AAC ATT GAA AAA ATA | 392  |
| Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn Ile Glu Lys Ile |      |
| 100 105 110                                                     |      |
| GTA ATG CTT AGC GGT GGC GTT TCA TCT AAC CCA CAA TTA GTC CAA GCG | 440  |
| Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln Leu Val Gln Ala |      |
| 115 120 125 130                                                 |      |
| TTG GAA AAA ATG CAA GAA CCC ATT ACT AAC CCT TTA GAA TTT GAA GAA | 488  |
| Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Phe Glu Glu |      |
| 135 140 145                                                     |      |
| AAC TTA AGA AAT TTA GAA GTG CAA TTT GCT CAA TCT CAA AAC CGC ATG | 536  |
| Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn Arg Met |      |
| 150 155 160                                                     |      |
| CTT TCT TCT TTA TCT TCT CAA ATC GCT GCC ATT TCA AAT TCC TTA AAC | 584  |
| Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser Leu Asn |      |
| 165 170 175                                                     |      |
| GCG CTT GAT CCT AAC TCT TAT TCT AAA AAC ATT TCA AGC ATG TAT GGG | 632  |
| Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met Tyr Gly |      |
| 180 185 190                                                     |      |
| GTG AGT TTG AGC GTA GGT TAT AAG CAT TTC TTT ACC AAG AAA AAA AAT | 680  |
| Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys Lys Asn |      |
| 195 200 205 210                                                 |      |
| CAA GGG TTG CGC TAT TAC TTG TTT TAT GAC TAT GGT TAC ACT AAT TTT | 728  |
| Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe |      |
| 215 220 225                                                     |      |
| GGT TTT GTG GGC AAT GGC TTT GAT GGT TTA GGC AAA ATG AAT AAC CAT | 776  |
| Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn Asn His |      |
| 230 235 240                                                     |      |
| CTC TAT GGG CTT GGG ATA GAC TAT CTT TAT AAT TTC ATT GAT AAT GCA | 824  |
| Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp Asn Ala |      |
| 245 250 255                                                     |      |
| AAA AAA CAC TCT AGC GTA GGT TTT TAT CTG GGT TTT GCT TTA GCG GGG | 872  |
| Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu Ala Gly |      |
| 260 265 270                                                     |      |
| AGT TCG TGG GTA GGG AGT GGT TTG AGC ATG TGG GTG AGC CAA ACG GAT | 920  |
| Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln Thr Asp |      |
| 275 280 285 290                                                 |      |
| TTT ATC AAC AAT TAC TTG ACG GGC TAT CAA GCT AAA ATG CAC ACG AGT | 968  |
| Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His Thr Ser |      |
| 295 300 305                                                     |      |
| TTT TTC CAG ATC CCT TTG AAT TTT GGG GTT CGT GTG AAT GTC AAT AGG | 1016 |
| Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val Asn Arg |      |
| 310 315 320                                                     |      |
| CAT AAT GGC TTT GAA ATG GGC TTG AAA ATC CCT TTA GCG ATG AAT TCC | 1064 |
| His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met Asn Ser |      |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Asn | Leu | Gly | Gly | Val | Leu | Gly | Gly | Gln | Ala | Tyr | Asp | Gly | Thr | Lys | Tyr |      |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |      |
| GAT | AGG | TGG | GCG | AAG | GAT | TTT | ACC | CCC | CCA | AGC | TAT | TGG | GAT | AAA | ACT | 392  |
| Asp | Arg | Trp | Ala | Lys | Asp | Phe | Thr | Pro | Pro | Ser | Tyr | Trp | Asp | Lys | Thr |      |
|     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |      |
| TCT | TGC | GGT | ACT | GAT | TCT | ATG | AGT | CTT | TGT | ATG | AAT | GCC | ACT | AAA | ATG | 440  |
| Ser | Cys | Gly | Thr | Asp | Ser | Met | Ser | Leu | Cys | Met | Asn | Ala | Thr | Lys | Met |      |
|     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |      |
| TGG | CAG | CAA | TCA | GGG | CCA | GGT | GGC | GTC | ATT | AAC | CCT | AGA | GGT | ATT | GGT | 488  |
| Trp | Gln | Gln | Ser | Gly | Pro | Gly | Gly | Val | Ile | Asn | Pro | Arg | Gly | Ile | Gly |      |
|     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |      |
| TGG | GAA | TAC | ATG | GGT | GAG | TGG | AAC | GGC | TTG | TTC | CCT | AAC | TAC | TAT | CCG | 536  |
| Trp | Glu | Tyr | Met | Gly | Glu | Trp | Asn | Gly | Leu | Phe | Pro | Asn | Tyr | Tyr | Pro |      |
|     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |      |
| GCT | AAC | GCC | TAC | TTG | CCT | GGT | GGC | TCA | AGG | CGC | TAT | CAA | GTC | TAT | AAA | 584  |
| Ala | Asn | Ala | Tyr | Leu | Pro | Gly | Gly | Ser | Arg | Arg | Tyr | Gln | Val | Tyr | Lys |      |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |      |
| GCA | AAT | TTG | ACC | TAT | GAT | AGC | GAC | AGG | GTC | CAT | ATG | GTA | ATG | GGG | CGT | 632  |
| Ala | Asn | Leu | Thr | Tyr | Asp | Ser | Asp | Arg | Val | His | Met | Val | Met | Gly | Arg |      |
|     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |      |
| TTT | GAC | ATT | ACC | GAG | CAG | GAG | CAA | ATG | GAT | TGG | ATT | TAC | CAA | TTG | TTC | 680  |
| Phe | Asp | Ile | Thr | Glu | Gln | Glu | Gln | Met | Asp | Trp | Ile | Tyr | Gln | Leu | Phe |      |
|     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |      |
| CAA | GGG | TTT | TAT | GGG | ACT | TTC | AAG | CTC | ACT | AAG | AAT | ATG | AAA | TTC | TTG | 728  |
| Gln | Gly | Phe | Tyr | Gly | Thr | Phe | Lys | Leu | Thr | Lys | Asn | Met | Lys | Phe | Leu |      |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |      |
| CTC | TTT | AGT | GGT | TGG | GGT | CGT | GGT | ATC | GCT | GAT | GGT | CAG | TGG | TTG | TTC | 776  |
| Leu | Phe | Ser | Gly | Trp | Gly | Arg | Gly | Ile | Ala | Asp | Gly | Gln | Trp | Leu | Phe |      |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |      |
| CCT | ATC | TAT | CGT | GAA | AAG | CCT | TGG | GGG | GTT | CAT | AAA | GCG | GGT | ATT | ATT | 824  |
| Pro | Ile | Tyr | Arg | Glu | Lys | Pro | Trp | Gly | Val | His | Lys | Ala | Gly | Ile | Ile |      |
|     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |      |
| TAT | CGC | CCT | ACA | AAG | AAT | TTG | ATG | ATC | CAC | CCT | TAT | GTG | TAT | CTT | ATC | 872  |
| Tyr | Arg | Pro | Thr | Lys | Asn | Leu | Met | Ile | His | Pro | Tyr | Val | Tyr | Leu | Ile |      |
|     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |      |
| CCA | ATG | GTA | GGC | ACA | TTG | CCT | GGT | GCT | AAA | ATA | GAA | TAC | GAT | ACC | AAT | 920  |
| Pro | Met | Val | Gly | Thr | Leu | Pro | Gly | Ala | Lys | Ile | Glu | Tyr | Asp | Thr | Asn |      |
|     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |      |
| CCT | GAA | TTT | AGC | GGT | AGG | GGC | ATT | AGG | AAC | AGA | ACG | ACT | TTC | TAT | GCG | 968  |
| Pro | Glu | Phe | Ser | Gly | Arg | Gly | Ile | Arg | Asn | Arg | Thr | Thr | Phe | Tyr | Ala |      |
|     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |      |
| TTG | TAT | GAC | TAT | CGT | TGG | AAT | AAC | GCT | GAA | TAC | GGT | CGT | TAC | GCG | CCC | 1016 |
| Leu | Tyr | Asp | Tyr | Arg | Trp | Asn | Asn | Ala | Glu | Tyr | Gly | Arg | Tyr | Ala | Pro |      |
|     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |      |





(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Lys | Lys | Arg | Lys | Val | Ala | Ala | Ala | Leu | Leu | Lys | Arg | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Pro | Leu | Leu | Phe | Thr | Thr | Gly | Ser | Leu | Gly | Ala | Val | Thr | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Val | His | Gly | Asp | Phe | Ile | Asn | Phe | Ala | Lys | Val | Gly | Phe | Asn | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Ile | Asn | Pro | Val | Lys | Gly | Ile | Tyr | Pro | Thr | Glu | Thr | Phe | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Thr | Gly | Lys | Leu | Glu | Gly | Ser | Val | His | Leu | Gly | Arg | Gly | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Val | Asn | Leu | Gly | Gly | Val | Leu | Gly | Gly | Gln | Ala | Tyr | Asp | Gly | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Tyr | Asp | Arg | Trp | Ala | Lys | Asp | Phe | Thr | Pro | Pro | Ser | Tyr | Trp | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Thr | Ser | Cys | Gly | Thr | Asp | Ser | Met | Ser | Leu | Cys | Met | Asn | Ala | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Met | Trp | Gln | Gln | Ser | Gly | Pro | Gly | Gly | Val | Ile | Asn | Pro | Arg | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Gly | Trp | Glu | Tyr | Met | Gly | Glu | Trp | Asn | Gly | Leu | Phe | Pro | Asn | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Pro | Ala | Asn | Ala | Tyr | Leu | Pro | Gly | Gly | Ser | Arg | Arg | Tyr | Gln | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Lys | Ala | Asn | Leu | Thr | Tyr | Asp | Ser | Asp | Arg | Val | His | Met | Val | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Arg | Phe | Asp | Ile | Thr | Glu | Gln | Glu | Gln | Met | Asp | Trp | Ile | Tyr | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Phe | Gln | Gly | Phe | Tyr | Gly | Thr | Phe | Lys | Leu | Thr | Lys | Asn | Met | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Leu | Leu | Phe | Ser | Gly | Trp | Gly | Arg | Gly | Ile | Ala | Asp | Gly | Gln | Trp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Phe | Pro | Ile | Tyr | Arg | Glu | Lys | Pro | Trp | Gly | Val | His | Lys | Ala | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ile | Tyr | Arg | Pro | Thr | Lys | Asn | Leu | Met | Ile | His | Pro | Tyr | Val | Tyr |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Ile | Pro | Met | Val | Gly | Thr | Leu | Pro | Gly | Ala | Lys | Ile | Glu | Tyr | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Thr | Asn | Pro | Glu | Phe | Ser | Gly | Arg | Gly | Ile | Arg | Asn | Arg | Thr | Thr | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Ala | Leu | Tyr | Asp | Tyr | Arg | Trp | Asn | Asn | Ala | Glu | Tyr | Gly | Arg | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ala | Pro | Ala | Arg | Tyr | Asn | Thr | Trp | Asp | Pro | Phe | Leu | Asp | Asn | Gly | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Trp | Arg | Gly | Leu | Gln | Gly | Pro | Gly | Gly | Ala | Thr | Leu | Leu | Leu | Arg | His |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| His | Ile | Asp | Ile | Asn | Asn | Tyr | Phe | Val | Val | Gly | Gly | Ala | Tyr | Leu | Asn |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Gly | Asn | Pro | Asn | Met | Asn | Leu | Gly | Thr | Trp | Gly | Asn | Pro | Val | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Asp | Gly | Ile | Glu | Gln | Trp | Val | Gly | Ser | Ile | Tyr | Ser | Leu | Gly | Phe |

|                 |                 |                 |                 |         |     |     |
|-----------------|-----------------|-----------------|-----------------|---------|-----|-----|
| 385             |                 | 390             |                 | 395     |     | 400 |
| Ala Gly Ile Asp | Asn Ile Thr Asp | Ala Asp         | Ala Phe Thr Glu | Tyr Val |     |     |
|                 | 405             |                 | 410             |         | 415 |     |
| Lys Gly Gly Gly | Lys His Gly Lys | Phe Ser Trp Ser | Val Tyr Gln Arg |         |     |     |
|                 | 420             | 425             | 430             |         |     |     |
| Phe Thr Thr Ala | Pro Arg Ala Leu | Glu Tyr Gly Ile | Gly Met Tyr Leu |         |     |     |
|                 | 435             | 440             | 445             |         |     |     |
| Asp Tyr Gln Phe | Ser Lys His Val | Lys Ala Gly Leu | Lys Leu Val Trp |         |     |     |
|                 | 450             | 455             | 460             |         |     |     |
| Leu Glu Phe Gln | Ile Arg Ala Gly | Tyr Asn Pro Gly | Thr Gly Phe Leu |         |     |     |
|                 | 465             | 470             | 475             |         | 480 |     |
| Gly Pro Asn Gly | Gln Pro Leu Asn | Leu Asn Thr Gly | Leu Phe Glu Ser |         |     |     |
|                 | 485             | 490             | 495             |         |     |     |
| Ser Ala Phe Ala | Gln Gly Pro Gln | Asn Met Gly Gly | Ile Ala Lys Ser |         |     |     |
|                 | 500             | 505             | 510             |         |     |     |
| Ile Thr Gln Asp | Arg Ser His Leu | Met Thr His Ile | Ser Tyr Ser Phe |         |     |     |
|                 | 515             | 520             | 525             |         |     |     |

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...359
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

|                                                                 |         |     |
|-----------------------------------------------------------------|---------|-----|
| TTTTGTCTGA TTTGTTGCTA CCAAACCAT TACCAACCAA AGCAGATCCC           | ATG TTT | 56  |
|                                                                 | Met Phe |     |
|                                                                 | 1       |     |
| TTG ATA CTA TCG AAT CCA TTC TTC AAC ACT TCT GCC ATA AAA TTC TTG |         | 104 |
| Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys Phe Leu |         |     |
| 5 10 15                                                         |         |     |
| ATA TTG TCC ATA GGC AAG TTG AAT TTT TTC CCT AAT ATT TCA TTA AGT |         | 152 |
| Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser Leu Ser |         |     |
| 20 25 30                                                        |         |     |
| CCC ATC ATT AAC ATC AGG AAG AAC AAA AAA TTT AAT ATC ATA GAA AAC |         | 200 |
| Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile Glu Asn |         |     |
| 35 40 45 50                                                     |         |     |
| AAA TCA CTG GAT AAA CCT GTA AAA AGA TTT GTT CCG CCA CCC AAC AAA |         | 248 |
| Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro Asn Lys |         |     |
| 55 60 65                                                        |         |     |
| GAA GCT AAA ATT TTT CCC ATG ATC AGT CCT TTT ATT TTT GGT TGT GTA |         | 296 |
| Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly Cys Val |         |     |
| 70 75 80                                                        |         |     |

AGT TCT TGC TTG TTC GGA TCT CTA ATG CGT GTT TTA GTA GGA AGC ATT 344  
 Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly Ser Ile  
           85                          90                          95

TCA CAA TGG CAT ACC TAAAGCTACT AAGAAAATTC TTGAATCTAT TGGTAAGATT A 400  
 Ser Gln Trp His Thr  
           100

CTCATGAAAT CA 412

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Ile | Leu | Ser | Asn | Pro | Phe | Phe | Asn | Thr | Ser | Ala | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Ile | Leu | Ser | Ile | Gly | Lys | Leu | Asn | Phe | Phe | Pro | Asn | Ile | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Pro | Ile | Ile | Asn | Ile | Arg | Lys | Asn | Lys | Lys | Phe | Asn | Ile | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asn | Lys | Ser | Leu | Asp | Lys | Pro | Val | Lys | Arg | Phe | Val | Pro | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Lys | Glu | Ala | Lys | Ile | Phe | Pro | Met | Ile | Ser | Pro | Phe | Ile | Phe | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Val | Ser | Ser | Cys | Leu | Phe | Gly | Ser | Leu | Met | Arg | Val | Leu | Val | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ile | Ser | Gln | Trp | His | Thr |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...405
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TCCAATCCGT CTAATATCTC TTTATTTTTCG CTCAATTCTT TAACCATAAC GGGTTTTTTTA 60  
 GCGCTT GTG GGG GTT ACT GGG CTA AAG TTT GGA GCG TTT TGC ACT TCT 108

| Val | Gly | Val | Thr   | Gly | Leu     | Lys        | Phe        | Gly     | Ala | Phe | Cys | Thr | Ser |     |     |     |
|-----|-----|-----|-------|-----|---------|------------|------------|---------|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |       | 5   |         |            |            | 10      |     |     |     |     |     |     |     |     |
| TTT | TCT | TCT | TTT   | TTT | AGA     | TTT        | TCC        | TTT     | ATC | ATT | TCT | TCT | ATC | CTT | CCT | 156 |
| Phe | Ser | Ser | Phe   | Phe | Arg     | Phe        | Ser        | Phe     | Ile | Ile | Ser | Ser | Ile | Leu | Pro |     |
| 15  |     |     |       |     | 20      |            |            |         | 25  |     |     |     |     |     | 30  |     |
| TCT | ATC | ATT | TCT   | TCT | TGC     | GTG        | TTT        | TCT     | TGT | GGG | TTT | TCT | TCT | TTT | TTA | 204 |
| Ser | Ile | Ile | Ser   | Ser | Cys     | Val        | Phe        | Ser     | Cys | Gly | Phe | Ser | Ser | Phe | Leu |     |
|     |     |     |       | 35  |         |            |            |         | 40  |     |     |     |     | 45  |     |     |
| GGG | TGG | TTG | GGG   | GTT | TTT     | TGG        | TTT        | TCT     | GTT | TTG | TTG | TCA | TTT | TCT | ATT | 252 |
| Gly | Trp | Leu | Gly   | Val | Phe     | Trp        | Phe        | Ser     | Val | Leu | Leu | Ser | Phe | Ser | Ile |     |
|     |     |     | 50    |     |         |            |            | 55      |     |     |     |     | 60  |     |     |     |
| ATG | GGT | GCA | AGT   | GTG | GGC     | ATG        | ATA        | GGT     | TTG | GGC | GTG | GTG | GGC | GTA | AGA | 300 |
| Met | Gly | Ala | Ser   | Val | Gly     | Met        | Ile        | Gly     | Leu | Gly | Val | Val | Gly | Val | Arg |     |
|     |     | 65  |       |     |         |            | 70         |         |     |     |     | 75  |     |     |     |     |
| GTT | TCT | TTT | GTA   | GGC | GTG     | GGT        | TCT        | CTT     | TCT | TTA | GTT | TCT | TGT | TTA | ATT | 348 |
| Val | Ser | Phe | Val   | Gly | Val     | Gly        | Ser        | Leu     | Ser | Leu | Val | Ser | Cys | Leu | Ile |     |
|     | 80  |     |       |     |         | 85         |            |         |     |     | 90  |     |     |     |     |     |
| TCT | TTT | AAA | GGG   | GGG | TTA     | GTG        | GGG        | TTA     | GTC | AAA | TCA | TCA | AAT | CGG | TTT | 396 |
| Ser | Phe | Lys | Gly   | Gly | Leu     | Val        | Gly        | Leu     | Val | Lys | Ser | Ser | Asn | Arg | Phe |     |
| 95  |     |     |       |     | 100     |            |            |         |     | 105 |     |     |     |     | 110 |     |
| CTT | TTA | GGG | TAAAT | GGT | GTAATGG | GTAGGGGGGT | GGGAGGAAAT | TTGGACT |     |     |     |     |     |     |     | 447 |
| Leu | Leu | Gly |       |     |         |            |            |         |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Val | Thr | Gly | Leu | Lys | Phe | Gly | Ala | Phe | Cys | Thr | Ser | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Phe | Phe | Arg | Phe | Ser | Phe | Ile | Ile | Ser | Ser | Ile | Leu | Pro | Ser | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Ser | Cys | Val | Phe | Ser | Cys | Gly | Phe | Ser | Ser | Phe | Leu | Gly | Trp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Val | Phe | Trp | Phe | Ser | Val | Leu | Leu | Ser | Phe | Ser | Ile | Met | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Ser | Val | Gly | Met | Ile | Gly | Leu | Gly | Val | Val | Gly | Val | Arg | Val | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Val | Gly | Val | Gly | Ser | Leu | Ser | Leu | Val | Ser | Cys | Leu | Ile | Ser | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Gly | Gly | Leu | Val | Gly | Leu | Val | Lys | Ser | Ser | Asn | Arg | Phe | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Gly

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1127
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

|                                                                 |         |     |
|-----------------------------------------------------------------|---------|-----|
| CCAAGAAAGA GTATAATAGC GCATAAGAAT TTAAGTATG AAGAGGTTTA           | ATG CTA | 56  |
|                                                                 | Met Leu |     |
|                                                                 | 1       |     |
| GAA AAT AGA GTT AAG ACC AAG CAA ATT TTT ATC GGT GGC GTG GCC ATA |         | 104 |
| Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val Ala Ile |         |     |
| 5 10 15                                                         |         |     |
| GGG GGT GAT GCT CCC ATA AGC ACG CAA AGC ATG ACC TTT AGC AAA ACC |         | 152 |
| Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser Lys Thr |         |     |
| 20 25 30                                                        |         |     |
| GCT GAT ATT GAA AGC ACT AAA AAT CAA ATT GAC AGA CTC AAA CTC GCC |         | 200 |
| Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys Leu Ala |         |     |
| 35 40 45 50                                                     |         |     |
| GGG GCC GAT TTA GTG AGG GTG GCG GTG AGT AAT GAA AAG GAC GCT CTA |         | 248 |
| Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp Ala Leu |         |     |
| 55 60 65                                                        |         |     |
| GCC TTA AAA GAA TTG AAA AAA GTG TCC CCT TTG CCT TTA ATC GCT GAT |         | 296 |
| Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile Ala Asp |         |     |
| 70 75 80                                                        |         |     |
| ATT CAT TTC CAT TAT AAA TTC GCT CTC ATT GCC GCT CAA AGC GTG GAT |         | 344 |
| Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser Val Asp |         |     |
| 85 90 95                                                        |         |     |
| GCG ATC AGG ATT AAC CCC GGA AAC ATC GGC TCT AAA GAG AAG ATC AAA |         | 392 |
| Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys Ile Lys |         |     |
| 100 105 110                                                     |         |     |
| GCG GTG GTT GAT GCT TGT AAA GAA AAA AAC ATT CCT ATA AGA ATT GGC |         | 440 |
| Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg Ile Gly |         |     |
| 115 120 125 130                                                 |         |     |
| GTG AAT GCT GGG AGT TTA GAA AAG CAG TTT GAT CAA AAA TAC GGA CCC |         | 488 |
| Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr Gly Pro |         |     |



## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein -

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Asn | Arg | Val | Lys | Thr | Lys | Gln | Ile | Phe | Ile | Gly | Gly | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Ile | Gly | Gly | Asp | Ala | Pro | Ile | Ser | Thr | Gln | Ser | Met | Thr | Phe | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Thr | Ala | Asp | Ile | Glu | Ser | Thr | Lys | Asn | Gln | Ile | Asp | Arg | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ala | Gly | Ala | Asp | Leu | Val | Arg | Val | Ala | Val | Ser | Asn | Glu | Lys | Asp |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Ala | Leu | Ala | Leu | Lys | Glu | Leu | Lys | Lys | Val | Ser | Pro | Leu | Pro | Leu | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Asp | Ile | His | Phe | His | Tyr | Lys | Phe | Ala | Leu | Ile | Ala | Ala | Gln | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Asp | Ala | Ile | Arg | Ile | Asn | Pro | Gly | Asn | Ile | Gly | Ser | Lys | Glu | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Lys | Ala | Val | Val | Asp | Ala | Cys | Lys | Glu | Lys | Asn | Ile | Pro | Ile | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Gly | Val | Asn | Ala | Gly | Ser | Leu | Glu | Lys | Gln | Phe | Asp | Gln | Lys | Tyr |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Gly | Pro | Thr | Pro | Lys | Gly | Met | Val | Glu | Ser | Ala | Leu | Tyr | Asn | Ala | Lys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Leu | Glu | Asp | Leu | Asp | Phe | Thr | Asn | Phe | Lys | Ile | Ser | Leu | Lys | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Asp | Val | Ile | Arg | Thr | Ile | Glu | Ala | Tyr | Arg | Met | Leu | Arg | Pro | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Val | Ile | Tyr | Pro | Phe | His | Leu | Gly | Val | Thr | Glu | Ala | Gly | Asn | Leu | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Ser | Ser | Ile | Lys | Ser | Ala | Met | Ala | Leu | Gly | Gly | Leu | Leu | Met | Glu |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Gly | Ile | Gly | Asp | Thr | Met | Arg | Val | Ser | Ile | Thr | Gly | Glu | Leu | Glu | Asn |
| 225 |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Glu | Ile | Lys | Val | Ala | Arg | Ala | Ile | Leu | Arg | His | Ser | Gly | Arg | Leu | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Glu | Gly | Ile | Asn | Trp | Ile | Ser | Cys | Pro | Thr | Cys | Gly | Arg | Ile | Glu | Ala |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asn | Leu | Val | Asp | Met | Ala | Ile | Lys | Val | Glu | Lys | Arg | Leu | Ser | His | Ile |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Thr | Pro | Leu | Asp | Ile | Ser | Val | Met | Gly | Cys | Val | Val | Asn | Ala | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Gly | Glu | Ala | Lys | His | Ala | Asp | Met | Ala | Ile | Ala | Phe | Gly | Asn | Arg | Ser |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Gly | Leu | Ile | Ile | Lys | Glu | Gly | Lys | Val | Ile | His | Lys | Leu | Ala | Glu | Lys |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Asp | Leu | Phe | Glu | Thr | Phe | Val | Ile | Glu | Val | Glu | Asn | Leu | Ala | Lys | Glu |

340  
Arg Glu Lys Ser Leu Lys Asp  
355

345

350

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1346
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GCCTATGAAA TCTTAAAGCG TTATCCGGCT AAAGCAAAGG TATAAATAAC ATG AAA  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| AAA TTT TTA ATC ACT TTA TTA TTA GGA GTT TTT ATG GGG TTA CAA GCG | 104 |
| Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu Gln Ala |     |
| 5 10 15                                                         |     |
| AGC GCT TTG ACA CAC CAA GAA ATC AAT CAA GCT AAA GTC CCT GTG ATT | 152 |
| Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro Val Ile |     |
| 20 25 30                                                        |     |
| TAT GAA GAA AAC CAT TTG TTG CCT ATG GGG TTT ATC CAT TTA GCC TTT | 200 |
| Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu Ala Phe |     |
| 35 40 45 50                                                     |     |
| AGG GGG GGT GGG AGC TTA AGC GAT AAA AAC CAG TTG GGT TTG GCG AAA | 248 |
| Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu Ala Lys |     |
| 55 60 65                                                        |     |
| TTA TTC GCG CAA GTT TTA AAC GAA GGC ACT AAA GAG CTT GGT GCG GTG | 296 |
| Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys Glu Leu Gly Ala Val |     |
| 70 75 80                                                        |     |
| GGG TTT GCG CAA CTT TTA GAG CAA AAA GCG ATC AGT TTG AAT GTG GAT | 344 |
| Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn Val Asp |     |
| 85 90 95                                                        |     |
| ACC AGC ACA GAA GAT TTG CAA ATC ACT TTA GAA TTT TTA AAA GAA TAC | 392 |
| Thr Ser Thr Glu Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys Glu Tyr |     |
| 100 105 110                                                     |     |
| GAA GAT GAA GCC ATT ACG CGC TTA AAA GAG CTT TTA AAA TCC CCT AAT | 440 |
| Glu Asp Glu Ala Ile Thr Arg Leu Lys Glu Leu Leu Lys Ser Pro Asn |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |      |
| TTC | ACG | CAA | AAC | GCT | TTA | GAA | AAA | GTC | AAA | ACC | CAA | ATG | TTA | GCC | GCA | 488  |
| Phe | Thr | Gln | Asn | Ala | Leu | Glu | Lys | Val | Lys | Thr | Gln | Met | Leu | Ala | Ala |      |
|     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |      |
| CTT | TTA | CAA | AAA | GAA | AGC | GAT | TTT | GAC | TAT | TTG | GCT | AAA | TTG | ACT | TTA | 536  |
| Leu | Leu | Gln | Lys | Glu | Ser | Asp | Phe | Asp | Tyr | Leu | Ala | Lys | Leu | Thr | Leu |      |
|     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |      |
| AAG | CAA | GAG | CTT | TTT | GCT | AAC | ACC | CCT | TTA | GCT | AAC | GCA | GCC | TTA | GGC | 584  |
| Lys | Gln | Glu | Leu | Phe | Ala | Asn | Thr | Pro | Leu | Ala | Asn | Ala | Ala | Leu | Gly |      |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |      |
| ACT | AAA | GAG | AGC | ATT | CAA | AAA | ATC | AAG | CTA | GAC | GAT | TTG | AAA | CAG | CAA | 632  |
| Thr | Lys | Glu | Ser | Ile | Gln | Lys | Ile | Lys | Leu | Asp | Asp | Leu | Lys | Gln | Gln |      |
|     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |     |     |      |
| TTT | GCT | AAG | GTC | TTT | GAA | CTC | AAT | AAG | CTC | GTG | GTG | GTG | CTT | GGG | GGC | 680  |
| Phe | Ala | Lys | Val | Phe | Glu | Leu | Asn | Lys | Leu | Val | Val | Val | Leu | Gly | Gly |      |
| 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |      |
| GAT | TTG | AAA | ATC | GAT | CAA | ACC | CTT | AAG | CGT | TTG | AAT | AAC | GCC | CTT | AAT | 728  |
| Asp | Leu | Lys | Ile | Asp | Gln | Thr | Leu | Lys | Arg | Leu | Asn | Asn | Ala | Leu | Asn |      |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     | 225 |     |     |      |
| TTC | TTG | CCA | CAA | GGT | AAA | GCG | TAT | GAA | GAG | CCT | TAT | TTT | GAA | ACG | AGC | 776  |
| Phe | Leu | Pro | Gln | Gly | Lys | Ala | Tyr | Glu | Glu | Pro | Tyr | Phe | Glu | Thr | Ser |      |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |      |
| GAT | AAA | AAA | AGC | GAA | AAA | GTC | CTC | TAT | AAA | GAC | ACT | GAG | CAG | GCT | TTC | 824  |
| Asp | Lys | Lys | Ser | Glu | Lys | Val | Leu | Tyr | Lys | Asp | Thr | Glu | Gln | Ala | Phe |      |
|     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |      |
| GTG | TAT | TTT | GGT | GCG | CCC | TTT | AAA | ATC | AAG | GAT | TTA | AAA | CAG | GAT | TTA | 872  |
| Val | Tyr | Phe | Gly | Ala | Pro | Phe | Lys | Ile | Lys | Asp | Leu | Lys | Gln | Asp | Leu |      |
| 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |      |
| GCG | AAA | TCT | AAA | GTC | ATG | ATG | TTT | GTG | CTT | GGT | GGG | GGG | TTT | GGC | TCT | 920  |
| Ala | Lys | Ser | Lys | Val | Met | Met | Phe | Val | Leu | Gly | Gly | Gly | Phe | Gly | Ser |      |
| 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |     |      |
| CGT | TTA | ATG | GAA | AAA | ATC | AGG | GTT | CAA | GAG | GGA | TTA | GCT | TAT | AGC | GTG | 968  |
| Arg | Leu | Met | Glu | Lys | Ile | Arg | Val | Gln | Glu | Gly | Leu | Ala | Tyr | Ser | Val |      |
|     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |      |
| TAT | ATC | CGC | TCC | AAT | TTT | TCT | AAA | GTG | GCG | CAT | TTT | GCG | AGC | GGG | TAT | 1016 |
| Tyr | Ile | Arg | Ser | Asn | Phe | Ser | Lys | Val | Ala | His | Phe | Ala | Ser | Gly | Tyr |      |
|     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |      |
| TTG | CAA | ACC | AAG | CTC | AGC | ACT | CAA | ACT | AAA | AGC | GTT | GCC | TTA | GTT | AAA | 1064 |
| Leu | Gln | Thr | Lys | Leu | Ser | Thr | Gln | Thr | Lys | Ser | Val | Ala | Leu | Val | Lys |      |
|     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |     |      |
| AAA | ATC | GTT | AAG | GAA | TTT | ATA | GAA | AAA | GGC | ATG | ACG | CAA | CAA | GAA | TTA | 1112 |
| Lys | Ile | Val | Lys | Glu | Phe | Ile | Glu | Lys | Gly | Met | Thr | Gln | Gln | Glu | Leu |      |
|     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |     |     |      |

GAC GAC GCT AAA AAG TTT TTA CTA GGC TCT GAG CCT TTA AGG AAT GAA 1160  
 Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu Pro Leu Arg Asn Glu  
 355 360 365 370

ACG ATC TCT AGC CGC TTG AAC ACC ACT TAC AAT TAT TTT TAT TTA GGT 1208  
 Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly  
 375 380 385

TTG CCT TTA AAT TTT AAC CAA ACG CTG CTC AAT CAA ATC CAA AAA ATG 1256  
 Leu Pro Leu Asn Phe Asn Gln Thr Leu Leu Asn Gln Ile Gln Lys Met  
 390 395 400

AGT TTG AAA GAA ATC AAT GAT TTC ATT AAA GCC CAC ACC GAA ATC AAC 1304  
 Ser Leu Lys Glu Ile Asn Asp Phe Ile Lys Ala His Thr Glu Ile Asn  
 405 410 415

GAC TTG ACT TTT GCT ATT GTG AGC AAT AAA AAG AAG GAC AAA TGATGCCAT 1355  
 Asp Leu Thr Phe Ala Ile Val Ser Asn Lys Lys Lys Asp Lys  
 420 425 430

TTGAAGCTGT AATCGGGCTA GAAGTCCATG TCCAAC TCAA CACC 1399

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Met Lys Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu  
 1 5 10 15  
 Gln Ala Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro  
 20 25 30  
 Val Ile Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu  
 35 40 45  
 Ala Phe Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu  
 50 55 60  
 Ala Lys Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys Glu Leu Gly  
 65 70 75 80  
 Ala Val Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn  
 85 90 95  
 Val Asp Thr Ser Thr Glu Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys  
 100 105 110  
 Glu Tyr Glu Asp Glu Ala Ile Thr Arg Leu Lys Glu Leu Leu Lys Ser  
 115 120 125  
 Pro Asn Phe Thr Gln Asn Ala Leu Glu Lys Val Lys Thr Gln Met Leu  
 130 135 140  
 Ala Ala Leu Leu Gln Lys Glu Ser Asp Phe Asp Tyr Leu Ala Lys Leu  
 145 150 155 160  
 Thr Leu Lys Gln Glu Leu Phe Ala Asn Thr Pro Leu Ala Asn Ala Ala  
 165 170 175  
 Leu Gly Thr Lys Glu Ser Ile Gln Lys Ile Lys Leu Asp Asp Leu Lys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gln | Gln | Phe | Ala | Lys | Val | Phe | Glu | Leu | Asn | Lys | Leu | Val | Val | Val | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gly | Gly | Asp | Leu | Lys | Ile | Asp | Gln | Thr | Leu | Lys | Arg | Leu | Asn | Asn | Ala |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Leu | Asn | Phe | Leu | Pro | Gln | Lys | Ala | Tyr | Glu | Glu | Pro | Tyr | Phe | Glu |     |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Thr | Ser | Asp | Lys | Lys | Ser | Glu | Lys | Val | Leu | Tyr | Lys | Asp | Thr | Glu | Gln |  |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| Ala | Phe | Val | Tyr | Phe | Gly | Ala | Pro | Phe | Lys | Ile | Lys | Asp | Leu | Lys | Gln |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asp | Leu | Ala | Lys | Ser | Lys | Val | Met | Met | Phe | Val | Leu | Gly | Gly | Gly | Phe |  |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |  |
| Gly | Ser | Arg | Leu | Met | Glu | Lys | Ile | Arg | Val | Gln | Glu | Gly | Leu | Ala | Tyr |  |
|     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |  |
| Ser | Val | Tyr | Ile | Arg | Ser | Asn | Phe | Ser | Lys | Val | Ala | His | Phe | Ala | Ser |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Gly | Tyr | Leu | Gln | Thr | Lys | Leu | Ser | Thr | Gln | Thr | Lys | Ser | Val | Ala | Leu |  |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     | 335 |     |     |  |
| Val | Lys | Lys | Ile | Val | Lys | Glu | Phe | Ile | Glu | Lys | Gly | Met | Thr | Gln | Gln |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Glu | Leu | Asp | Asp | Ala | Lys | Lys | Phe | Leu | Leu | Gly | Ser | Glu | Pro | Leu | Arg |  |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |  |
| Asn | Glu | Thr | Ile | Ser | Ser | Arg | Leu | Asn | Thr | Thr | Tyr | Asn | Tyr | Phe | Tyr |  |
|     |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Leu | Gly | Leu | Pro | Leu | Asn | Phe | Asn | Gln | Thr | Leu | Asn | Gln | Ile | Gln |     |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |  |
| Lys | Met | Ser | Leu | Lys | Glu | Ile | Asn | Asp | Phe | Ile | Lys | Ala | His | Thr | Glu |  |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |     |  |
| Ile | Asn | Asp | Leu | Thr | Phe | Ala | Ile | Val | Ser | Asn | Lys | Lys | Lys | Asp | Lys |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...521  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

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THE UNIVERSITY OF CHICAGO

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...950  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

271

| Gly                               | Ser        | Val        | Phe        | Val        | Ser        | Val        | Val        | Asp        | Pro        | Gly        | Val        | Gly        | Thr        | Lys        | Arg        |      |
|-----------------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
|                                   |            | 85         |            |            |            |            | 90         |            |            |            |            | 95         |            |            |            |      |
| AAA<br>Lys                        | TCG<br>Ser | GTG<br>Val | GTA<br>Val | CTA<br>Leu | AAA<br>Lys | ACT<br>Thr | AAA<br>Lys | AAC<br>Asn | GGC<br>Gly | CAG<br>Gln | TAT<br>Tyr | TTC<br>Phe | GTC<br>Val | TCG<br>Ser | CCG<br>Pro | 392  |
| GAT<br>Asp                        | AAC<br>Asn | GGC<br>Gly | ACG<br>Thr | CTG<br>Leu | ACT<br>Thr | TTG<br>Leu | GTG<br>Val | GCA<br>Ala | CAA<br>Gln | ACT<br>Thr | TTG<br>Leu | GGG<br>Gly | ATT<br>Ile | GAT<br>Asp | AGC<br>Ser | 440  |
| GTG<br>Val                        | CGT<br>Arg | GAA<br>Glu | ATT<br>Ile | GAT<br>Asp | GAA<br>Glu | AAA<br>Lys | GCT<br>Ala | AAC<br>Asn | CGC<br>Arg | TTG<br>Leu | AAA<br>Lys | GGT<br>Gly | TCT<br>Ser | GAA<br>Glu | AAA<br>Lys | 488  |
| TCC<br>Ser                        | TAT<br>Tyr | ACT<br>Thr | TTC<br>Phe | CAT<br>His | GGT<br>Gly | CGT<br>Arg | GAT<br>Asp | GTG<br>Val | TAT<br>Tyr | GCT<br>Ala | TAC<br>Tyr | ACC<br>Thr | GGT<br>Gly | GCA<br>Ala | CGC<br>Arg | 536  |
| TTG<br>Leu                        | GCT<br>Ala | TCT<br>Ser | GGG<br>Gly | GCG<br>Ala | ATC<br>Ile | ACA<br>Thr | TTC<br>Phe | GAG<br>Glu | CAG<br>Gln | GTC<br>Val | GGG<br>Gly | CCA<br>Pro | GAG<br>Glu | CTT<br>Leu | CCC<br>Pro | 584  |
| CCA<br>Pro                        | AAA<br>Lys | GTC<br>Val | GTT<br>Val | GAA<br>Glu | ATT<br>Ile | CCT<br>Pro | TAC<br>Tyr | CAA<br>Gln | AAA<br>Lys | GCG<br>Ala | AAA<br>Lys | GCC<br>Ala | ACA<br>Thr | AAA<br>Lys | GGG<br>Gly | 632  |
| GAA<br>Glu                        | GTG<br>Val | AAA<br>Lys | GGT<br>Gly | AAT<br>Asn | ATC<br>Ile | CCG<br>Pro | ATT<br>Ile | TTG<br>Leu | GAT<br>Asp | ATT<br>Ile | CAA<br>Gln | TAT<br>Tyr | GGC<br>Gly | AAT<br>Asn | GTT<br>Val | 680  |
| TGG<br>Trp                        | AGC<br>Ser | AAC<br>Asn | ATC<br>Ile | AGC<br>Ser | GAT<br>Asp | AAA<br>Lys | TTA<br>Leu | CTC<br>Leu | AAT<br>Asn | CAA<br>Gln | GCA<br>Ala | AAA<br>Lys | ATC<br>Ile | AAA<br>Lys | CTC<br>Leu | 728  |
| AAT<br>Asn                        | GAC<br>Asp | ACG<br>Thr | CTG<br>Leu | TGT<br>Cys | GTA<br>Val | ACG<br>Thr | ATT<br>Ile | TTT<br>Phe | AAA<br>Lys | GGT<br>Gly | TCT<br>Ser | AAG<br>Lys | AAA<br>Lys | CAA<br>Gln | TAC<br>Tyr | 776  |
| GAA<br>Glu                        | GGG<br>Gly | AAA<br>Lys | ATG<br>Met | CCG<br>Pro | TAT<br>Tyr | GTC<br>Val | GCA<br>Ala | AGC<br>Ser | TTT<br>Phe | GGC<br>Gly | GAT<br>Asp | GTG<br>Val | CCA<br>Pro | GAA<br>Glu | GGC<br>Gly | 824  |
| CAG<br>Gln                        | CCG<br>Pro | TTA<br>Leu | GTT<br>Val | TAT<br>Tyr | TTA<br>Leu | AAC<br>Asn | AGC<br>Ser | TTG<br>Leu | TTA<br>Leu | AAT<br>Asn | GTT<br>Val | TCC<br>Ser | GTG<br>Val | GCG<br>Ala | CTG<br>Leu | 872  |
| AAT<br>Asn                        | AGG<br>Arg | GAT<br>Asp | AAT<br>Asn | TTC<br>Phe | GCG<br>Ala | CAA<br>Gln | AAA<br>Lys | TAT<br>Tyr | CAA<br>Gln | ATC<br>Ile | AAA<br>Lys | TCC<br>Ser | GGT<br>Gly | GCT<br>Ala | GAC<br>Asp | 920  |
| TGG<br>Trp                        | AAT<br>Asn | ATT<br>Ile | GAT<br>Asp | ATA<br>Ile | AAG<br>Lys | AAG<br>Lys | TGC<br>Cys | GCT<br>Ala | AAG<br>Lys | TAAAGCGCTG | TTTAGAAAAT | TAA        |            |            |            | 973  |
| GGGGCGGTGAA ACGCCCTAAC CGCTAAAGAT |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            | 1003 |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Thr | Ile | Ser | Ala | Leu | Phe | Leu | Ser | Ala | Cys | Ile | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Val | Tyr | Ala | Asp | Asn | Ala | Leu | Ile | Leu | Gln | Thr | Asp | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Asp | Gly | Ala | Val | Ser | Ala | Met | Lys | Gly | Val | Ala | Phe | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser | His | Leu | Lys | Ile | Phe | Asp | Leu | Thr | His | Glu | Ile | Pro | Pro | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Ile | Trp | Glu | Gly | Ala | Tyr | Arg | Leu | Tyr | Gln | Thr | Ala | Ser | Tyr | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Lys | Gly | Ser | Val | Phe | Val | Ser | Val | Val | Asp | Pro | Gly | Val | Gly | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Arg | Lys | Ser | Val | Val | Leu | Lys | Thr | Lys | Asn | Gly | Gln | Tyr | Phe | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Pro | Asp | Asn | Gly | Thr | Leu | Thr | Leu | Val | Ala | Gln | Thr | Leu | Gly | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ser | Val | Arg | Glu | Ile | Asp | Glu | Lys | Ala | Asn | Arg | Leu | Lys | Gly | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Lys | Ser | Tyr | Thr | Phe | His | Gly | Arg | Asp | Val | Tyr | Ala | Tyr | Thr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Arg | Leu | Ala | Ser | Gly | Ala | Ile | Thr | Phe | Glu | Gln | Val | Gly | Pro | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Pro | Pro | Lys | Val | Val | Glu | Ile | Pro | Tyr | Gln | Lys | Ala | Lys | Ala | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Gly | Glu | Val | Lys | Gly | Asn | Ile | Pro | Ile | Leu | Asp | Ile | Gln | Tyr | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Val | Trp | Ser | Asn | Ile | Ser | Asp | Lys | Leu | Leu | Asn | Gln | Ala | Lys | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Leu | Asn | Asp | Thr | Leu | Cys | Val | Thr | Ile | Phe | Lys | Gly | Ser | Lys | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Tyr | Glu | Gly | Lys | Met | Pro | Tyr | Val | Ala | Ser | Phe | Gly | Asp | Val | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Gly | Gln | Pro | Leu | Val | Tyr | Leu | Asn | Ser | Leu | Leu | Asn | Val | Ser | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Leu | Asn | Arg | Asp | Asn | Phe | Ala | Gln | Lys | Tyr | Gln | Ile | Lys | Ser | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Asp | Trp | Asn | Ile | Asp | Ile | Lys | Lys | Cys | Ala | Lys |     |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| ATA GAC TAT TCT AGC CTG GTT AAA AAC ATC CAA TCC ACT TTA AAA GGC   | 632  |
| Ile Asp Tyr Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu Lys Gly   |      |
| 180 185 190                                                       |      |
| ACT TCT TTT GAA ATG CTT ATA GGT AGC GTT TGG GAA AGA TTT GAA ACA   | 680  |
| Thr Ser Phe Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe Glu Thr   |      |
| 195 200 205 210                                                   |      |
| AAG GTT CTA GGG GAG TTT AGC GCT TAT AAT ATC GCT TCA GCC ATT TTA   | 728  |
| Lys Val Leu Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala Ile Leu   |      |
| 215 220 225                                                       |      |
| ATC GCT AAG CAT TTA GGC TTA GAG ACC GAA AGG ATC AAA CGG CTT GTT   | 776  |
| Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val   |      |
| 230 235 240                                                       |      |
| TTA GAA CTC AAC CCT ATT GCT CAT CGT TTG CAA CTT TTG GAA GTG AAT   | 824  |
| Leu Glu Leu Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu Val Asn   |      |
| 245 250 255                                                       |      |
| CAA AAA ATC ATC ATA GAC GAT AGC TTT AAT GGG AAT TTA AAG GGC ATG   | 872  |
| Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met   |      |
| 260 265 270                                                       |      |
| TTA GAG GGC ATT CGT TTA GCG AGT TTG CAC AAA GGG CGT AAA GTC ATT   | 920  |
| Leu Glu Gly Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys Val Ile   |      |
| 275 280 285 290                                                   |      |
| GTA ACA CCG GGC TTA GTG GAA AGC AAT ACA GAA AGT AAT GAG GCT TTA   | 968  |
| Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu   |      |
| 295 300 305                                                       |      |
| GCG CAA AAA ATA GAC GGG GTT TTT GAT GTC GCT ATC ATC ACA GGG GAG   | 1016 |
| Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu   |      |
| 310 315 320                                                       |      |
| TTG AAT TCC AAA ACG ATT GCT TCA CAA TTG AAA ACC CCC CAA AAA ATC   | 1064 |
| Leu Asn Ser Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln Lys Ile   |      |
| 325 330 335                                                       |      |
| TTA CTC AAG GAT AAG GCG CAA TTG GAA AAT ATC TTA CAA GCC ACC ACG   | 1112 |
| Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr   |      |
| 340 345 350                                                       |      |
| ATT CAA GGC GAT TTG ATT TTA TTC GCT AAT GAC GCC CCT AAT TAC ATT T | 1161 |
| Ile Gln Gly Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn Tyr Ile   |      |
| 355 360 365 370                                                   |      |
| AGGAAATGAA CATGCAACAT TTATACGCTC CTTGGCGCGA AAGTTATTTG AA         | 1213 |

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Gly | Phe | Xaa | Leu | Ala | Leu | Gly | Tyr | Leu | Cys | Leu | Phe | Ile | Phe | Val | 1   | 5   | 10  | 15 |
| Leu | Ser | Ala | Ser | Leu | Ile | Ser | Glu | Lys | Ala | Leu | Ser | Lys | Gln | Tyr | Leu | 20  | 25  | 30  |    |
| Gln | Thr | Ala | Lys | Asp | Lys | Ile | Thr | Ser | Leu | Lys | Asn | Leu | Lys | Val | Ile | 35  | 40  | 45  |    |
| Ala | Ile | Thr | Gly | Ser | Phe | Gly | Lys | Thr | Ser | Thr | Lys | Asn | Phe | Leu | Leu | 50  | 55  | 60  |    |
| Gln | Ile | Leu | Gln | Thr | Thr | Phe | Asn | Ala | His | Ala | Ser | Pro | Lys | Ser | Val | 65  | 70  | 75  |    |
| Asn | Thr | Leu | Leu | Gly | Leu | Ala | Asn | Asp | Ile | Asn | Gln | Asn | Leu | Asp | Asp | 85  | 90  | 95  |    |
| Arg | Ser | Glu | Ile | Tyr | Ile | Ala | Glu | Ala | Gly | Ala | Arg | Asn | Lys | Gly | Asp | 100 | 105 | 110 |    |
| Ile | Lys | Glu | Ile | Thr | Cys | Leu | Ile | Glu | Pro | His | Leu | Val | Val | Val | Ala | 115 | 120 | 125 |    |
| Glu | Val | Gly | Glu | Gln | His | Leu | Glu | Tyr | Phe | Lys | Thr | Leu | Glu | Asn | Ile | 130 | 135 | 140 |    |
| Cys | Glu | Thr | Lys | Ala | Glu | Leu | Leu | Asp | Ser | Lys | Arg | Leu | Glu | Lys | Ala | 145 | 150 | 155 |    |
| Phe | Cys | Tyr | Ser | Val | Glu | Lys | Ile | Lys | Pro | Tyr | Ala | Pro | Lys | Asp | Ser | 165 | 170 | 175 |    |
| Pro | Leu | Ile | Asp | Tyr | Ser | Ser | Leu | Val | Lys | Asn | Ile | Gln | Ser | Thr | Leu | 180 | 185 | 190 |    |
| Lys | Gly | Thr | Ser | Phe | Glu | Met | Leu | Ile | Gly | Ser | Val | Trp | Glu | Arg | Phe | 195 | 200 | 205 |    |
| Glu | Thr | Lys | Val | Leu | Gly | Glu | Phe | Ser | Ala | Tyr | Asn | Ile | Ala | Ser | Ala | 210 | 215 | 220 |    |
| Ile | Leu | Ile | Ala | Lys | His | Leu | Gly | Leu | Glu | Thr | Glu | Arg | Ile | Lys | Arg | 225 | 230 | 235 |    |
| Leu | Val | Leu | Glu | Leu | Asn | Pro | Ile | Ala | His | Arg | Leu | Gln | Leu | Leu | Glu | 245 | 250 | 255 |    |
| Val | Asn | Gln | Lys | Ile | Ile | Ile | Asp | Asp | Ser | Phe | Asn | Gly | Asn | Leu | Lys | 260 | 265 | 270 |    |
| Gly | Met | Leu | Glu | Gly | Ile | Arg | Leu | Ala | Ser | Leu | His | Lys | Gly | Arg | Lys | 275 | 280 | 285 |    |
| Val | Ile | Val | Thr | Pro | Gly | Leu | Val | Glu | Ser | Asn | Thr | Glu | Ser | Asn | Glu | 290 | 295 | 300 |    |
| Ala | Leu | Ala | Gln | Lys | Ile | Asp | Gly | Val | Phe | Asp | Val | Ala | Ile | Ile | Thr | 305 | 310 | 315 |    |
| Gly | Glu | Leu | Asn | Ser | Lys | Thr | Ile | Ala | Ser | Gln | Leu | Lys | Thr | Pro | Gln | 325 | 330 | 335 |    |
| Lys | Ile | Leu | Leu | Lys | Asp | Lys | Ala | Gln | Leu | Glu | Asn | Ile | Leu | Gln | Ala | 340 | 345 | 350 |    |
| Thr | Thr | Ile | Gln | Gly | Asp | Leu | Ile | Leu | Phe | Ala | Asn | Asp | Ala | Pro | Asn | 355 | 360 | 365 |    |
| Tyr | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 370 |     |     |    |

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1303 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...1250  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCTTGTGGTC TCATTTGTTT CTGTTTACT TGTAGCTTGG AGGACTAGGC ATG TAT   | 56  |
| Met Tyr                                                         |     |
| 1                                                               |     |
| AAA TTA GGG GTG TTT TTG TTA GCC ACC TTA CTA TCA GCT AAC ACG CAA | 104 |
| Lys Leu Gly Val Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn Thr Gln |     |
| 5 10 15                                                         |     |
| AAA GTG AGC GAT ATT GCT AAA GAT ATC CAA CAT AAA GAA ACC CTT TTG | 152 |
| Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr Leu Leu |     |
| 20 25 30                                                        |     |
| AAA AAA ACC CAT GAA GAA AAA AAC CAA CTA AAC AGC CGT TTG AGT TCT | 200 |
| Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu Ser Ser |     |
| 35 40 45 50                                                     |     |
| TTA GGC GAA GCG ATC CGC TCT AAA GAG CTT CAA AAG GCT GAG ATG GAG | 248 |
| Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu Met Glu |     |
| 55 60 65                                                        |     |
| CGC CAA ATG ATC GCT TTA AAA AAG AGT CTT GAA AAA AAT CGT AAC GAA | 296 |
| Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg Asn Glu |     |
| 70 75 80                                                        |     |
| AGT TTG GCG CAA GAA AAA GTC CTA ACC AAC TAC CGC AAG TCT TTA GAT | 344 |
| Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser Leu Asp |     |
| 85 90 95                                                        |     |
| CAT TTG CAA AAA AAG CGA TCA TTT TTA CAA AAG AGG GTG TTT GAT ACG | 392 |
| His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe Asp Thr |     |
| 100 105 110                                                     |     |
| CTT TTA CAG GAT TTC CTT TTT TCA CAA GCC CTA AAG GGG CAG AAT TTA | 440 |
| Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln Asn Leu |     |
| 115 120 125 130                                                 |     |
| GCC TCT TCT AAT GAT GTT GTT TTG CAA GTG GCG TTT GAA AAC TTG CAC | 488 |
| Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn Leu His |     |
| 135 140 145                                                     |     |
| CAA AGC ACT CTG TCT AAA ATG TCG CAA CTG AGC CAA GAA GAA AAG GAA | 536 |
| Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu Lys Glu |     |
| 150 155 160                                                     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| CTC AAT ACG CAA GCT TTA AAA GTC AAA AAC AGC ATT CAA AAA ATC TCA<br>Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys Ile Ser<br>165 170 175     | 584  |
| TCC ATC ATA GAT GAG CAA AAA ACT CGT GAA GTA ACC TTA AAA TCC TTG<br>Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys Ser Leu<br>180 185 190     | 632  |
| AAA ACC GAA CAA GAT AAG CTC ATT TTG AGC ATG CAA AAA GAT TAT GCG<br>Lys Thr Glu Gln Asp Lys Leu Ile Leu Ser Met Gln Lys Asp Tyr Ala<br>195 200 205 210 | 680  |
| ATC TAC AAC CAA CGC CTA ACC CTT TTA GAA AAA GAG CGC CAG AAT TTA<br>Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln Asn Leu<br>215 220 225     | 728  |
| AAC GCT CTT TTA AAA CGC TTG AAT ATC ATC AAA CAA AAC AGA GAA AAT<br>Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg Glu Asn<br>230 235 240     | 776  |
| GAA GAA AAA GTC AGT TTG AAA AAA TCT TCT CAA GCC TTA GAA GTC AAA<br>Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu Val Lys<br>245 250 255     | 824  |
| CAA GTG GCT AGC TCT TAT CAA AAT ATC AAC ACC ACG AGC TAT AAC GGA<br>Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr Asn Gly<br>260 265 270     | 872  |
| CCA AAA ACG ATC GCT CCC TTG AAC GAT TAT GAA GTG GTG CAA AAA TTT<br>Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln Lys Phe<br>275 280 285 290 | 920  |
| GGC CCC TAT ATT GAC CCG GTT TAT AAT TTA AAA ATT TTT AGC GAG TCT<br>Gly Pro Tyr Ile Asp Pro Val Tyr Asn Leu Lys Ile Phe Ser Glu Ser<br>295 300 305     | 968  |
| ATT ACG CTC GTG TCA AAA ACC CCA AAC GCT TTG GTG CGT AAT GTT TTA<br>Ile Thr Leu Val Ser Lys Thr Pro Asn Ala Leu Val Arg Asn Val Leu<br>310 315 320     | 1016 |
| GAC GGG AAA ATC GTG TTC GCT AAA GAA ATC AAC ATG CTT AAA AAA GTC<br>Asp Gly Lys Ile Val Phe Ala Lys Glu Ile Asn Met Leu Lys Lys Val<br>325 330 335     | 1064 |
| GTT ATC ATT GAG CAT AAA AAT GGG ATC CGC ACG ATT TAT TCT CAA TTG<br>Val Ile Ile Glu His Lys Asn Gly Ile Arg Thr Ile Tyr Ser Gln Leu<br>340 345 350     | 1112 |
| GAT AAA ATC GCT CCC ACC ATT AAA AGC GGC ATG CGG ATC CAA AAA GGC<br>Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln Lys Gly<br>355 360 365 370 | 1160 |
| TAT GTT TTA GGG CGC ATT GAT CAA CGC TTG GGC TTT GAA GTT ACC ATG<br>Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val Thr Met<br>375 380 385     | 1208 |
| AGA GAA AAA CAC ATC AAC CCC TTA GAA CTC ATC GCA CGC AAT TAAACAAAT<br>Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn                          | 1259 |

390

395

400

CGTTTATTATT GCCGATATTG GCTAAAGAAT TTATGCAAAC AAAT

1303

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Lys | Leu | Gly | Val | Phe | Leu | Leu | Ala | Thr | Leu | Leu | Ser | Ala | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gln | Lys | Val | Ser | Asp | Ile | Ala | Lys | Asp | Ile | Gln | His | Lys | Glu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Lys | Lys | Thr | His | Glu | Glu | Lys | Asn | Gln | Leu | Asn | Ser | Arg | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Leu | Gly | Glu | Ala | Ile | Arg | Ser | Lys | Glu | Leu | Gln | Lys | Ala | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Glu | Arg | Gln | Met | Ile | Ala | Leu | Lys | Lys | Ser | Leu | Glu | Lys | Asn | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Glu | Ser | Leu | Ala | Gln | Glu | Lys | Val | Leu | Thr | Asn | Tyr | Arg | Lys | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asp | His | Leu | Gln | Lys | Lys | Arg | Ser | Phe | Leu | Gln | Lys | Arg | Val | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Thr | Leu | Leu | Gln | Asp | Phe | Leu | Phe | Ser | Gln | Ala | Leu | Lys | Gly | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Leu | Ala | Ser | Ser | Asn | Asp | Val | Val | Leu | Gln | Val | Ala | Phe | Glu | Asn |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | His | Gln | Ser | Thr | Leu | Ser | Lys | Met | Ser | Gln | Leu | Ser | Gln | Glu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Glu | Leu | Asn | Thr | Gln | Ala | Leu | Lys | Val | Lys | Asn | Ser | Ile | Gln | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ser | Ser | Ile | Ile | Asp | Glu | Gln | Lys | Thr | Arg | Glu | Val | Thr | Leu | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Leu | Lys | Thr | Glu | Gln | Asp | Lys | Leu | Ile | Leu | Ser | Met | Gln | Lys | Asp |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Ala | Ile | Tyr | Asn | Gln | Arg | Leu | Thr | Leu | Leu | Glu | Lys | Glu | Arg | Gln |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Leu | Asn | Ala | Leu | Leu | Lys | Arg | Leu | Asn | Ile | Ile | Lys | Gln | Asn | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Asn | Glu | Glu | Lys | Val | Ser | Leu | Lys | Lys | Ser | Ser | Gln | Ala | Leu | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Lys | Gln | Val | Ala | Ser | Ser | Tyr | Gln | Asn | Ile | Asn | Thr | Thr | Ser | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Gly | Pro | Lys | Thr | Ile | Ala | Pro | Leu | Asn | Asp | Tyr | Glu | Val | Val | Gln |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Phe | Gly | Pro | Tyr | Ile | Asp | Pro | Val | Tyr | Asn | Leu | Lys | Ile | Phe | Ser |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Ser | Ile | Thr | Leu | Val | Ser | Lys | Thr | Pro | Asn | Ala | Leu | Val | Arg | Asn |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Val | Leu | Asp | Gly | Lys | Ile | Val | Phe | Ala | Lys | Glu | Ile | Asn | Met | Leu | Lys |









|                                                                   |      |
|-------------------------------------------------------------------|------|
| AAG CAT GAT TTA AGC ATG CAA AAA GCG AAT GAA AAA GCC TTA AGG AGC   | 920  |
| Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu Arg Ser   |      |
| 275 280 285 290                                                   |      |
| TAT ATC GCT CTA AAA AAA GCG AAC GCG CAA AAC TAC ACC ACA CAA GAT   | 968  |
| Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr Gln Asp   |      |
| 295 300 305                                                       |      |
| TTT GAA GAG AAC AAC TCC CCC TAT ACT GCT GAA ATC ACG CAA AAA CTC   | 1016 |
| Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys Leu   |      |
| 310 315 320                                                       |      |
| ACC GCT CTC AAA CCC CTT GAA ATC CTA AAG CCA GAG CCT TTT AAA GAT   | 1064 |
| Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe Lys Asp   |      |
| 325 330 335                                                       |      |
| GGT TTT ATT GTG GTG CAA CTC ATC TCT CAA ATT AAA GAC GAA TTG CAA   | 1112 |
| Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu Leu Gln   |      |
| 340 345 350                                                       |      |
| AAT TTT AAT GAA GCT AAA AGC GCT CTT AAA ACC CGC CTA ACT CAA GAA   | 1160 |
| Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln Glu   |      |
| 355 360 365 370                                                   |      |
| AAA ACC CTT ATG GCG TTG CAA ACT TTA GCC AAA GAA AAG CTT AAG GAT   | 1208 |
| Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys Asp   |      |
| 375 380 385                                                       |      |
| TTT AAG GGC AAA AGC GTG GGC TAT GTA AGC CCT AAT TTT GGA GGC ACT   | 1256 |
| Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly Thr   |      |
| 390 395 400                                                       |      |
| ATT AGT GAG CTT AAC CAA GAA GAA AGT GCT AAG TTT ATC AAC GCT CTT   | 1304 |
| Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Ala Leu   |      |
| 405 410 415                                                       |      |
| TTT AAC CGC CAG GAA AAA AAG GGG TTT ATC GCT ATT AAT AAT AAA GTG   | 1352 |
| Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn Lys Val   |      |
| 420 425 430                                                       |      |
| GTG CTC TAT CAA ATC ACA GAA CAA AAT TTC AAC CAC TCA TTT AGT GCA   | 1400 |
| Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe Ser Ala   |      |
| 435 440 445 450                                                   |      |
| GAA GAA AGC CAG TAT ATG CAG CGT TTA GTC AAT AAC ACT AAA ACG GAT   | 1448 |
| Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr Asp   |      |
| 455 460 465                                                       |      |
| TTT TTT GAT AAA GCG TTG ATA GAA GAA TTG AAA AAA CGC TAT AAG ATA   | 1496 |
| Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys Ile   |      |
| 470 475 480                                                       |      |
| GTC AAA TAC ATT CAA TAAATGCAAG GGGAAATCAT GGAACATAAA GAAATCGTTA T | 1552 |
| Val Lys Tyr Ile Gln                                               |      |
| 485                                                               |      |
| AGGGGTTGAT CT                                                     | 1564 |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Glu | Trp | Met | Gln | Asn | His | Arg | Lys | Tyr | Leu | Val | Val | Thr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Ile | Ser | Thr | Ile | Ala | Phe | Ile | Ala | Ala | Gly | Met | Ile | Gly | Trp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Tyr | Ser | Phe | Ser | Leu | Asp | Ser | Asp | Ser | Ala | Ala | Lys | Val | Gly | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Lys | Ile | Ser | Gln | Glu | Glu | Leu | Ala | Gln | Glu | Tyr | Arg | Arg | Leu | Lys |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Ala | Tyr | Ala | Glu | Ser | Ile | Pro | Asp | Phe | Lys | Glu | Leu | Thr | Lys | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Ile | Lys | Ala | Met | His | Leu | Glu | Lys | Ser | Ala | Leu | Asp | Ser | Leu | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Gln | Ala | Leu | Leu | Arg | Asn | Leu | Ala | Leu | Asp | Leu | Gly | Leu | Gly | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Lys | Gln | Glu | Val | Ala | Lys | Glu | Ile | Arg | Lys | Thr | Ser | Val | Phe | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Asp | Gly | Val | Phe | Asp | Glu | Glu | Leu | Tyr | Lys | Asn | Ile | Leu | Lys | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | His | Tyr | Arg | Pro | Lys | His | Phe | Glu | Glu | Ser | Val | Glu | Arg | Leu | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Leu | Gln | Lys | Ile | Ser | Thr | Leu | Phe | Pro | Lys | Thr | Thr | Thr | Pro | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Gln | Ser | Ser | Leu | Ser | Leu | Trp | Ala | Lys | Leu | Gln | Asp | Lys | Leu | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Ile | Leu | Asn | Pro | Ser | Asp | Val | Lys | Ile | Ser | Leu | Asn | Glu | Glu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Met | Lys | Lys | Tyr | Tyr | Glu | Ser | His | Lys | Lys | Asp | Phe | Lys | Lys | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Ser | Phe | Lys | Thr | Arg | Ser | Leu | Tyr | Phe | Asp | Ala | Ser | Leu | Glu | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Asp | Leu | Lys | Glu | Leu | Glu | Glu | Tyr | Tyr | His | Lys | Asn | Lys | Val | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Tyr | Leu | Asp | Lys | Glu | Gly | Lys | Leu | Gln | Asp | Phe | Lys | Ser | Val | Gln | Glu |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Gln | Val | Lys | His | Asp | Leu | Ser | Met | Gln | Lys | Ala | Asn | Glu | Lys | Ala | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ser | Tyr | Ile | Ala | Leu | Lys | Lys | Ala | Asn | Ala | Gln | Asn | Tyr | Thr | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | Asp | Phe | Glu | Glu | Asn | Ser | Pro | Tyr | Thr | Ala | Glu | Ile | Thr | Gln |     |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Lys | Leu | Thr | Ala | Leu | Lys | Pro | Leu | Glu | Ile | Leu | Lys | Pro | Glu | Pro | Phe |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Lys | Asp | Gly | Phe | Ile | Val | Val | Gln | Leu | Ile | Ser | Gln | Ile | Lys | Asp | Glu |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Leu | Gln | Asn | Phe | Asn | Glu | Ala | Lys | Ser | Ala | Leu | Lys | Thr | Arg | Leu | Thr |









(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...197  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATATAATCTT TTCTTAATTT TGAAGTTTAG CAAATTTTAA GGAAGTAACC ATG ATG    | 56  |
| Met Met                                                           |     |
| 1                                                                 |     |
| AAA AAA ACC CTT TTT ATC TCT TTG GCT TTA GCG TTA AGC TTG AAT GCG   | 104 |
| Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu Asn Ala   |     |
| 5 10 15                                                           |     |
| GGC AAT ATC CAA ATC CAG AGC ATG CCC AAA GTT AAA GAG CGA GTG AGT   | 152 |
| Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg Val Ser   |     |
| 20 25 30                                                          |     |
| GTC CCC TCT AAA GAC GAT ACG GAT CTA TTC TTA CCA CGA TTC TAT TAAGG | 202 |
| Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe Tyr       |     |
| 35 40 45                                                          |     |
| ACTCTATTAA GGCGGTGGTG AATATCTCCA CTGAAAAGAA GATTAAAA              | 250 |

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Met Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu |  |
| 1 5 10 15                                                       |  |
| Asn Ala Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg |  |
| 20 25 30                                                        |  |
| Val Ser Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe |  |
| 35 40 45                                                        |  |
| Tyr                                                             |  |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 328 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear





Glu Arg Ser Ser Leu Leu Lys Thr Arg Leu Trp  
65 70 75

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...596
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CGAATTGCTG TATAGTTAGC GTTTTTAATT CAAAATGAAG TGAGGAAACA ATG AAA  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| AAA GCG TTA ATA TCC ACC CTT TTT GGT GTT AGT TTG GCG TTT GCA AAA | 104 |
| Lys Ala Leu Ile Ser Thr Leu Phe Gly Val Ser Leu Ala Phe Ala Lys |     |
| 5 10 15                                                         |     |
| CCT TAT ACG ATT GAT AAG GCA AAC TCT AGC GTG TGG TTT GAG GTC AAA | 152 |
| Pro Tyr Thr Ile Asp Lys Ala Asn Ser Ser Val Trp Phe Glu Val Lys |     |
| 20 25 30                                                        |     |
| CAC TTC ACG TTC AAT GAA ACA AGA GGC GCG TTT GAT AAT TTT GAT GGC | 200 |
| His Phe Thr Phe Asn Glu Thr Arg Gly Ala Phe Asp Asn Phe Asp Gly |     |
| 35 40 45 50                                                     |     |
| AAA ATT GAT CTA GAG CCC AAC ACT AAA ATG CTC AGC GTT TTT GAA GGC | 248 |
| Lys Ile Asp Leu Glu Pro Asn Thr Lys Met Leu Ser Val Phe Glu Gly |     |
| 55 60 65                                                        |     |
| AAT ATT GAT GTG AAA AGC GTC AAT ACT AGG GAT AGA AAA AGA GAT AAC | 296 |
| Asn Ile Asp Val Lys Ser Val Asn Thr Arg Asp Arg Lys Arg Asp Asn |     |
| 70 75 80                                                        |     |
| CAC TTG AAA ACA GCG GAC TTT TTT GAT GTG GTA AAA TAC CCC AAA GGG | 344 |
| His Leu Lys Thr Ala Asp Phe Phe Asp Val Val Lys Tyr Pro Lys Gly |     |
| 85 90 95                                                        |     |
| AGC TTT AAA ATG ACC AAA TAC GAA GAT GGT AAA ATC TAT GGG GAT TTG | 392 |
| Ser Phe Lys Met Thr Lys Tyr Glu Asp Gly Lys Ile Tyr Gly Asp Leu |     |
| 100 105 110                                                     |     |
| ACT CTT CGT GGC GTA ACC AAG CCT GTC GTA TTG GAA GCC AAA ATC CAA | 440 |
| Thr Leu Arg Gly Val Thr Lys Pro Val Val Leu Glu Ala Lys Ile Gln |     |
| 115 120 125 130                                                 |     |



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...425
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TCCGTTTCGCA ACAAGAATTT TCTTGTTATC TTAATGTAAA GGTCAAAACG ATG AAA   | 56  |
| Met Lys                                                           |     |
| 1                                                                 |     |
| AAG TTA GCC GCT TTA TTT TTA GTA AGC GTG TTG GGG GTT ATG GGT TTA   | 104 |
| Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly Leu   |     |
| 5 10 15                                                           |     |
| AAC GCA TGG GAG CAA ACC CTA AAA GCT AAT GAC TTG GAA GTG AAA ATC   | 152 |
| Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys Ile   |     |
| 20 25 30                                                          |     |
| AAA TCC GTG GGT AAC CCC ATT AAA GGC GAT AAC ACT TTC ATT CTC AGC   | 200 |
| Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu Ser   |     |
| 35 40 45 50                                                       |     |
| CCC ACT TTA AAA GGT AAG GCT TTA GAA AAA GCT ATC GTT AGG GTG CAG   | 248 |
| Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val Gln   |     |
| 55 60 65                                                          |     |
| TTT ATG ATG CCT GAA ATG CCC GGC ATG CCA GCG ATG AAA GAA ATG GCG   | 296 |
| Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met Ala   |     |
| 70 75 80                                                          |     |
| CAA GTG AGT GAA AAA AAC GGC CTT TAT GAA GCT AAA ACC AAT CTT TCT   | 344 |
| Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu Ser   |     |
| 85 90 95                                                          |     |
| ATG AAC GGG ACA TGG CAG GTT AGG GTG GAT ATT AAA TCT AAA GAG GGT   | 392 |
| Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu Gly   |     |
| 100 105 110                                                       |     |
| CAG GTT TAT CGC GCT AAA ACA AGC CTG GAT TTA TAAGAGCATG CTATCTTTTA | 445 |
| Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu                       |     |
| 115 120 125                                                       |     |
| TAAGCGCGTT TGATAAAAGG GCGGTTTCAA TAC                              | 478 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:



|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| CAA ACC CGT TTT AAT ATT TCC ACC ACT AAG GTC ATA GAA AAA GAA TTT<br>Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys Glu Phe<br>35 40 45 50     | 200 |
| TCT CAA AGC CGG CGC TAT TAC GCG CTT TTA GAG CCC AAT GAA GCG CTG<br>Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu Ala Leu<br>55 60 65        | 248 |
| ATT TTT TCT CAA ACC CTG CGT TTT GAT GGC TAT GTG GAA AAG CTT TAT<br>Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys Leu Tyr<br>70 75 80        | 296 |
| GCG AAT AAA ACC TAT ACC CCC ATT AAA AAG GGC GAC AGG TTA TTG AGC<br>Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu Leu Ser<br>85 90 95        | 344 |
| GTG TAT TCC CCT GAA TTA GTG AGC GCT CAA AGC GAA TTG CTA TCA TCA<br>Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu Ser Ser<br>100 105 110     | 392 |
| TTG AAA TTC AAC CAA CAA GTG GGA GCG ATT AAA GAA AAA TTA AAA CTA<br>Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu Lys Leu<br>115 120 125 130 | 440 |
| TTA GGG TTA GAA AAC TCT AGC ATT GAA AAA ATC ATT AGC AGC CAT AAA<br>Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser His Lys<br>135 140 145     | 488 |
| GTC CAA AAT GAA ATG ACT ATT TAC TCT CAC TTC AAC GGC ATT ATT TTT<br>Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile Ile Phe<br>150 155 160     | 536 |
| AAA AAA AGC CCG GAT CTC AAT GAG GGG AGC TTC ATT AAA AAA GGG CAA<br>Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys Gly Gln<br>165 170 175     | 584 |
| GAG TTG TTT CAA ATC ATA GAT TTA AGC CAA TTG TGG GCG CTG GTT AAA<br>Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu Val Lys<br>180 185 190     | 632 |
| GTC AAT CAA GAG GAT TTA GAA TTT TTA AAA AAC ACG CAT AAA GCG ATC<br>Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys Ala Ile<br>195 200 205 210 | 680 |
| TTG TTT GTA GAA GGG ATT AAA GGC GAG CAA GAA ATC ACG CTT GAA AAT<br>Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu Glu Asn<br>215 220 225     | 728 |
| ATC AAC CCC ATC ATC AAC AAA GAA GAT AAA ATG CTA GAA GCG GCG TTC<br>Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala Arg Phe<br>230 235 240     | 776 |
| AAT GTG CCT AAT GTT AAA CAG ATT TAT TAC CCT AAC ATG TTC GCT CAA<br>Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe Ala Gln<br>245 250 255     | 824 |
| GTA GAA ATC TTT CAA AAA CCA CAA AAA ATG AAG ATT TTG CCT AAA GAA<br>Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro Lys Glu                    | 872 |

| 260                                                               | 265 | 270 |      |
|-------------------------------------------------------------------|-----|-----|------|
| GCG GTT TTG ATT AAA GGG GGG AAA GCT ATC GTG TTT AAA AAA GAC GAT   |     |     | 920  |
| Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys Asp Asp   |     |     |      |
| 275                                                               | 280 | 285 | 290  |
| TTT GGC TTA AGC CCG TTA GAA ATT AAA GCC GTC CGC TTG AGC GAT GGG   |     |     | 968  |
| Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser Asp Gly   |     |     |      |
|                                                                   | 295 | 300 | 305  |
| AGT TAT GAG ATT TTA GAG GGT TTA AAG GCG GGC GAA GAA GTC GCT AAT   |     |     | 1016 |
| Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val Ala Asn   |     |     |      |
|                                                                   | 310 | 315 | 320  |
| AAC GCT TTA TTC GTG CTA GAC GCT GAC GCT CAA AAC AAT GGG GAT TAT T |     |     | 1065 |
| Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly Asp Tyr   |     |     |      |
|                                                                   | 325 | 330 | 335  |
| GAATGATAGA AAAGATCATT GATTTAAGCG TTAAAAACAA ACTCCTTACC AC         |     |     | 1117 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ile | Leu | Trp | Leu | Ala | Leu | Ile | Leu | Phe | Phe | Ser | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ala | Asn | Ala | Gln | Lys | Thr | Gln | Glu | Ile | Lys | Lys | Thr | Lys | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ser | Gln | Thr | Arg | Phe | Asn | Ile | Ser | Thr | Thr | Lys | Val | Ile | Glu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Phe | Ser | Gln | Ser | Arg | Arg | Tyr | Tyr | Ala | Leu | Leu | Glu | Pro | Asn | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Leu | Ile | Phe | Ser | Gln | Thr | Leu | Arg | Phe | Asp | Gly | Tyr | Val | Glu | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Tyr | Ala | Asn | Lys | Thr | Tyr | Thr | Pro | Ile | Lys | Lys | Gly | Asp | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Ser | Val | Tyr | Ser | Pro | Glu | Leu | Val | Ser | Ala | Gln | Ser | Glu | Leu | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Ser | Leu | Lys | Phe | Asn | Gln | Gln | Val | Gly | Ala | Ile | Lys | Glu | Lys | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Leu | Leu | Gly | Leu | Glu | Asn | Ser | Ser | Ile | Glu | Lys | Ile | Ile | Ser | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Lys | Val | Gln | Asn | Glu | Met | Thr | Ile | Tyr | Ser | His | Phe | Asn | Gly | Ile |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Phe | Lys | Lys | Ser | Pro | Asp | Leu | Asn | Glu | Gly | Ser | Phe | Ile | Lys | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Gln | Glu | Leu | Phe | Gln | Ile | Ile | Asp | Leu | Ser | Gln | Leu | Trp | Ala | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Val | Lys | Val | Asn | Gln | Glu | Asp | Leu | Glu | Phe | Leu | Lys | Asn | Thr | His | Lys |

195 200 205  
 Ala Ile Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu  
 210 215 220  
 Glu Asn Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala  
 225 230 235 240  
 Arg Phe Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe  
 245 250 255  
 Ala Gln Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro  
 260 265 270  
 Lys Glu Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys  
 275 280 285  
 Asp Asp Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser  
 290 295 300  
 Asp Gly Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val  
 305 310 315 320  
 Ala Asn Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly  
 325 330 335  
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1196
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAACTTAGA TAAAATAACA CGATAAAACC ATAGTAATAA AGATAACCCC ATG AGA  | 56  |
| Met Arg                                                         |     |
| 1                                                               |     |
| TTT TTT TGC TTT TTC TTA TTT TTT CTA ACC TTT TCA AAC GCA CAG ATA | 104 |
| Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala Gln Ile |     |
| 5 10 15                                                         |     |
| ATG ATG ACT TTT GAT TCT CAA ACT AAC GCC AAA CTC TCG CGC TCT AAC | 152 |
| Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg Ser Asn |     |
| 20 25 30                                                        |     |
| GAA CAG CTT TCA GAC ATG CTC TAT AAA CTC AAT GAA AGT TTA AGA ATC | 200 |
| Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu Arg Ile |     |
| 35 40 45 50                                                     |     |
| TAT CAA AGC GTG CTT TCC AAT AAC CAA GAT CAA CTC AAA GAA ATC AAA | 248 |
| Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu Ile Lys |     |
| 55 60 65                                                        |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAA GCT AAC AGC ACC CTA AAT AGC CAA AGG CGT TTT TTT AAC GCC AGC | 296 |
| Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn Ala Ser |     |
| 70 75 80                                                        |     |
| CAG ATC CGC CTT ATG GAC ACT GAT GCA CTA TTG AAA CAA AGC GCT TTG | 344 |
| Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser Ala Leu |     |
| 85 90 95                                                        |     |
| GAA TTA GAA AAA TTA CAA GCT TTA GAA AAA CAC ATA AAA AAG GGC ATG | 392 |
| Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys Gly Met |     |
| 100 105 110                                                     |     |
| GAA CAA GAA CGC TTA ATA GAA GAA TCC CAA ACG CTT TTT TTA CAA GAG | 440 |
| Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu Gln Glu |     |
| 115 120 125 130                                                 |     |
| CAT TGC CCT TAT TTG AGC GGC GTT AAG AAT TTA GAA GAG GCT TCA AAC | 488 |
| His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala Ser Asn |     |
| 135 140 145                                                     |     |
| GCT TTA GAA GTC CAA GAG CAA AAC AAC GCC CTT TTC TTA CTC AAA GAG | 536 |
| Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu Lys Glu |     |
| 150 155 160                                                     |     |
| CCT AAA CTC GCC CGT TTG CTC TCA CGA TTG GAT TTG ATG AGC GCT TTA | 584 |
| Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser Ala Leu |     |
| 165 170 175                                                     |     |
| AAC GCC TTG TGC GAT CAG GTT TTA GAA AAC CAA GCC CAT AAC CAA CAA | 632 |
| Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn Gln Gln |     |
| 180 185 190                                                     |     |
| TCC CAT AAC AAA ATT TTA GAA TAC AAC GCT CTT AAA AAC CAT GAT TTT | 680 |
| Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His Asp Phe |     |
| 195 200 205 210                                                 |     |
| CAA GCC TAT AAA GCC ATG CGT TTG AAA AAA TTT AAA AAC AAG CTT CAA | 728 |
| Gln Ala Tyr Lys Ala Met Arg Leu Lys Lys Phe Lys Asn Lys Leu Gln |     |
| 215 220 225                                                     |     |
| AGT CAA ATC CAA GCC CAA GAA GAC GCT CTA AAA ACC TTT TTA CCC TTA | 776 |
| Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu Pro Leu |     |
| 230 235 240                                                     |     |
| GAA AAA CGC TTG GAA ACT TTA AAA ACG CAT TTT TTA TGC GAT AAA GAA | 824 |
| Glu Lys Arg Leu Glu Thr Leu Lys Thr His Phe Leu Cys Asp Lys Glu |     |
| 245 250 255                                                     |     |
| AAC CTA AAA TCA TGC GCT AAA GAA TTG CAC CAA CGC TAC CAA AAC GCC | 872 |
| Asn Leu Lys Ser Cys Ala Lys Glu Leu His Gln Arg Tyr Gln Asn Ala |     |
| 260 265 270                                                     |     |
| CTT ATA GAG CGA GAT AAA GAA TTA AAA AAC GCT AAA AAT AAT AAA GAA | 920 |
| Leu Ile Glu Arg Asp Lys Glu Leu Lys Asn Ala Lys Asn Asn Lys Glu |     |
| 275 280 285 290                                                 |     |
| AAG CAT GCT CTA ATC TTA GCC AAT TAC GAG CAT ACT TTA AAA ACC TTG | 968 |
| Lys His Ala Leu Ile Leu Ala Asn Tyr Glu His Thr Leu Lys Thr Leu |     |



| 295        |     |     |     |     |     |     |     |     |     |     |     |            |     |     |     | 300        |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 305        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|-----|-----|-----|------------|------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|------------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|---------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|------|
| AAT        | ATA | GAA | TTT | TTA | AGC | GAA | TTA | AAT | AAG | CAA | ATG | GCG        | TTT | TTG | AAT | 1016       |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| Asn        | Ile | Glu | Phe | Leu | Ser | Glu | Leu | Asn | Lys | Gln | Met | Ala        | Phe | Leu | Asn |            |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| 310        |     |     |     |     |     |     |     |     |     |     |     |            |     |     |     | 315        |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 320        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| GAA        | ACC | ATG | GCG | TTA | AAC | GCC | CGA | GTT | TTA | GCC | CTT | TTA        | GCC | AAA | CAG | 1064       |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| Glu        | Thr | Met | Ala | Leu | Asn | Ala | Arg | Val | Leu | Ala | Leu | Leu        | Ala | Lys | Gln |            |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| 325        |     |     |     |     |     |     |     |     |     |     |     |            |     |     |     | 330        |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 335        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| CAT        | GCC | AAA | ACG | CCA | AAG | CCT | TTC | AAT | TTG | AGC | GGT | GGT        | TTA | AGC | GGT | 1112       |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| His        | Ala | Lys | Thr | Pro | Lys | Pro | Phe | Asn | Leu | Ser | Gly | Gly        | Leu | Ser | Gly |            |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| 340        |     |     |     |     |     |     |     |     |     |     |     |            |     |     |     | 345        |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 350        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| GAT        | TTG | AGC | GGT | GGG | AAA | GCT | CTT | ATT | AAA | AAT | ATC | CGC        | TTA | GAT | CCG | 1160       |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| Asp        | Leu | Ser | Gly | Gly | Lys | Ala | Leu | Ile | Lys | Asn | Ile | Arg        | Leu | Asp | Pro |            |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| 355        |     |     |     |     |     |     |     |     |     |     |     |            |     |     |     | 360        |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 365        |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 370     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| CAT        | GGA | TTC | CCT | AGC | TTT | AAA | AAT | TTT | AAG | CAA | GAG | TAGGACAATA |     |     |     | TTTGAC     | 1212 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| His        | Gly | Phe | Pro | Ser | Phe | Lys | Asn | Phe | Lys | Gln | Glu |            |     |     |     |            |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| 375        |     |     |     |     |     |     |     |     |     |     |     |            |     |     |     | 380        |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |            |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |         |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |      |
| AAGCAAAAAC |     |     |     |     |     |     |     |     |     |     |     |            |     |     |     | AATTATAGTA |      |  |  |  |  |  |  |  |  |  |  |  |  |  |  | AAATAAGAGC |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | ATAACTT |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1249 |

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Phe | Phe | Cys | Phe | Phe | Leu | Phe | Phe | Leu | Thr | Phe | Ser | Asn | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Ile | Met | Met | Thr | Phe | Asp | Ser | Gln | Thr | Asn | Ala | Lys | Leu | Ser | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asn | Glu | Gln | Leu | Ser | Asp | Met | Leu | Tyr | Lys | Leu | Asn | Glu | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ile | Tyr | Gln | Ser | Val | Leu | Ser | Asn | Asn | Gln | Asp | Gln | Leu | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Lys | Lys | Ala | Asn | Ser | Thr | Leu | Asn | Ser | Gln | Arg | Arg | Phe | Phe | Asn |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ser | Gln | Ile | Arg | Leu | Met | Asp | Thr | Asp | Ala | Leu | Leu | Lys | Gln | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Leu | Glu | Leu | Glu | Lys | Leu | Gln | Ala | Leu | Glu | Lys | His | Ile | Lys | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gly | Met | Glu | Gln | Glu | Arg | Leu | Ile | Glu | Glu | Ser | Gln | Thr | Leu | Phe | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gln | Glu | His | Cys | Pro | Tyr | Leu | Ser | Gly | Val | Lys | Asn | Leu | Glu | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Asn | Ala | Leu | Glu | Val | Gln | Glu | Gln | Asn | Asn | Ala | Leu | Phe | Leu | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Glu | Pro | Lys | Leu | Ala | Arg | Leu | Leu | Ser | Arg | Leu | Asp | Leu | Met | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Asn | Ala | 165 | Leu | Cys | Asp | Gln | Val | 170 | Leu | Glu | Asn | Gln | Ala | 175 | His | Asn |
| Gln | Gln | Ser | His | 180 | Asn | Lys | Ile | Leu | Glu | 185 | Tyr | Asn | Ala | Leu | Lys | Asn | His |     |
| Asp | Phe | Gln | Ala | 195 | Tyr | Lys | Ala | Met | Arg | 200 | Leu | Lys | Lys | Phe | Lys | Asn | Lys |     |
| Leu | Gln | Ser | Gln | 210 | Ile | Gln | Ala | Gln | Glu | 215 | Asp | Ala | Leu | Lys | Thr | Phe | Leu |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |     |     | 240 |
| Pro | Leu | Glu | Lys | 245 | Arg | Leu | Glu | Thr | Leu | 250 | Lys | Thr | His | Phe | Leu | Cys | Asp |     |
| Lys | Glu | Asn | Leu | 260 | Lys | Ser | Cys | Ala | Lys | 265 | Glu | Leu | His | Gln | Arg | Tyr | Gln |     |
| Asn | Ala | Leu | Ile | 275 | Glu | Arg | Asp | Lys | Glu | 280 | Leu | Lys | Asn | Ala | Lys | Asn | Asn |     |
| Lys | Glu | Lys | His | 290 | Ala | Leu | Ile | Leu | Ala | 295 | Asn | Tyr | Glu | His | Thr | Leu | Lys |     |
| Thr | Leu | Asn | Ile | 305 | Glu | Phe | Leu | Ser | Glu | 310 | Leu | Asn | Lys | Gln | Met | Ala | Phe |     |
| Leu | Asn | Glu | Thr | 325 | Met | Ala | Leu | Asn | Ala | 330 | Arg | Val | Leu | Ala | Leu | Leu | Ala |     |
| Lys | Gln | His | Ala | 340 | Lys | Thr | Pro | Lys | Pro | 345 | Phe | Asn | Leu | Ser | Gly | Gly | Leu |     |
| Ser | Gly | Asp | Leu | 355 | Ser | Gly | Gly | Lys | Ala | 360 | Leu | Ile | Lys | Asn | Ile | Arg | Leu |     |
| Asp | Pro | His | Gly | 370 | Phe | Pro | Ser | Phe | Lys | 375 | Asn | Phe | Lys | Gln | Glu |     |     |     |

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...437
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

|                                                                 |            |            |            |            |         |     |
|-----------------------------------------------------------------|------------|------------|------------|------------|---------|-----|
| TTGTTGAGAA                                                      | AATCCGATGT | TTTGAGCGAA | AAATTCAGGA | TCATGAAAAA | ATG AAA | 56  |
|                                                                 |            |            |            |            | Met Lys |     |
|                                                                 |            |            |            |            | 1       |     |
| AGC ATC AGA AGA GGC GAT GGG CTG AAT GTT GTC CCT TTC ATT GAT ATT |            |            |            |            |         | 104 |
| Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile Asp Ile |            |            |            |            |         |     |
| 5                                                               |            |            | 10         |            | 15      |     |
| ATG CTC GTT TTG CTA GCG ATT GTG TTG AGC ATT TCT ACT TTT ATT GCA |            |            |            |            |         | 152 |
| Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe Ile Ala |            |            |            |            |         |     |
| 20                                                              |            |            | 25         |            | 30      |     |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CAA GGT AAG ATT AAG GTC AGT CTC CCT AAC GCT AAA AAT GCG GAA AAA   | 200 |
| Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys   |     |
| 35 40 45 50                                                       |     |
| TCC CAG CCA AAC GAT CAA AAA GTG GTG GTC ATC TCT GTA GAT GAG CAT   | 248 |
| Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp Glu His   |     |
| 55 60 65                                                          |     |
| GAC AAT ATT TTC GTA GAT GAC AAA CCG ATG AAT TTA GAA GCT TTG AGC   | 296 |
| Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser   |     |
| 70 75 80                                                          |     |
| GCT GTA GTC AAA CAA ACA GAC CCT AAA ACC CTT ATA GAC TTA AAA AGC   | 344 |
| Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser   |     |
| 85 90 95                                                          |     |
| GAC AAA AGC TCT CGT TTT GAA ACT TTT ATC AGC ATT ATG GAT ATT TTA   | 392 |
| Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu   |     |
| 100 105 110                                                       |     |
| AAA GAG CAT AAT CAT GAA AAT TTC TCC ATC TCC ACG CAA GCT CAG TAAAG | 442 |
| Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln       |     |
| 115 120 125                                                       |     |
| TTTCAACGAG TGTTAGCTTT TTAATCTCTT TTGCCCTATA CGCTATAG              | 490 |

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile |  |
| 1 5 10 15                                                       |  |
| Asp Ile Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe |  |
| 20 25 30                                                        |  |
| Ile Ala Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala |  |
| 35 40 45                                                        |  |
| Glu Lys Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp |  |
| 50 55 60                                                        |  |
| Glu His Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala |  |
| 65 70 75 80                                                     |  |
| Leu Ser Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu |  |
| 85 90 95                                                        |  |
| Lys Ser Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp |  |
| 100 105 110                                                     |  |
| Ile Leu Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala |  |
| 115 120 125                                                     |  |
| Gln                                                             |  |



|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCT AAA GAG GAA GCT AAA GAA AAA AGC GCT CCT AAA CAA GTA ACA ACT   | 536 |
| Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val Thr Thr   |     |
| 150 155 160                                                       |     |
| AAG GAT ATA GTC AAA GAA AAA GAC AAG CAA GAA GAA TCC AAC AAA ACC   | 584 |
| Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn Lys Thr   |     |
| 165 170 175                                                       |     |
| TCT GAG GGG GCC ACT TCT GAA GCT CAA GCT TAT AAC CCA GGG GTG AGC   | 632 |
| Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly Val Ser   |     |
| 180 185 190                                                       |     |
| AAC GAA TTT TTA ATG AAG ATC CAA ACC GCT ATT TCT TCT AAA AAC CGC   | 680 |
| Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys Asn Arg   |     |
| 195 200 205 210                                                   |     |
| TAC CCT AAA ATG GCG CAG ATT AGG GGT ATT GAG GGC GAA GTG TTG GTG   | 728 |
| Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val Leu Val   |     |
| 215 220 225                                                       |     |
| AGC TTT ACG ATC AAT GCT GAT GGG AGC GTT ACG GAC ATT AAA GTG GTC   | 776 |
| Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys Val Val   |     |
| 230 235 240                                                       |     |
| AAA AGC AAC ACC ACA GAT ATT TTA AAC CAT GCG GCT TTA GAA GCC ATT   | 824 |
| Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu Ala Ile   |     |
| 245 250 255                                                       |     |
| AAA AGC GCG GCA CAT CTA TTC CCT AAA CCA GAA GAA ACC GTG CAT CTA   | 872 |
| Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Thr Val His Leu       |     |
| 260 265 270                                                       |     |
| AAA ATC CCT ATC GCT TAT AGC TTG AAA GAA GAC TGATTAGTCT TTCTTTTAGG | 925 |
| Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp                       |     |
| 275 280 285                                                       |     |
| GGCGATTCAA GCCTTAAAAG CCGGGTCAAA ATC                              | 958 |

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

|                                                                 |
|-----------------------------------------------------------------|
| Met Lys Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser |
| 1 5 10 15                                                       |
| Val Ser Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr |
| 20 25 30                                                        |
| Phe Leu Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr |
| 35 40 45                                                        |
| Thr Lys Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr |

|                                                                 |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|----|
| 50                                                              |     | 55  |     | 60 |
| Lys Thr Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys |     |     |     |    |
| 65                                                              | 70  | 75  | 80  |    |
| Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr |     |     |     |    |
|                                                                 | 85  | 90  | 95  |    |
| Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro |     |     |     |    |
|                                                                 | 100 | 105 | 110 |    |
| Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro |     |     |     |    |
|                                                                 | 115 | 120 | 125 |    |
| Lys Val Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys |     |     |     |    |
|                                                                 | 130 | 135 | 140 |    |
| Glu Glu Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val |     |     |     |    |
| 145                                                             | 150 | 155 | 160 |    |
| Thr Thr Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn |     |     |     |    |
|                                                                 | 165 | 170 | 175 |    |
| Lys Thr Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly |     |     |     |    |
|                                                                 | 180 | 185 | 190 |    |
| Val Ser Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys |     |     |     |    |
|                                                                 | 195 | 200 | 205 |    |
| Asn Arg Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val |     |     |     |    |
|                                                                 | 210 | 215 | 220 |    |
| Leu Val Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys |     |     |     |    |
| 225                                                             | 230 | 235 | 240 |    |
| Val Val Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu |     |     |     |    |
|                                                                 | 245 | 250 | 255 |    |
| Ala Ile Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val |     |     |     |    |
|                                                                 | 260 | 265 | 270 |    |
| His Leu Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp             |     |     |     |    |
|                                                                 | 275 | 280 | 285 |    |

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...704
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTGATGAAAA AAATAACGCT CCTCTTTTAA AAACCTCTTTT AGAGGATGCC ATG AGA | 56  |
| Met Arg                                                         |     |
| 1                                                               |     |
| GTG TCT TCT AAA GAG ATT TTA CTC ATT GTG GGG GGG AGC AGT TTT TAC | 104 |
| Val Ser Ser Lys Glu Ile Leu Leu Ile Val Gly Gly Ser Ser Phe Tyr |     |
| 5 10 15                                                         |     |
| CTC AAA TCC ATT TTA GAA GGT TTG AGC CGC ATG CCA AAA CTG AGC GGT | 152 |

|            |          |     |     |     |     |     |     |            |            |            |     |     |     |     |     |     |     |
|------------|----------|-----|-----|-----|-----|-----|-----|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|
| Leu        | Lys      | Ser | Ile | Leu | Glu | Gly | Leu | Ser        | Arg        | Met        | Pro | Lys | Leu | Ser | Gly |     |     |
| 20         |          |     |     |     |     | 25  |     |            |            |            | 30  |     |     |     |     |     |     |
| GAG        | GAG      | GTT | GTA | AAA | ATA | GAG | CGA | GAA        | ATT        | GCC        | ACT | CTT | TCT | AAC | CCT | 200 |     |
| Glu        | Glu      | Val | Val | Lys | Ile | Glu | Arg | Glu        | Ile        | Ala        | Thr | Leu | Ser | Asn | Pro | 50  |     |
| 35         |          |     |     | 40  |     |     |     |            | 45         |            |     |     |     |     |     |     |     |
| TAT        | ATA      | TTT | TTA | AAA | TCC | ATT | GAC | CCT        | AAC        | ATG        | GCT | TTT | AAA | ATC | CAT | 248 |     |
| Tyr        | Ile      | Phe | Leu | Lys | Ser | Ile | Asp | Pro        | Asn        | Met        | Ala | Phe | Lys | Ile | His | 65  |     |
|            |          |     |     | 55  |     |     |     | 60         |            |            |     |     |     |     |     |     |     |
| CCA        | AAC      | GAC | ACT | TAC | CGC | ACC | CAT | AAG        | GCT        | TTA        | GAA | ATC | TTT | TAT | GCC | 296 |     |
| Pro        | Asn      | Asp | Thr | Tyr | Arg | Thr | His | Lys        | Ala        | Leu        | Glu | Ile | Phe | Tyr | Ala | 80  |     |
|            |          |     | 70  |     |     |     |     | 75         |            |            |     |     |     |     |     |     |     |
| ACC        | TGC      | ACG | CCC | CCA | AGC | GAG | TAT | TTT        | AAG        | GCC        | AAC | CCT | AAA | AAA | CCC | 344 |     |
| Thr        | Cys      | Thr | Pro | Pro | Ser | Glu | Tyr | Phe        | Lys        | Ala        | Asn | Pro | Lys | Lys | Pro | 95  |     |
|            |          | 85  |     |     |     |     | 90  |            |            |            |     |     |     |     |     |     |     |
| TTT        | GAG      | CAT | GCT | ATC | TCC | TTA | TTC | GCT        | CTG        | TCT        | ATT | GAA | AAA | AGC | GCG | 392 |     |
| Phe        | Glu      | His | Ala | Ile | Ser | Leu | Phe | Ala        | Leu        | Ser        | Ile | Glu | Lys | Ser | Ala | 110 |     |
| 100        |          |     |     |     |     | 105 |     |            |            |            |     |     |     |     |     |     |     |
| CTC        | CAT      | AAC | AAT | ATC | AAA | CGG | CGC | ACC        | AAA        | AAC        | ATG | CTC | CAT | TCA | GGG | 440 |     |
| Leu        | His      | Asn | Asn | Ile | Lys | Arg | Arg | Thr        | Lys        | Asn        | Met | Leu | His | Ser | Gly | 130 |     |
| 115        |          |     |     |     | 120 |     |     |            | 125        |            |     |     |     |     |     |     |     |
| CTT        | GTT      | GAA | GAA | ATC | AAA | GCC | CTC | TAT        | ACT        | CAA        | TAC | CCT | AAA | GAT | TCG | 488 |     |
| Leu        | Val      | Glu | Glu | Ile | Lys | Ala | Leu | Tyr        | Thr        | Gln        | Tyr | Pro | Lys | Asp | Ser | 145 |     |
|            |          |     |     | 135 |     |     |     |            | 140        |            |     |     |     |     |     |     |     |
| CAG        | CCT      | TTT | AAA | GCC | ATA | GGC | GTT | AAA        | GAG        | AGC        | GTT | CTT | TTT | TTA | GAA | 536 |     |
| Gln        | Pro      | Phe | Lys | Ala | Ile | Gly | Val | Lys        | Glu        | Ser        | Val | Leu | Phe | Leu | Glu | 160 |     |
|            |          |     | 150 |     |     |     |     | 155        |            |            |     |     |     |     |     |     |     |
| AAA        | CGA      | CTC | ACT | TTA | AAG | GAG | CTA | GAA        | GAA        | GCG        | ATT | ACC | TCT | AAC | ACC | 584 |     |
| Lys        | Arg      | Leu | Thr | Leu | Lys | Glu | Leu | Glu        | Glu        | Ala        | Ile | Thr | Ser | Asn | Thr | 175 |     |
|            |          | 165 |     |     |     |     | 170 |            |            |            |     |     |     |     |     |     |     |
| ATG        | AAA      | TTA | GCC | AAG | CGC | CAA | AAC | ACT        | TTC        | AAT        | AAA | ACC | CAA | TTC | AAT | 632 |     |
| Met        | Lys      | Leu | Ala | Lys | Arg | Gln | Asn | Thr        | Phe        | Asn        | Lys | Thr | Gln | Phe | Asn | 190 |     |
| 180        |          |     |     |     |     | 185 |     |            |            |            |     |     |     |     |     |     |     |
| AAC        | CTT      | TAT | GTG | GGG | AGC | GCT | GAA | GAA        | GTT        | AGG        | CAT | GCG | ATT | TTA | AAA | 680 |     |
| Asn        | Leu      | Tyr | Val | Gly | Ser | Ala | Glu | Glu        | Val        | Arg        | His | Ala | Ile | Leu | Lys | 210 |     |
| 195        |          |     |     |     | 200 |     |     |            | 205        |            |     |     |     |     |     |     |     |
| CAC        | TCA      | AAA | AGC | GGC | ATT | AAA | GGA | TAATCTAATG | GATACACAAA | ACTTACCCGA | 734 |     |     |     |     |     |     |
| His        | Ser      | Lys | Ser | Gly | Ile | Lys | Gly |            |            |            |     |     |     |     |     |     |     |
|            |          |     |     | 215 |     |     |     |            |            |            |     |     |     |     |     |     |     |
| TCAAATTATC | CCTATTTT | TGA |     |     |     |     |     |            |            |            |     |     |     |     |     |     | 757 |

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid





1

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAC AAT AAA ACG CCT TTT TTG AGC GCG ATT TTT ACG GCA TCA ATT AGG   | 104 |
| Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser Ile Arg   |     |
| 5 10 15                                                           |     |
| GGT TAC CAA CGC TTT TTT TCG GCT TTC ACC CCT TCA AGC TGC CGG TTT   | 152 |
| Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys Arg Phe   |     |
| 20 25 30                                                          |     |
| TAC CCC ACT TGT TCC AAC TAC GCT CTG TGG TTG CTC TGT TTT GAA AGC   | 200 |
| Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe Glu Ser   |     |
| 35 40 45 50                                                       |     |
| CCT TTG AGC GCT ATG GGT AAG ATC GCT ATA AGG ATA CTC TCA TGC AAC   | 248 |
| Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser Cys Asn   |     |
| 55 60 65                                                          |     |
| CCT TTT TGC TCT GGG GGC ATT GCT TAC CCT ACT ACT CGC TTG AAA CGC   | 296 |
| Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu Lys Arg   |     |
| 70 75 80                                                          |     |
| CCA AGC CTG ATC CAA TCT CAT AAA GAT TCT AAT CGC AAT TTT AAA ACC   | 344 |
| Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe Lys Thr   |     |
| 85 90 95                                                          |     |
| ATC ACT TTT TGG CTC GTT CCC ACA AAA AGC CAC GCA ACT TAC TAC ATC   | 392 |
| Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr Tyr Ile   |     |
| 100 105 110                                                       |     |
| ATT AAG GTT TAATCACAAT GGATAAAAAC AACAATAATC TCCGCTTGAT TTTAGCGAT | 450 |
| Ile Lys Val                                                       |     |
| 115                                                               |     |
| CGCT                                                              | 454 |

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Arg Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser |  |
| 1 5 10 15                                                       |  |
| Ile Arg Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys |  |
| 20 25 30                                                        |  |
| Arg Phe Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe |  |
| 35 40 45                                                        |  |
| Glu Ser Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser |  |
| 50 55 60                                                        |  |
| Cys Asn Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu |  |



|                                                                    |      |
|--------------------------------------------------------------------|------|
| CAC CTT TTA AGC TCC CCA ACG GTG TAT AAC TCT GTG TTT AAC GAT GTG    | 440  |
| His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn Asp Val    |      |
| 115 120 125 130                                                    |      |
| CAG TTT TGG GAT GGC AGG GTT ACG CAT TTA AAC GAA CAG GCG CAA GGG    | 488  |
| Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala Gln Gly    |      |
| 135 140 145                                                        |      |
| CCC ATC CAG TCT TCT TTT GAA ATG GGG GCT GAT CCC AAA GTG GTG GTA    | 536  |
| Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val Val Val    |      |
| 150 155 160                                                        |      |
| GAA AAA ATC AAT TCC ATG CCA GGC TAT GTC AAG CTC TTT AGA AAA GCC    | 584  |
| Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg Lys Ala    |      |
| 165 170 175                                                        |      |
| TAT GGC TCT AAA GTC AAA ATT GAT TTT AAA TTG ATC GCT GAT AGT ATC    | 632  |
| Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp Ser Ile    |      |
| 180 185 190                                                        |      |
| GCT ATG TTT GAA GCC ACG CTT ATT ACC CCA AGC CGT TAC GAC GAT TTT    | 680  |
| Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp Asp Phe    |      |
| 195 200 205 210                                                    |      |
| TTA AGA GGC AAT CCT AAA GCG CTC AGC AAA GCC GAA AAA GAG GGG CTG    | 728  |
| Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu Gly Leu    |      |
| 215 220 225                                                        |      |
| AAT TTA TTC ATT TCT AAA GGC TGT GTG GCT TGC CAT AAC GGC ATT AAT    | 776  |
| Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly Ile Asn    |      |
| 230 235 240                                                        |      |
| CTT GGG GGA ACG ATG CAG CCT TTT GGG GTG GTC AAA CCT TAT AAA TTC    | 824  |
| Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr Lys Phe    |      |
| 245 250 255                                                        |      |
| GCT AAT GTG GGC GAT TTC AAA GGC GAT AAA AAC GGG CTT GTG AAA GTG    | 872  |
| Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val Lys Val    |      |
| 260 265 270                                                        |      |
| CCT ACT TTA AGG AAT ATC ACC GAA ACG ATG CCC TAT TTC CAT AAC GGG    | 920  |
| Pro Thr Leu Arg Asn Ile Thr Glu Thr Met Pro Tyr Phe His Asn Gly    |      |
| 275 280 285 290                                                    |      |
| CAA TTC TGG GAT GTT AAG GAT GCG ATT AAA GAA ATG GGC TCT ATC CAG    | 968  |
| Gln Phe Trp Asp Val Lys Asp Ala Ile Lys Glu Met Gly Ser Ile Gln    |      |
| 295 300 305                                                        |      |
| TTA GGC ATT GAA ATC AGC GAT GAA GAA GCG AAA AAA ATT GAA ACT TTC    | 1016 |
| Leu Gly Ile Glu Ile Ser Asp Glu Glu Ala Lys Lys Ile Glu Thr Phe    |      |
| 310 315 320                                                        |      |
| TTT GGA GCC TTA AGG GGT AAA AAA CCT AAA ATA ATC TAC CCA GAA CTC    | 1064 |
| Phe Gly Ala Leu Arg Gly Lys Lys Pro Lys Ile Ile Tyr Pro Glu Leu    |      |
| 325 330 335                                                        |      |
| CCC ATA ATG ACA GAC AAA ACC CCT AAA CCC TCT TTT TGATT TAAAA AAGTCC | 1116 |
| Pro Ile Met Thr Asp Lys Thr Pro Lys Pro Ser Phe                    |      |

340

345

350

TTTTAGGGGT CTTTGGCGCT AAATCTAAAA AATACTC

1153

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ser | Ile | Leu | Leu | Gly | Val | Cys | Leu | Ala | Phe | Ser | Cys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Ala | Leu | Asn | Asp | Leu | Glu | Leu | Ile | Lys | Lys | Ala | Arg | Glu | Ser | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Pro | Met | Pro | Met | Gly | Lys | Ala | Leu | Lys | Glu | Tyr | Gln | Ile | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Thr | Arg | Asp | Val | Gly | Ile | Gly | Thr | Lys | Asn | Ser | Glu | Ile | Met | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Ala | Gln | Val | Glu | Leu | Gly | Lys | Met | Leu | Tyr | Phe | Asp | Pro | Arg | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Thr | Ser | Tyr | Leu | Val | Ser | Cys | Asn | Thr | Cys | His | Asn | Leu | Gly | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Gly | Val | Asp | Leu | Val | Pro | Ser | Ala | Ile | Gly | Ser | Gln | Trp | Lys | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asn | Pro | His | Leu | Leu | Ser | Ser | Pro | Thr | Val | Tyr | Asn | Ser | Val | Phe | Asn |
|     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Asp | Val | Gln | Phe | Trp | Asp | Gly | Arg | Val | Thr | His | Leu | Asn | Glu | Gln | Ala |
| 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Gln | Gly | Pro | Ile | Gln | Ser | Phe | Glu | Met | Gly | Ala | Asp | Pro | Lys | Val |     |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Val | Glu | Lys | Ile | Asn | Ser | Met | Pro | Gly | Tyr | Val | Lys | Leu | Phe | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Lys | Ala | Tyr | Gly | Ser | Lys | Val | Lys | Ile | Asp | Phe | Lys | Leu | Ile | Ala | Asp |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ser | Ile | Ala | Met | Phe | Glu | Ala | Thr | Leu | Ile | Thr | Pro | Ser | Arg | Tyr | Asp |
|     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Asp | Phe | Leu | Arg | Gly | Asn | Pro | Lys | Ala | Leu | Ser | Lys | Ala | Glu | Lys | Glu |
| 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Gly | Leu | Asn | Leu | Phe | Ile | Ser | Lys | Gly | Cys | Val | Ala | Cys | His | Asn | Gly |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Asn | Leu | Gly | Gly | Thr | Met | Gln | Pro | Phe | Gly | Val | Val | Lys | Pro | Tyr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Lys | Phe | Ala | Asn | Val | Gly | Asp | Phe | Lys | Gly | Asp | Lys | Asn | Gly | Leu | Val |
|     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Lys | Val | Pro | Thr | Leu | Arg | Asn | Ile | Thr | Glu | Thr | Met | Pro | Tyr | Phe | His |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Asn | Gly | Gln | Phe | Trp | Asp | Val | Lys | Asp | Ala | Ile | Lys | Glu | Met | Gly | Ser |
| 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Ile | Gln | Leu | Gly | Ile | Glu | Ile | Ser | Asp | Glu | Glu | Ala | Lys | Lys | Ile | Glu |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Thr | Phe | Phe | Gly | Ala | Leu | Arg | Gly | Lys | Lys | Pro | Lys | Ile | Ile | Tyr | Pro |

325 330 335  
 Glu Leu Pro Ile Met Thr Asp Lys Thr Pro Lys Pro Ser Phe  
 340 345 350

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...374
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GTTAGAGATT TCTCCCAATT CTCAAGTGGG AGCGAGCGTG AAAATCCGCT ATG AAA 56  
 Met Lys  
 1

GCA ATC TTT AGC CTC TTT TTC CTT CTT ATT GTT TTA AAA GCA AAC CCC 104  
 Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala Asn Pro  
 5 10 15

ATA AAC CCT TTA TTA GAG CCG TTA TAT TTC CCC AGT TAC GCG CAA TTT 152  
 Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala Gln Phe  
 20 25 30

TTA AAC TTA GCA CCT CAC TTT GTC ATT AAA AAA AAG CGC GCT TAT AGA 200  
 Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala Tyr Arg  
 35 40 45 50

CCC TTT CAA TGG GGG AAT ACC ATT ATC ATC AAA CGC CAT GAT TTA GAA 248  
 Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp Leu Glu  
 55 60 65

GAA CGC CAA AGC AAC CAG CCA AGC GAT ATT TTC CGC CAA AAC GCT GAA 296  
 Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn Ala Glu  
 70 75 80

ATC AAT GTG TCT TCT CAA ACT TTT TTA AAA GGA ATG AGC AAC GCT TCT 344  
 Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn Ala Ser  
 85 90 95

TCA CGA ACA GTG CTT GAT TCA GCC GCT CAG TAAATGCTA AAACCTTTTTT TAA 397  
 Ser Arg Thr Val Leu Asp Ser Ala Ala Gln  
 100 105

TCACATTTTT CTTGGTATTT TCTTAATCC 426

(2) INFORMATION FOR SEQ ID NO:236:











(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...968  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTACTGATTT TTCTTTGTGT GAGCTTTGGC TTAGTTTTGT AAGGAATGAG ATG ATA  | 56  |
| Met Ile                                                         |     |
| 1                                                               |     |
| AAG AGT TGG ACT AAA AAG TGG TTT TTG ATT TTA TTT TTA ATG GCA AGT | 104 |
| Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser |     |
| 5 10 15                                                         |     |
| TGT TCC AGT TAT TTG GTG GCT ACA ACC GGT GAG AAA TAT TTT AAA ATG | 152 |
| Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met |     |
| 20 25 30                                                        |     |
| GCT ACT CAA GCC TTT AAG AGA GGG GAC TAC CAT AAA GCG GTG GCT TTT | 200 |
| Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val Ala Phe |     |
| 35 40 45 50                                                     |     |
| TAT AAG AGG AGC TGT AAT TTA AGG GTG GGG GTT GGT TGC ACG AGT TTA | 248 |
| Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr Ser Leu |     |
| 55 60 65                                                        |     |
| GGC TCT ATG TAT GAA GAT GGC GAT GGC GTG GAT CAG AAT ATT ACA AAA | 296 |
| Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys |     |
| 70 75 80                                                        |     |
| GCC GTT TTT TAT TAC AGA AGA GGG TGT AAT TTA AGG AAT CAT CTC GCT | 344 |
| Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala |     |
| 85 90 95                                                        |     |
| TGC GCG AGT CTA GGC TCT ATG TAT GAA GAT GGC GAT GGT GTG CAA AAA | 392 |
| Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys |     |
| 100 105 110                                                     |     |
| AAC CTT CCA AAG GCT ATC TAT TAT TAC AGG AGA GGG TGC CAC TTA AAG | 440 |
| Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys |     |
| 115 120 125 130                                                 |     |
| GGT GGG GTG AGC TGT GGG AGT TTA GGT TTT ATG TAT TTT AAT GGC ACG | 488 |
| Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr |     |
| 135 140 145                                                     |     |
| GGC GTT AAG CAA AAT TAT GCC AAA GCC CTT TTT CTT TCT AAA TAC GCT | 536 |
| Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala |     |
| 150 155 160                                                     |     |
| TGC AGT TTG AAT TAC GGC ATT AGT TGT AAC TTT GTA GGG TAT ATG TAT | 584 |
| Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr |     |
| 165 170 175                                                     |     |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AGG AAC GCC AAA GGC GTA CAG AAG GAT TTG AAA AAA GCC CTT GCG AAT   | 632  |
| Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn   |      |
| 180 185 190                                                       |      |
| TTT AAA AGA GGG TGC CAT TTG AAA GAC GGA GCG AGT TGT GTG AGC TTG   | 680  |
| Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu   |      |
| 195 200 205 210                                                   |      |
| GGA TAC ATG TAT GAA GTC GGT ATG GAT GTC AAA CAA AAT GGA GAG CAA   | 728  |
| Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln   |      |
| 215 220 225                                                       |      |
| GCC TTG AAT CTT TAT AAA AAG GGT TGT TAT TTA AAA AGG GGG AGC GGT   | 776  |
| Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly   |      |
| 230 235 240                                                       |      |
| TGT CAT AAT GTG GCG GTG ATG TAT TAC ACC GGT AAG GGC GTT CCA AAG   | 824  |
| Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys   |      |
| 245 250 255                                                       |      |
| GAT TTA GAT AAA GCC ATT TCG TAT TAT AAG AAA GGT TGC ACT CTA GGC   | 872  |
| Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly   |      |
| 260 265 270                                                       |      |
| TTT AGT GGT AGC TGT AAA GTG TTA GAA GAA GTG ATT GGC AAG AAG TCT   | 920  |
| Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser   |      |
| 275 280 285 290                                                   |      |
| GAT GAT TTG CAA GAT GAC GCG CAA AAC GAC ACG CAA GAT GAT ATG CAA T | 969  |
| Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln   |      |
| 295 300 305                                                       |      |
| AAGTTAAAGC TTATGGACTA ATGATTAAAA CTCATCTTAT AGAAATCTTT CT         | 1021 |

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met |  |
| 1 5 10 15                                                       |  |
| Ala Ser Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe |  |
| 20 25 30                                                        |  |
| Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val |  |
| 35 40 45                                                        |  |
| Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr |  |
| 50 55 60                                                        |  |
| Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile |  |
| 65 70 75 80                                                     |  |
| Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Cys | Ala | Ser | Leu | Gly | Ser | Met | Tyr | Glu | Asp | Gly | Asp | Gly | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gln | Lys | Asn | Leu | Pro | Lys | Ala | Ile | Tyr | Tyr | Tyr | Arg | Arg | Gly | Cys | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Lys | Gly | Gly | Val | Ser | Cys | Gly | Ser | Leu | Gly | Phe | Met | Tyr | Phe | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Thr | Gly | Val | Lys | Gln | Asn | Tyr | Ala | Lys | Ala | Lys | Phe | Leu | Ser | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Ala | Cys | Ser | Leu | Asn | Tyr | Gly | Ile | Ser | Cys | Asn | Phe | Val | Gly | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Tyr | Arg | Asn | Ala | Lys | Gly | Val | Gln | Lys | Asp | Leu | Lys | Lys | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asn | Phe | Lys | Arg | Gly | Cys | His | Leu | Lys | Asp | Gly | Ala | Ser | Cys | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Leu | Gly | Tyr | Met | Tyr | Glu | Val | Gly | Met | Asp | Val | Lys | Gln | Asn | Gly |
|     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Glu | Gln | Ala | Leu | Asn | Leu | Tyr | Lys | Lys | Gly | Cys | Tyr | Leu | Lys | Arg | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Gly | Cys | His | Asn | Val | Ala | Val | Met | Tyr | Tyr | Thr | Gly | Lys | Gly | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | Lys | Asp | Leu | Asp | Lys | Ala | Ile | Ser | Tyr | Tyr | Lys | Lys | Gly | Cys | Thr |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     |     | 270 |     |     |
| Leu | Gly | Phe | Ser | Gly | Ser | Cys | Lys | Val | Leu | Glu | Glu | Val | Ile | Gly | Lys |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Lys | Ser | Asp | Asp | Leu | Gln | Asp | Asp | Ala | Gln | Asn | Asp | Thr | Gln | Asp | Asp |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Met | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...947
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CTATAATGTG AATTTAATGA TGAAAATTAG TTTAGAGTGG AGAACACACA ATG AAA  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| AAA AAT ATC TTA AAT TTA GCG TTA GTG GGT GCG TTG AGC ACG TCG TTT | 104 |
| Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr Ser Phe |     |
| 5 10 15                                                         |     |
| TTG ATG GCT AAG CCG GCT CAT AAC GCA AAT AAC GCT ACG CAT AAC ACG | 152 |



ACT TAT ACT TAT GAA CAG GCT AAA CCT ACC ATT AAG GGG ATG TTA CAA 872  
 Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met Leu Gln  
 260 265 270

GAA AAG CTT TTC CAA GAA CGC ATG AAT CAA CGC ATT GAG GAA CTA AGA 920  
 Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu Leu Arg  
 275 280 285 290

AAG CAC GCT AAA ATT GTT ATC AAC AAG TAATTGATGA GGTGTTATCA TGTTAGT 974  
 Lys His Ala Lys Ile Val Ile Asn Lys  
 295

TAAAGGCAAT GAAATTTTAT TGAAAG 1000

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Lys Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr  
 1 5 10 15  
 Ser Phe Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ala Thr His  
 20 25 30  
 Asn Thr Lys Lys Thr Thr Asp Ser Ser Ala Gly Val Leu Ala Thr Val  
 35 40 45  
 Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg  
 50 55 60  
 Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala  
 65 70 75 80  
 Leu Ile Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys  
 85 90 95  
 Thr Glu Lys Leu Asp Ser Thr Pro Glu Phe Lys Ala Met Met Glu Ala  
 100 105 110  
 Val Lys Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu  
 115 120 125  
 Glu Val Lys Lys Val Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr  
 130 135 140  
 Asn Ala Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg  
 145 150 155 160  
 His Ile Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu  
 165 170 175  
 Ile Asp Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu  
 180 185 190  
 Ala Asn Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly  
 195 200 205  
 Gly Asp Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser  
 210 215 220  
 Lys Ala Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val  
 225 230 235 240  
 Lys Thr Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser







|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TAT ATG GAG AGG ATT TAT GGC GTC ATA GAC GCA AGC TCT GGT TAC GCT | 248 |
| Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly Tyr Ala |     |
| 55 60 65                                                        |     |
| AAC GGC AAG ACT TCA AGC ACG AAT TAT GAG AAA TTG CAT GAA AGT GAT | 296 |
| Asn Gly Lys Thr Ser Ser Thr Asn Tyr Glu Lys Leu His Glu Ser Asp |     |
| 70 75 80                                                        |     |
| CAT GCT GAA AGC GTG AAA GTC ATT TAT GAT CCT AAA AAA ATC AGT TTG | 344 |
| His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile Ser Leu |     |
| 85 90 95                                                        |     |
| GAC AAA TTG TTG CGT TAC TAT TTT AAG GTG GTT GAT CCG GTG AGC GTG | 392 |
| Asp Lys Leu Leu Arg Tyr Phe Lys Val Val Asp Pro Val Ser Val     |     |
| 100 105 110                                                     |     |
| AAC AAG CAG GGT AAT GAT GTG GGC AGG CAG TAT CGC ACG GGG ATT TAT | 440 |
| Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly Ile Tyr |     |
| 115 120 125 130                                                 |     |
| TAT GTC AAT AGC GCG GAT AAA GAA GTG ATA GAT CAT GCC TTA AAA GCG | 488 |
| Tyr Val Asn Ser Ala Asp Lys Glu Val Ile Asp His Ala Leu Lys Ala |     |
| 135 140 145                                                     |     |
| TTA CAG AAA GAA GTG AAA GGT AAA ATC GCT ATT GAA GTA GAG CCT TTA | 536 |
| Leu Gln Lys Glu Val Lys Gly Lys Ile Ala Ile Glu Val Glu Pro Leu |     |
| 150 155 160                                                     |     |
| AAA AAT TAT GTG AGG GCT GAA GAG TAT CAT CAG GAT TAT TTG AAG AAA | 584 |
| Lys Asn Tyr Val Arg Ala Glu Tyr His Gln Asp Tyr Leu Lys Lys     |     |
| 165 170 175                                                     |     |
| CAC CCT AGT GGT TAT TGC CAT ATT GAT TTG AAA AAG GCG GAT GAA GTG | 632 |
| His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp Glu Val |     |
| 180 185 190                                                     |     |
| ATT GTG GAT GAC GAT AAA TAC ACC AAA CCT AGC GAT GAA GTT TTA AAG | 680 |
| Ile Val Asp Asp Asp Lys Tyr Thr Lys Pro Ser Asp Glu Val Leu Lys |     |
| 195 200 205 210                                                 |     |
| AAA AAA CTC ACC AAA CTC CAG TAT GAG GTT ACG CAA AAC AAA CAC ACT | 728 |
| Lys Lys Leu Thr Lys Leu Gln Tyr Glu Val Thr Gln Asn Lys His Thr |     |
| 215 220 225                                                     |     |
| GAG AAA CCC TTT GAA AAC GAG TAT TAC AAC AAA GAA GAA GAG GGC ATT | 776 |
| Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu Gly Ile |     |
| 230 235 240                                                     |     |
| TAT GTG GAT ATT ACC ACA GGC GAG CCG TTA TTT TCT TCA GCG GAT AAA | 824 |
| Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Ser Ser Ala Asp Lys |     |
| 245 250 255                                                     |     |
| TAC GAC TCC GGT TGC GGG TGG CCA AGC TTT TCT AAG CCT ATC AAT AAA | 872 |
| Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile Asn Lys |     |
| 260 265 270                                                     |     |
| GAT GTG GTG AAA TAC GAA GAC GAT GAG AGC CTT AAT AGG AAA CGC ATT | 920 |
| Asp Val Val Lys Tyr Glu Asp Asp Glu Ser Leu Asn Arg Lys Arg Ile |     |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE: internal

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Lys        | Val        | Leu        | Ser<br>5  | Tyr        | Leu        | Lys        | Asn        | Phe<br>10 | Tyr        | Leu        | Phe        | Leu        | Ala       | Ile        |
| Gly        | Ala        | Ile        | Met<br>20  | Gln       | Ala        | Ser        | Glu        | Asn<br>25  | Met       | Gly        | Ser        | Gln        | His<br>30  | Gln       | Lys        |
| Thr        | Asp        | Glu<br>35  | Arg        | Val       | Ile        | Tyr        | Leu<br>40  | Ala        | Gly       | Gly        | Cys        | Phe<br>45  | Trp        | Gly       | Leu        |
| Glu        | Ala<br>50  | Tyr        | Met        | Glu       | Arg        | Ile<br>55  | Tyr        | Gly        | Val       | Ile        | Asp<br>60  | Ala        | Ser        | Ser       | Gly        |
| Tyr<br>65  | Ala        | Asn        | Gly        | Lys       | Thr<br>70  | Ser        | Ser        | Thr        | Asn       | Tyr<br>75  | Glu        | Lys        | Leu        | His       | Glu<br>80  |
| Ser        | Asp        | His        | Ala        | Glu<br>85 | Ser        | Val        | Lys        | Val        | Ile<br>90 | Tyr        | Asp        | Pro        | Lys        | Lys<br>95 | Ile        |
| Ser        | Leu        | Asp        | Lys<br>100 | Leu       | Leu        | Arg        | Tyr        | Tyr<br>105 | Phe       | Lys        | Val        | Val        | Asp<br>110 | Pro       | Val        |
| Ser        | Val        | Asn<br>115 | Lys        | Gln       | Gly        | Asn        | Asp<br>120 | Val        | Gly       | Arg        | Gln        | Tyr<br>125 | Arg        | Thr       | Gly        |
| Ile        | Tyr<br>130 | Tyr        | Val        | Asn       | Ser        | Ala<br>135 | Asp        | Lys        | Glu       | Val        | Ile<br>140 | Asp        | His        | Ala       | Leu        |
| Lys<br>145 | Ala        | Leu        | Gln        | Lys       | Glu<br>150 | Val        | Lys        | Gly        | Lys       | Ile<br>155 | Ala        | Ile        | Glu        | Val       | Glu<br>160 |
| Pro        | Leu        | Lys        | Asn        | Tyr       | Val        | Arg        | Ala        | Glu        | Glu       | Tyr        | His        | Gln        | Asp        | Tyr       | Leu        |



|     |     |     |     |     |     |     |             |            |            |      |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-------------|------------|------------|------|-----|-----|-----|-----|-----|-----|--|
| Leu | Val | Ser | Val | Ile | Glu | Lys | Gln         | Thr        | Asn        | Lys  | Lys | Val | Arg | Ile | Leu |     |  |
| 35  |     |     |     |     | 40  |     |             |            |            | 45   |     |     |     |     | 50  |     |  |
| GAA | ATC | AAA | CCT | TTA | AAA | TCT | AGC         | CAG        | GAT        | TTA  | AAA | ATG | GTC | GTT | ATT | 248 |  |
| Glu | Ile | Lys | Pro | Leu | Lys | Ser | Ser         | Gln        | Asp        | Leu  | Lys | Met | Val | Val | Ile |     |  |
|     |     |     |     | 55  |     |     |             |            | 60         |      |     |     |     | 65  |     |     |  |
| GAA | GAT | CCG | GAC | ACT | AAA | TAC | AAT         | ATC        | CCG        | CTT  | GTG | GTG | AGT | AAG | GAT | 296 |  |
| Glu | Asp | Pro | Asp | Thr | Lys | Tyr | Asn         | Ile        | Pro        | Leu  | Val | Val | Ser | Lys | Asp |     |  |
|     |     |     | 70  |     |     |     |             | 75         |            |      |     |     | 80  |     |     |     |  |
| GGT | AAT | TTA | ATC | ATA | GGG | CTT | AGC         | AAC        | ATA        | TTC  | TTT | AGC | AAT | AAA | AGC | 344 |  |
| Gly | Asn | Leu | Ile | Ile | Gly | Leu | Ser         | Asn        | Ile        | Phe  | Phe | Ser | Asn | Lys | Ser |     |  |
|     | 85  |     |     |     |     |     | 90          |            |            |      |     | 95  |     |     |     |     |  |
| GAT | GAT | GTG | CAA | TTA | GTT | GCA | GAA         | ACC        | AAT        | CAA  | AAA | GTT | CAA | GCT | CTT | 392 |  |
| Asp | Asp | Val | Gln | Leu | Val | Ala | Glu         | Thr        | Asn        | Gln  | Lys | Val | Gln | Ala | Leu |     |  |
|     | 100 |     |     |     |     | 105 |             |            |            |      | 110 |     |     |     |     |     |  |
| AAC | GCC | ACC | CAA | CAA | AAT | AGC | GCG         | AAA        | TTG        | AAC  | GCT | ATT | TTT | AAT | GAA | 440 |  |
| Asn | Ala | Thr | Gln | Gln | Asn | Ser | Ala         | Lys        | Leu        | Asn  | Ala | Ile | Phe | Asn | Glu |     |  |
|     | 115 |     |     |     | 120 |     |             |            | 125        |      |     |     |     |     | 130 |     |  |
| ATA | CCG | GCT | GAT | TAT | GCG | ATA | GAG         | TTG        | CCC        | TCT  | ACT | AAC | GCT | GCA | AAT | 488 |  |
| Ile | Pro | Ala | Asp | Tyr | Ala | Ile | Glu         | Leu        | Pro        | Ser  | Thr | Asn | Ala | Ala | Asn |     |  |
|     |     |     |     | 135 |     |     |             |            | 140        |      |     |     |     | 145 |     |     |  |
| AAG | GAT | AAA | ATC | CTT | TAT | ATT | GTC         | TCT        | GAT        | CCC  | ATG | TGC | CCA | CAT | TGC | 536 |  |
| Lys | Asp | Lys | Ile | Leu | Tyr | Ile | Val         | Ser        | Asp        | Pro  | Met | Cys | Pro | His | Cys |     |  |
|     |     |     | 150 |     |     |     |             | 155        |            |      |     |     | 160 |     |     |     |  |
| CAA | AAA | GAG | CTC | ACT | AAA | CTT | AGG         | GAT        | CAT        | TTA  | AAA | GAA | AAC | ACC | GTG | 584 |  |
| Gln | Lys | Glu | Leu | Thr | Lys | Leu | Arg         | Asp        | His        | Leu  | Lys | Glu | Asn | Thr | Val |     |  |
|     |     | 165 |     |     |     |     | 170         |            |            |      |     | 175 |     |     |     |     |  |
| AGA | ATG | GTC | GTG | GTG | GGG | TGG | CTT         | GGG        | GTC        | AAT  | TCA | GCT | AAA | AAA | GCG | 632 |  |
| Arg | Met | Val | Val | Val | Gly | Trp | Leu         | Gly        | Val        | Asn  | Ser | Ala | Lys | Lys | Ala |     |  |
|     | 180 |     |     |     |     | 185 |             |            |            |      | 190 |     |     |     |     |     |  |
| GCT | TTA | ATC | CAA | GAA | GAA | ATG | GCG         | AAA        | GCT        | AGG  | GCT | AGG | GGA | GCG | AGC | 680 |  |
| Ala | Leu | Ile | Gln | Glu | Glu | Met | Ala         | Lys        | Ala        | Arg  | Ala | Arg | Gly | Ala | Ser |     |  |
|     | 195 |     |     |     | 200 |     |             |            | 205        |      |     |     |     |     | 210 |     |  |
| GTG | GAA | GAT | AAG | ATC | TCT | ATT | CTT         | GAA        | AAG        | ATT  | TAT | TCC | ACC | CAA | TAC | 728 |  |
| Val | Glu | Asp | Lys | Ile | Ser | Ile | Leu         | Glu        | Lys        | Ile  | Tyr | Ser | Thr | Gln | Tyr |     |  |
|     |     |     |     | 215 |     |     |             |            | 220        |      |     |     |     | 225 |     |     |  |
| GAT | ATT | AAC | GCT | CAA | AAA | GAG | CCT         | GAA        | GAT        | TTA  | CGC | ACT | AAA | GTG | GAA | 776 |  |
| Asp | Ile | Asn | Ala | Gln | Lys | Glu | Pro         | Glu        | Asp        | Leu  | Arg | Thr | Lys | Val | Glu |     |  |
|     |     |     | 230 |     |     |     |             | 235        |            |      |     |     | 240 |     |     |     |  |
| AAT | ACC | ACT | AAA | AAG | ATT | TTT | GAA         | TCT        | GGC        | GTG  | ATT | AAG | GGT | GTG | CCT | 824 |  |
| Asn | Thr | Thr | Lys | Lys | Ile | Phe | Glu         | Ser        | Gly        | Val  | Ile | Lys | Gly | Val | Pro |     |  |
|     |     | 245 |     |     |     |     | 250         |            |            |      |     | 255 |     |     |     |     |  |
| TTC | TTA | TAC | CAT | TAT | AAG | GCA | ATGATATAAGG | TTGCTCTCAT | GAAAAAACCC | TATA |     |     |     |     |     | 879 |  |
| Phe | Leu | Tyr | His | Tyr | Lys | Ala |             |            |            |      |     |     |     |     |     |     |  |
|     | 260 |     |     |     |     | 265 |             |            |            |      |     |     |     |     |     |     |  |

GGAAGATTTTC TGATTATGC

898

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Arg | Ala | Ser | Val | Leu | Ser | Ala | Leu | Leu | Leu | Val | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Ala | Pro | Lys | His | Ser | Val | Ser | Ala | Asn | Asp | Lys | Arg | Met | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Asn | Leu | Val | Ser | Val | Ile | Glu | Lys | Gln | Thr | Asn | Lys | Lys | Val | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Leu | Glu | Ile | Lys | Pro | Leu | Lys | Ser | Ser | Gln | Asp | Leu | Lys | Met | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Ile | Glu | Asp | Pro | Asp | Thr | Lys | Tyr | Asn | Ile | Pro | Leu | Val | Val | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Asp | Gly | Asn | Leu | Ile | Ile | Gly | Leu | Ser | Asn | Ile | Phe | Phe | Ser | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ser | Asp | Asp | Val | Gln | Leu | Val | Ala | Glu | Thr | Asn | Gln | Lys | Val | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Asn | Ala | Thr | Gln | Gln | Asn | Ser | Ala | Lys | Leu | Asn | Ala | Ile | Phe |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asn | Glu | Ile | Pro | Ala | Asp | Tyr | Ala | Ile | Glu | Leu | Pro | Ser | Thr | Asn | Ala |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ala | Asn | Lys | Asp | Lys | Ile | Leu | Tyr | Ile | Val | Ser | Asp | Pro | Met | Cys | Pro |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| His | Cys | Gln | Lys | Glu | Leu | Thr | Lys | Leu | Arg | Asp | His | Leu | Lys | Glu | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Val | Arg | Met | Val | Val | Val | Gly | Trp | Leu | Gly | Val | Asn | Ser | Ala | Lys |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Lys | Ala | Ala | Leu | Ile | Gln | Glu | Glu | Met | Ala | Lys | Ala | Arg | Ala | Arg | Gly |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ala | Ser | Val | Glu | Asp | Lys | Ile | Ser | Ile | Leu | Glu | Lys | Ile | Tyr | Ser | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Gln | Tyr | Asp | Ile | Asn | Ala | Gln | Lys | Glu | Pro | Glu | Asp | Leu | Arg | Thr | Lys |
|     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Val | Glu | Asn | Thr | Thr | Lys | Lys | Ile | Phe | Glu | Ser | Gly | Val | Ile | Lys | Gly |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Val | Pro | Phe | Leu | Tyr | His | Tyr | Lys | Ala |     |     |     |     |     |     |     |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...707  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

|                                                                 |            |            |            |            |         |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|---------|----|
| TCTTTTAGAC                                                      | GAAAACGCCA | TGATTTTACA | CTGGCAAAAA | GAGGGCTTGC | ATG CGT | 56 |
|                                                                 |            |            |            |            | Met Arg |    |
|                                                                 |            |            |            |            | 1       |    |
| AAA ATC TTG TTA TTG GGT CTG ATT TTA CAA GCG CTC TTC AGC GAA GAA | 104        |            |            |            |         |    |
| Lys Ile Leu Leu Leu Gly Leu Ile Leu Gln Ala Leu Phe Ser Glu Glu |            |            |            |            |         |    |
| 5                                                               | 10         | 15         |            |            |         |    |
| GCC GCG CAA GAA TTG TTG CAA TGC TCT GCG ATT TTT GAA TCT AAA AAA | 152        |            |            |            |         |    |
| Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser Lys Lys |            |            |            |            |         |    |
| 20                                                              | 25         | 30         |            |            |         |    |
| GCC GAA TTG AAA GAC GAT TTG CGC CGA TTG AGT GAA AAA GAG CAG TCT | 200        |            |            |            |         |    |
| Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu Gln Ser |            |            |            |            |         |    |
| 35                                                              | 40         | 45         |            |            | 50      |    |
| TTA AGG ATC TTG CAA ACC GAA AAC GCC CGC CTT TTA GAT GAA AAA ACC | 248        |            |            |            |         |    |
| Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu Lys Thr |            |            |            |            |         |    |
| 55                                                              | 60         | 65         |            |            |         |    |
| GAT CTG TTG AAC CAA AAA GAA AAA GAA GTG GAA GAA AAA CTG AAA AAT | 296        |            |            |            |         |    |
| Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu Lys Asn |            |            |            |            |         |    |
| 70                                                              | 75         | 80         |            |            |         |    |
| TTA GCC GCT AAA GAA GAA GCC TTT AAA ACC TTA CAA ACG GAA GAA AAA | 344        |            |            |            |         |    |
| Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu Glu Lys |            |            |            |            |         |    |
| 85                                                              | 90         | 95         |            |            |         |    |
| AAA CGC CTT AAA AAT TTG ATA GAA GAA AAC GAA GGC ATT TTA AGA GAA | 392        |            |            |            |         |    |
| Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu Arg Glu |            |            |            |            |         |    |
| 100                                                             | 105        | 110        |            |            |         |    |
| ATC AAG CAG GCT AAA GAC AGC AAG ATT GGC GAG ACT TAT TCT AAA ATG | 440        |            |            |            |         |    |
| Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser Lys Met |            |            |            |            |         |    |
| 115                                                             | 120        | 125        |            |            | 130     |    |
| AAA GAT TCT AAA TCG GCT CTG ATT TTA GAA AAT TTA CCC ACT CAA AAC | 488        |            |            |            |         |    |
| Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr Gln Asn |            |            |            |            |         |    |
| 135                                                             | 140        | 145        |            |            |         |    |
| GCA TTA GAA ATT TTA ATG GCG CTA AAA CCC CAA GAA CTC GGT AAA ATT | 536        |            |            |            |         |    |
| Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly Lys Ile |            |            |            |            |         |    |
| 150                                                             | 155        | 160        |            |            |         |    |
| TTA GCC AAA ATG GAT CCT AAA AAA GCG GCG GCT TTG ACA GAG TTG TGG | 584        |            |            |            |         |    |
| Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu Leu Trp |            |            |            |            |         |    |
| 165                                                             | 170        | 175        |            |            |         |    |



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1340
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CTAAAGTGCG CTAAATTCA CTTCAAGTGAT AAAAAAAGG AAATAAAATA ATG AAT   | 56  |
| Met Asn                                                         |     |
| 1                                                               |     |
| ATT CAA ATA AAG AAA AGG TTT TTA GCA AAT TTG TTG CTT TTT AGC CTG | 104 |
| Ile Gln Ile Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe Ser Leu |     |
| 5 10 15                                                         |     |
| TTT TGC CTT AAG GCT GAA ACC CTT TCA GAA GAT CAT CAA ATC CTG TTG | 152 |
| Phe Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln Ile Leu Leu |     |
| 20 25 30                                                        |     |
| AGT TCA GAC GCT TTC CAT AGA GGG GAT TTT GCT GCC GCT CAA AAA GGC | 200 |
| Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Ala Ala Gln Lys Gly |     |
| 35 40 45 50                                                     |     |
| TAT ATG AAT CTC TAT AAG CAA ACC AAT AAG GTG GTG TAT GCT AAA GAA | 248 |
| Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr Ala Lys Glu |     |
| 55 60 65                                                        |     |
| GCG GCC ATT TCA GCG GCG AGC TTA GGG GAT ATT AAA ACC GCT ATG CAT | 296 |
| Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala Met His |     |
| 70 75 80                                                        |     |
| TTA GCC ATG CTC TAT CAA AAA ATC ACC AAT AAT CGT AAT GAT GTT TCT | 344 |
| Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp Val Ser |     |
| 85 90 95                                                        |     |
| ATC AAT AAG ATT TTA GTG GAT GGC TAT GCG CAA ATG GGG CAG ATT GAT | 392 |
| Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln Ile Asp |     |
| 100 105 110                                                     |     |
| AAG GCG ATT GAA TTG CTG CAC AAA ATC CGT AAA GAA GAA AAG ACC ATA | 440 |
| Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys Thr Ile |     |
| 115 120 125 130                                                 |     |
| GCC ACA GAC AAT GTG TTA GGG ACT TTG TAT TTG ACT CAA AAG CGT TTG | 488 |
| Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys Arg Leu |     |
| 135 140 145                                                     |     |
| GAT AAG GCT TTC CCA TTG TTG AAT AAG TTT TAT AAC CAA GTG CAT GAT | 536 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Asp | Lys | Ala | Phe | Pro | Leu | Leu | Asn | Lys | Phe | Tyr | Asn | Gln | Val | His | Asp |      |
|     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |      |
| GAA | GAC | AGC | CTA | GAA | AAA | CTC | ATT | ACG | ATC | TAT | TTT | TTG | CAA | AAT | CGT | 584  |
| Glu | Asp | Ser | Leu | Glu | Lys | Leu | Ile | Thr | Ile | Tyr | Phe | Leu | Gln | Asn | Arg |      |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |      |
| AAA | AAA | GAG | GGC | TTG | GAT | TTG | TTG | CAA | TCT | CAT | ATA | GAC | AGG | TAT | GGT | 632  |
| Lys | Lys | Glu | Gly | Leu | Asp | Leu | Leu | Gln | Ser | His | Ile | Asp | Arg | Tyr | Gly |      |
|     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |      |
| TGC | TCA | GAG | CAA | TTG | TGC | CAA | AAA | GCG | CTC | AAC | ACT | TTC | ACG | CAA | TTT | 680  |
| Cys | Ser | Glu | Gln | Leu | Cys | Gln | Lys | Ala | Leu | Asn | Thr | Phe | Thr | Gln | Phe |      |
| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |      |
| AAC | GAG | CTT | GAT | TTG | GCT | AAA | ACG | ACT | TTT | GCT | CGT | TTG | TAT | GAA | AAA | 728  |
| Asn | Glu | Leu | Asp | Leu | Ala | Lys | Thr | Thr | Phe | Ala | Arg | Leu | Tyr | Glu | Lys |      |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |      |
| AAC | CCT | ATT | GTT | CAA | AAT | GCT | CAG | TTT | TAC | ATA | GGG | GTA | TTA | ATC | TTG | 776  |
| Asn | Pro | Ile | Val | Gln | Asn | Ala | Gln | Phe | Tyr | Ile | Gly | Val | Leu | Ile | Leu |      |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |      |
| TTA | AAA | GAG | TTT | GAT | AAG | GCC | CAG | AAA | ATC | GCA | GAA | TTA | TTC | CCT | TTT | 824  |
| Leu | Lys | Glu | Phe | Asp | Lys | Ala | Gln | Lys | Ile | Ala | Glu | Leu | Phe | Pro | Phe |      |
|     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |      |
| GAC | AGG | CGT | TTG | TTG | TTA | GAC | TTA | TAC | ACC | GCA | CAA | AAA | AAA | TTC | GAT | 872  |
| Asp | Arg | Arg | Leu | Leu | Leu | Asp | Leu | Tyr | Thr | Ala | Gln | Lys | Lys | Phe | Asp |      |
|     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |      |
| CAA | GCT | TCC | AAA | CAA | GCT | TCT | TTG | ATC | TAT | CAA | GAA | AAA | AAA | GAC | CCT | 920  |
| Gln | Ala | Ser | Lys | Gln | Ala | Ser | Leu | Ile | Tyr | Gln | Glu | Lys | Lys | Asp | Pro |      |
| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |      |
| AAA | TTC | TTA | GGA | TTA | GAG | GCC | ATT | TAT | CAT | TAT | GAA | AGC | TTG | AGT | GCG | 968  |
| Lys | Phe | Leu | Gly | Leu | Glu | Ala | Ile | Tyr | His | Tyr | Glu | Ser | Leu | Ser | Ala |      |
|     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |      |
| AAT | AAG | AAA | AAG | CTC | ACC | AAA | GAA | GAG | ATG | TTG | CCT | ATC | ATT | CAA | AAA | 1016 |
| Asn | Lys | Lys | Lys | Leu | Thr | Lys | Glu | Glu | Met | Leu | Pro | Ile | Ile | Gln | Lys |      |
|     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |      |
| TTA | GAG | CAA | GCC | ACC | AAA | GAG | CGC | CAA | GCA | TGG | CTC | GCT | AAA | ACC | AAA | 1064 |
| Leu | Glu | Gln | Ala | Thr | Lys | Glu | Arg | Gln | Ala | Trp | Leu | Ala | Lys | Thr | Lys |      |
|     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |     |      |
| GAT | AAA | GAA | GAC | GCG | CAA | GAC | GCT | TTC | TTT | TAT | AAT | TTT | TTA | GGG | TAT | 1112 |
| Asp | Lys | Glu | Asp | Ala | Gln | Asp | Ala | Phe | Phe | Tyr | Asn | Phe | Leu | Gly | Tyr |      |
|     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |      |
| TCC | TTA | ATA | GAT | TAT | GAC | ATG | GAT | ATT | AAA | AGG | GGC | ATG | GAT | TTT | GTG | 1160 |
| Ser | Leu | Ile | Asp | Tyr | Asp | Met | Asp | Ile | Lys | Arg | Gly | Met | Asp | Phe | Val |      |
| 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     | 370 |      |
| AGG | AAA | GCC | TTA | GCG | TTG | GAT | TCT | GGA | TCA | GTG | CTT | TAT | TTG | GAT | TCT | 1208 |
| Arg | Lys | Ala | Leu | Ala | Leu | Asp | Ser | Gly | Ser | Val | Leu | Tyr | Leu | Asp | Ser |      |
|     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     | 385 |     |      |

|                                          |     |     |     |     |     |     |     |     |     |     |     |             |     |     |        |      |
|------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------------|-----|-----|--------|------|
| TTA                                      | GCA | TGG | GGT | TAT | TAC | AAA | TTA | GGG | AAT | TGT | TTG | GAA         | GCT | AAA | AAA    | 1256 |
| Leu                                      | Ala | Trp | Gly | Tyr | Tyr | Lys | Leu | Gly | Asn | Cys | Leu | Glu         | Ala | Lys | Lys    |      |
|                                          |     |     | 390 |     |     |     |     | 395 |     |     |     |             | 400 |     |        |      |
|                                          |     |     |     |     |     |     |     |     |     |     |     |             |     |     |        |      |
| ATC                                      | TTT | TCT | AGC | ATC | GCT | AAA | GAG | TCT | ATC | CAA | GCC | GAA         | CCT | GAA | TTG    | 1304 |
| Ile                                      | Phe | Ser | Ser | Ile | Ala | Lys | Glu | Ser | Ile | Gln | Ala | Glu         | Pro | Glu | Leu    |      |
|                                          |     |     | 405 |     |     |     | 410 |     |     |     |     | 415         |     |     |        |      |
|                                          |     |     |     |     |     |     |     |     |     |     |     |             |     |     |        |      |
| AAA                                      | GAA | CAC | AAT | AAA | ATC | ATT | CAA | GAA | TGC | AAG | AAA | TAGGGATT'TT |     |     | AGAAAA | 1356 |
| Lys                                      | Glu | His | Asn | Lys | Ile | Ile | Gln | Glu | Cys | Lys | Lys |             |     |     |        |      |
|                                          |     |     | 420 |     |     | 425 |     |     |     |     | 430 |             |     |     |        |      |
|                                          |     |     |     |     |     |     |     |     |     |     |     |             |     |     |        |      |
| TTTACAAAAA AGCTTAGCCT TAAAAGAGGG CATGCTT |     |     |     |     |     |     |     |     |     |     |     |             |     |     | 1393   |      |

(2) INFORMATION FOR SEO ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- ```

7. SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: protein

```
(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEO ID NO:254:

Met 1	Asn	Ile	Gln	Ile 5	Lys	Lys	Arg	Phe	Leu 10	Ala	Asn	Leu	Leu	Leu 15	Phe
Ser	Leu	Phe	Cys 20	Leu	Lys	Ala	Glu	Thr 25	Leu	Ser	Glu	Asp	His 30	Gln	Ile
Leu	Leu	Ser 35	Ser	Asp	Ala	Phe	His 40	Arg	Gly	Asp	Phe	Ala 45	Ala	Ala	Gln
Lys	Gly	Tyr	Met	Asn	Leu	Tyr 55	Lys	Gln	Thr	Asn	Lys	Val	Val	Tyr	Ala
Lys 65	Glu	Ala	Ala	Ile	Ser 70	Ala	Ala	Ser	Leu	Gly 75	Asp	Ile	Lys	Thr	Ala 80
Met	His	Leu	Ala	Met 85	Leu	Tyr	Gln	Lys	Ile 90	Thr	Asn	Asn	Arg	Asn 95	Asp
Val	Ser	Ile	Asn 100	Lys	Ile	Leu	Val	Asp 105	Gly	Tyr	Ala	Gln	Met 110	Gly	Gln
Ile	Asp	Lys 115	Ala	Ile	Glu	Leu	Leu 120	His	Lys	Ile	Arg	Lys 125	Glu	Glu	Lys
Thr	Ile	Ala	Thr	Asp	Asn	Val 135	Leu	Gly	Thr	Leu	Tyr	Leu	Thr	Gln	Lys
Arg 145	Leu	Asp	Lys	Ala	Phe 150	Pro	Leu	Leu	Asn	Lys 155	Phe	Tyr	Asn	Gln	Val 160
His	Asp	Glu	Asp	Ser 165	Leu	Glu	Lys	Leu	Ile 170	Thr	Ile	Tyr	Phe	Leu 175	Gln
Asn	Arg	Lys	Lys 180	Glu	Gly	Leu	Asp	Leu 185	Leu	Gln	Ser	His	Ile 190	Asp	Arg
Tyr	Gly	Cys 195	Ser	Glu	Gln	Leu	Cys 200	Gln	Lys	Ala	Leu	Asn 205	Thr	Phe	Thr
Gln	Phe	Asn	Glu	Leu	Asp	Leu 215	Ala	Lys	Thr	Thr	Phe	Ala	Arg	Leu	Tyr
Glu 225	Lys	Asn	Pro	Ile	Val 230	Gln	Asn	Ala	Gln	Phe	Tyr	Ile	Gly	Val	Leu 240
Ile	Leu	Leu	Lys	Glu	Phe	Asp	Lys	Ala	Gln	Lys	Ile	Ala	Glu	Leu	Phe

				245					250					255			
Pro	Phe	Asp	Arg	Arg	Leu	Leu	Leu	Asp	Leu	Tyr	Thr	Ala	Gln	Lys	Lys		
			260					265					270				
Phe	Asp	Gln	Ala	Ser	Lys	Gln	Ala	Ser	Leu	Ile	Tyr	Gln	Glu	Lys	Lys		
		275					280					285					
Asp	Pro	Lys	Phe	Leu	Gly	Leu	Glu	Ala	Ile	Tyr	His	Tyr	Glu	Ser	Leu		
	290					295					300						
Ser	Ala	Asn	Lys	Lys	Lys	Leu	Thr	Lys	Glu	Glu	Met	Leu	Pro	Ile	Ile		
305					310					315					320		
Gln	Lys	Leu	Glu	Gln	Ala	Thr	Lys	Glu	Arg	Gln	Ala	Trp	Leu	Ala	Lys		
			325						330					335			
Thr	Lys	Asp	Lys	Glu	Asp	Ala	Gln	Asp	Ala	Phe	Phe	Tyr	Asn	Phe	Leu		
		340						345					350				
Gly	Tyr	Ser	Leu	Ile	Asp	Tyr	Asp	Met	Asp	Ile	Lys	Arg	Gly	Met	Asp		
		355				360					365						
Phe	Val	Arg	Lys	Ala	Leu	Ala	Leu	Asp	Ser	Gly	Ser	Val	Leu	Tyr	Leu		
	370				375					380							
Asp	Ser	Leu	Ala	Trp	Gly	Tyr	Tyr	Lys	Leu	Gly	Asn	Cys	Leu	Glu	Ala		
385					390					395					400		
Lys	Lys	Ile	Phe	Ser	Ile	Ala	Lys	Glu	Ser	Ile	Gln	Ala	Glu	Pro			
			405					410					415				
Glu	Leu	Lys	Glu	His	Asn	Lys	Ile	Ile	Gln	Glu	Cys	Lys	Lys				
			420					425					430				

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1037
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TTACCCTAAA ACGCTATTTT TAAATAATC CATTAAATA AAGCGAGGA ATG AAA	56
Met Lys	
1	
AGA TTT GTT TTG TTT TTA TTG TTC ATG TGC GTT TGC GTT CAA GCT TAC	104
Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln Ala Tyr	
5 10 15	
GCC GAG CAA GAT TAC TTT TTT AGG GAT TTT AAA TCT AGA GAT TTG CCC	152
Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp Leu Pro	
20 25 30	
CAA AAA CTC CAT CTT GAT AAA AAG CTC TCC CAA ACA ATA CAG CCA TGC	200
Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln Pro Cys	
35 40 45 50	

ATG CAA CTT AAC GCA TCA AAA CAC TAC ACT TCT ACC GGG GTT AGA GAG	248
Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val Arg Glu	
55 60 65	
CCT GAT AAA TGC ACA AAG AGT TTT AAA AAA TCC GCT CTC ATG TCC TAT	296
Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met Ser Tyr	
70 75 80	
GAC TTA GCG CTA GGT TAT TTG GTG AGT AAG AAT AAG CAA TAC GGC TTA	344
Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr Gly Leu	
85 90 95	
AAG GCT ATA GAA ATT TTA AAC GCT TGG GCT AAA GAG CTT CAA AGC GTG	392
Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln Ser Val	
100 105 110	
GAT ACT TAT CAG AGC GAG GAT AAT ATC AAT TTT TAC ATG CCT TAT ATG	440
Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro Tyr Met	
115 120 125 130	
AAC ATG GCT TAT TGG TTT GTC AAA AAG GCG TTT CCT AGC CCA GAA TAT	488
Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro Glu Tyr	
135 140 145	
GAA GAT TTC ATT AAG CGG ATG CGC CAG TAT TCT CAA TCA GCT CTT AAC	536
Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala Leu Asn	
150 155 160	
ACT AAC CAT GGG GCG TGG GGC ATT CTT TTT GAT GTG AGT TCT GCG CTA	584
Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser Ala Leu	
165 170 175	
GCG TTA GAC GAT AAT GCC CTT TTG CAC AAT AGC GCT AAT CGG TGG CAG	632
Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg Trp Gln	
180 185 190	
GAG TGG GTG TTT AAA GCC ATA GAT GAG AAT GGG GTT ATT GNT AGC GCG	680
Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Xaa Ser Ala	
195 200 205 210	
ATC ACT AGG AGC GAT ACG AGC GAT TAT CAT GGC GGC CCT ACA AAG GGC	728
Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr Lys Gly	
215 220 225	
ATT AAG GGG ATA GCT TAT ACC AAT TTC GCG CTT CTT GCG CTA ACC ATA	776
Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu Thr Ile	
230 235 240	
TCA GGC GAA TTG CTT TTT GAG AAC GGG TAT GAT TTG TGG GGT AGT GGA	824
Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly Ser Gly	
245 250 255	
GCT GGG AAA AGG CTC TCT GTG GCG TAT AAC AAA GTT GCA ACA TGG ATT	872
Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr Trp Ile	
260 265 270	
TTA AAC CCT GAA ACT TTC CCT TAT TTC CAG CCT AAC CTT ATC GGG GTG	920
Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile Gly Val	

[illegible]

(2) INFORMATION FOR SEO ID NO:256:

- (A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (v) FRAGMENT TYPE: internal

Met 1	Lys	Arg	Phe	Val 5	Leu	Phe	Leu	Leu	Phe 10	Met	Cys	Val	Cys	Val 15	Gln
Ala	Tyr	Ala	Glu	Gln	Asp	Tyr	Phe	Phe	Arg	Asp	Phe	Lys	Ser	Arg	Asp
		20						25					30		
Leu	Pro	Gln	Lys	Leu	His	Leu	Asp	Lys	Lys	Leu	Ser	Gln	Thr	Ile	Gln
		35					40					45			
Pro	Cys	Met	Gln	Leu	Asn	Ala	Ser	Lys	His	Tyr	Thr	Ser	Thr	Gly	Val
	50					55					60				
Arg	Glu	Pro	Asp	Lys	Cys	Thr	Lys	Ser	Phe	Lys	Lys	Ser	Ala	Leu	Met
65					70					75				80	
Ser	Tyr	Asp	Leu	Ala	Leu	Gly	Tyr	Leu	Val	Ser	Lys	Asn	Lys	Gln	Tyr
				85					90					95	
Gly	Leu	Lys	Ala	Ile	Glu	Ile	Leu	Asn	Ala	Trp	Ala	Lys	Glu	Leu	Gln
			100					105					110		
Ser	Val	Asp	Thr	Tyr	Gln	Ser	Glu	Asp	Asn	Ile	Asn	Phe	Tyr	Met	Pro
		115					120					125			
Tyr	Met	Asn	Met	Ala	Tyr	Trp	Phe	Val	Lys	Lys	Ala	Phe	Pro	Ser	Pro
	130					135					140				
Glu	Tyr	Glu	Asp	Phe	Ile	Lys	Arg	Met	Arg	Gln	Tyr	Ser	Gln	Ser	Ala
145					150					155					160
Leu	Asn	Thr	Asn	His	Gly	Ala	Trp	Gly	Ile	Leu	Phe	Asp	Val	Ser	Ser
				165					170					175	
Ala	Leu	Ala	Leu	Asp	Asp	Asn	Ala	Leu	Leu	His	Asn	Ser	Ala	Asn	Arg
			180					185					190		
Trp	Gln	Glu	Trp	Val	Phe	Lys	Ala	Ile	Asp	Glu	Asn	Gly	Val	Ile	Xaa
		195					200					205			
Ser	Ala	Ile	Thr	Arg	Ser	Asp	Thr	Ser	Asp	Tyr	His	Gly	Gly	Pro	Thr
	210					215					220				
Lys	Gly	Ile	Lys	Gly	Ile	Ala	Tyr	Thr	Asn	Phe	Ala	Leu	Leu	Ala	Leu

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(A) NAME/KEY: Coding Sequence

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

336

373

(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(v) FRAGMENT TYPE: internal
```

Val 1	Asn	Phe	Leu	Lys 5	Lys	Pro	Lys	Tyr	Tyr 10	Lys	Phe	Ile	Glu	Gly 15	Ala
Asn	Tyr	Leu	Ser 20	Leu	Gly	Leu	Ser	Met 25	Val	Val	Ala	Ile	Leu 30	Met	Gly
Val	Ala	Ile 35	Gly	Tyr	Gly	Leu	Lys 40	Lys	Leu	Thr	His	Ile 45	Ser	Trp	Leu
Phe	Trp 50	Leu	Gly	Val	Ile	Trp 55	Gly	Val	Leu	Ala	Ser 60	Phe	Leu	Asn	Val
Tyr 65	Lys	Ala	Tyr	Lys	Asn 70	Met	Gln	Lys	Asp 75	Tyr	Glu	Glu	Leu	Ala	Lys 80
Asp	Pro	Lys	Tyr	Thr 85	Gln	Asn	Lys	Thr	Lys 90						

(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION:

TTGGTTGGTT	GT	TTTTATCA	TAGAGTGTA	TTTAAAATA	GGATCATTTG	ATG	TTA	56								
						Met	Leu									
						1										
AAC	AAG	TTT	AAA	AAA	ATC	GTT	GGC	GTT	AGT	GTG	TTA	GTG	GGC	TGT	TTA	104
Asn	Lys	Phe	Lys	Lys	Ile	Val	Gly	Val	Ser	Val	Leu	Val	Gly	Cys	Leu	
		5					10					15				
GGG	GTT	TTG	CAA	GCT	AAA	AAC	AGC	TTA	TTT	GTC	TTA	CCT	TAT	GAG	CAA	152

Gly 20	Val	Leu	Gln	Ala	Lys	Asn 25	Ser	Leu	Phe	Val	Leu 30	Pro	Tyr	Glu	Gln	
AAA Lys 35	GAC Asp	GCT Ala	CTC Leu	AAT Asn	TCT Ser 40	TTA Leu	GTT Val	TCT Ser	GGC Gly 45	ATT Ile	AGT Ser	AAC Asn	GCC Ala	AGA Arg	GAG Glu 50	200
AGC Ser	GTG Val	AAA Lys	ATC Ile	GCT Ala 55	ATC Ile	TAT Tyr	AGT Ser	TTC Phe	ACG Thr 60	CAC His	AGA Arg	GAT Asp	ATT Ile	GCA Ala 65	AGA Arg	248
GCG Ala	ATT Ile	AAA Lys	AGC Ser 70	GTA Val	GCG Ala	AGT Ser	AGG Arg	GGG Gly 75	ATT Ile	AAG Lys	GTG Val	CAA Gln	ATC Ile 80	ATT Ile	TAT Tyr	296
GAT Asp	TAT Tyr	GAA Glu 85	AGC Ser	AAT Asn	CAT His	CAT His	AAC Asn 90	AAG Lys	CAA Gln	TCC Ser	ACT Thr	ATT Ile 95	GGC Gly	TAT Tyr	CTG Leu	344
GAC Asp	AAA Lys 100	TAC Tyr	CCT Pro	AAC Asn	ACG Thr	AAA Lys 105	GTG Val	TGC Cys	TTA Leu	TTG Leu	AAA Lys 110	GGG Gly	CTT Leu	AAG Lys	GCT Ala	392
AAA Lys 115	AAC Asn	GGG Gly	AAT Asn	TAT Tyr	TAC Tyr 120	GGC Gly	ATC Ile	ATG Met	CAC His	CAA Gln 125	AAA Lys	GTA Val	GCG Ala	ATC Ile	ATT Ile 130	440
GAT Asp	GAT Asp	AAG Lys	ATC Ile	GTG Val 135	TTT Phe	TTA Leu	GGC Gly	TCA Ser	GCG Ala 140	AAT Asn	TGG Trp	AGC Ser	AAA Lys	AAC Asn	GCT Ala	488
TTT Phe	GAA Glu	AAC Asn	AAT Asn 150	TAT Tyr	GAA Glu	GTG Val	CTT Leu	TTA Leu 155	AAA Lys	ACC Thr	GAT Asp	GAC Asp	ACA Thr 160	GAA Glu	ACG Thr	536
ATC Ile	CTC Leu	AAA Lys 165	GCC Ala	AAG Lys	AGC Ser	TAT Tyr	TAC Tyr 170	CAA Gln	AAG Lys	ATG Met	TTA Leu	GGG Gly 175	AGT Ser	TGC Cys	GTT Val	584
GGG Gly	TTT Phe 180	TAAAAGCCCT			TTAGAAGTGG			TAATTATACC			CCACATAAAA			GGCAAAGACC CT		642

A

643

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:260:

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}, \quad \frac{d}{dt} \left(\frac{\partial L}{\partial \dot{y}} \right) = \frac{\partial L}{\partial y}, \quad \frac{d}{dt} \left(\frac{\partial L}{\partial \dot{z}} \right) = \frac{\partial L}{\partial z}$$

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Genomic DNA

(A) NAME/KEY: Coding Sequence

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

339

35	40	45	50	
AGT TTT GGG CAG GGT GAG CGC CCC TTG TTT GCG GAC AGG AGG GCG				248
Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg Arg Ala	55	60	65	
ATG AAG CCT AAC GAT TTG ATC ACA ATC ATT GTT TCT GAA AAA GCG AGC				296
Met Lys Pro Asn Asp Leu Ile Thr Ile Val Ser Glu Lys Ala Ser	70	75	80	
GCG AAT TAT TCC AGC TCT AAA GAT TAT AAA AGC GCT TCA GGG GGT AAT				344
Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly Gly Asn	85	90	95	
TCC ACG CCC CCA AGA CTC ACT TAT AAC GGG CTA GAT GAA AGA AAG AAA				392
Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg Lys Lys	100	105	110	
AAA GAA GCG GAG TAT TTA GAC GAT AAG AAT AAT TAC AAT TTC ACC AAA				440
Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe Thr Lys	115	120	125	130
TCC AGC AAT AAC ACG AAT TTT AAA GGC GGT GGC TCG CAA AAA AAG AGC				488
Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys Lys Ser	135	140	145	
GAA GAT TTA GAG ATT GTG TTG AGC GCT CGA ATC ATT AAG GTG CTA GAA				536
Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val Leu Glu	150	155	160	
AAC GGG AAT TAT TTC ATC TAT GGG AAT AAG GAA GTG CTA GTG GAT GGG				584
Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val Asp Gly	165	170	175	
GAA AAG CAA ATC CTT AAG GTG AGT GGG GTG ATC CGC CCT TAT GAT ATT				632
Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr Asp Ile	180	185	190	
GAA AGG AAT AAC ACC ATC CAA TCC AAG TTT TTA GCC GAC GCT AAG ATT				680
Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala Lys Ile	195	200	205	210
GAA TAC ACG AAT TTA GGG CAT TTG AGC GAT TCC AAT AAG AAG AAA TTC				728
Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys Lys Phe	215	220	225	
GCT GCT GAT GCG ATG GAA ACC CAA ATG CCT TAT TAAAAAGAGC AAAGCCTAGC				781
Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr	230	235		
ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGT				814

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met	Lys	Lys	Ala	Leu	Tyr	Leu	Gly	Ala	Val	Ala	Phe	Ser	Val	Ala	Phe
1				5					10					15	
Ser	Met	Ala	Ser	Ala	Asn	Glu	Pro	Lys	Ile	Asp	Phe	Asn	Pro	Pro	Asn
		20						25					30		
Tyr	Val	Glu	Glu	Thr	Pro	Ser	Lys	Glu	Phe	Ile	Pro	Glu	Leu	Asn	Lys
		35					40					45			
Leu	Gly	Ser	Leu	Phe	Gly	Gln	Gly	Glu	Arg	Pro	Leu	Phe	Ala	Asp	Arg
	50					55					60				
Arg	Ala	Met	Lys	Pro	Asn	Asp	Leu	Ile	Thr	Ile	Ile	Val	Ser	Glu	Lys
65					70					75				80	
Ala	Ser	Ala	Asn	Tyr	Ser	Ser	Ser	Lys	Asp	Tyr	Lys	Ser	Ala	Ser	Gly
			85						90					95	
Gly	Asn	Ser	Thr	Pro	Pro	Arg	Leu	Thr	Tyr	Asn	Gly	Leu	Asp	Glu	Arg
			100						105				110		
Lys	Lys	Lys	Glu	Ala	Glu	Tyr	Leu	Asp	Asp	Lys	Asn	Asn	Tyr	Asn	Phe
		115					120					125			
Thr	Lys	Ser	Ser	Asn	Asn	Thr	Asn	Phe	Lys	Gly	Gly	Gly	Ser	Gln	Lys
	130					135					140				
Lys	Ser	Glu	Asp	Leu	Glu	Ile	Val	Leu	Ser	Ala	Arg	Ile	Ile	Lys	Val
145					150					155				160	
Leu	Glu	Asn	Gly	Asn	Tyr	Phe	Ile	Tyr	Gly	Asn	Lys	Glu	Val	Leu	Val
			165						170					175	
Asp	Gly	Glu	Lys	Gln	Ile	Leu	Lys	Val	Ser	Gly	Val	Ile	Arg	Pro	Tyr
			180				185					190			
Asp	Ile	Glu	Arg	Asn	Asn	Thr	Ile	Gln	Ser	Lys	Phe	Leu	Ala	Asp	Ala
		195				200						205			
Lys	Ile	Glu	Tyr	Thr	Asn	Leu	Gly	His	Leu	Ser	Asp	Ser	Asn	Lys	Lys
	210					215					220				
Lys	Phe	Ala	Ala	Asp	Ala	Met	Glu	Thr	Gln	Met	Pro	Tyr			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...797
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TTGGGTAAGA TTAGGAATTG ATTTTAAAGA AAAAGAAAGA AAGGAATTTA ATG AAA

56

ACC AAA GAG TTA AGC AAA AAA CAC ATG GAA CAT TAT GAA AAA GTT TCT 776
 Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys Val Ser
 230 235 240

AGT GAA ATG AAA AAA CGA AAG TAGTTTTTAA GAAACGAAAA GCTTAAAAAT CATT 831
 Ser Glu Met Lys Lys Arg Lys
 245

GAGAGCTATT TTTAAAAAA 850

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Lys Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser
 1 5 10 15
 Gly Ala Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln
 20 25 30
 His Asn Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile
 35 40 45
 Lys Gly Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu
 50 55 60
 Pro Lys Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu
 65 70 75 80
 Phe Glu Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys
 85 90 95
 Gly Tyr Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp
 100 105 110
 Ile Lys Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala
 115 120 125
 Ile Leu Glu Asp Ile Val Glu Ser Asp Ala Leu Ser Glu Glu Lys
 130 135 140
 Val Ile Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro
 145 150 155 160
 Lys Ser Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile
 165 170 175
 Lys Ala Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly
 180 185 190
 Phe Val Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp
 195 200 205
 Gln Ala Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val
 210 215 220
 His Ile Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys
 225 230 235 240
 Val Ser Ser Glu Met Lys Lys Arg Lys
 245

(2) INFORMATION FOR SEQ ID NO:265:

(The following information was obtained from the records of the Federal Bureau of Investigation, Department of Justice.)

- ```
(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:
```

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...788  
(D) OTHER INFORMATION:

|                                                                                 |                  |                   |            |                   |                   |                  |                  |                   |                  |                   |                  |                  |                  |                   |                   |     |
|---------------------------------------------------------------------------------|------------------|-------------------|------------|-------------------|-------------------|------------------|------------------|-------------------|------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|-----|
| TACAAATAGG TATAATCACC AATTCCAATC ATT'TAATCAA AGGGAGTTCT ATG AAA<br>Met Lys<br>1 |                  |                   |            |                   |                   |                  |                  |                   |                  |                   |                  |                  |                  |                   | 56                |     |
| AAT<br>Asn                                                                      | ACT<br>Thr       | TTC<br>Phe<br>5   | AAA<br>Lys | GCG<br>Ala        | TTT<br>Phe        | GCC<br>Ala       | TTT<br>Phe<br>10 | TTA<br>Leu        | ATT<br>Ile       | GTA<br>Val        | TTT<br>Phe<br>15 | TTT<br>Phe       | TCA<br>Ser       | AGC<br>Ser        | GCT<br>Ala        | 104 |
| TTA<br>Leu<br>20                                                                | TTA<br>Leu       | GCG<br>Ala        | CAG<br>Gln | GAT<br>Asp        | TTA<br>Leu        | AAA<br>Lys<br>25 | ATC<br>Ile       | GCT<br>Ala        | GCT<br>Ala       | GCT<br>Ala<br>30  | GCT<br>Ala       | AAT<br>Asn       | CTT<br>Leu       | ACA<br>Thr        | CGC<br>Arg        | 152 |
| GCT<br>Ala<br>35                                                                | TTA<br>Leu       | AAA<br>Lys        | GCC<br>Ala | CTT<br>Leu<br>40  | GTT<br>Val        | AAA<br>Lys       | GAA<br>Glu       | TTT<br>Phe        | CAA<br>Gln       | AAA<br>Lys<br>45  | GAA<br>Glu       | CAC<br>His       | CCC<br>Pro       | AAA<br>Lys<br>50  | GAC<br>Asp        | 200 |
| ACT<br>Thr                                                                      | GTT<br>Val       | AAT<br>Asn        | ATT<br>Ile | AGC<br>Ser<br>55  | TTT<br>Phe        | AAT<br>Asn       | TCT<br>Ser       | TCA<br>Ser        | GGC<br>Gly<br>60 | AAA<br>Lys        | CTC<br>Leu       | TAC<br>Tyr       | GCT<br>Ala<br>65 | CAA<br>Gln        | ATC<br>Ile        | 248 |
| ATT<br>Ile                                                                      | CAA<br>Gln       | AAC<br>Asn<br>70  | GCC<br>Ala | CCT<br>Pro        | TTT<br>Phe        | GAT<br>Asp       | TTA<br>Leu<br>75 | TTC<br>Phe        | ATT<br>Ile       | TCA<br>Ser        | GCA<br>Ala       | GAT<br>Asp<br>80 | ATG<br>Met       | ATT<br>Ile        | AGA<br>Arg        | 296 |
| CCT<br>Pro                                                                      | AAA<br>Lys<br>85 | AAG<br>Lys        | CTT<br>Leu | TAT<br>Tyr        | GAT<br>Asp        | AAA<br>Lys       | AAA<br>Lys<br>90 | ATA<br>Ile        | ACC<br>Thr       | CCT<br>Pro        | TTT<br>Phe<br>95 | AAA<br>Lys       | GAA<br>Glu       | GAA<br>Glu        | GTC<br>Val        | 344 |
| TAT<br>Tyr<br>100                                                               | GCT<br>Ala       | AAA<br>Lys        | GGC<br>Gly | GTG<br>Val        | TTG<br>Leu<br>105 | GTT<br>Val       | TTA<br>Leu       | TGG<br>Trp        | AGT<br>Ser       | GAA<br>Glu<br>110 | GAT<br>Asp       | CTA<br>Leu       | AAA<br>Lys       | ATG<br>Met        | GAT<br>Asp        | 392 |
| TCT<br>Ser<br>115                                                               | TTA<br>Leu       | GAA<br>Glu        | ATT<br>Ile | CTT<br>Leu<br>120 | AAA<br>Lys        | AAT<br>Asn       | CCT<br>Pro       | AAA<br>Lys        | ATC<br>Ile       | AAG<br>Lys<br>125 | CGT<br>Arg       | ATC<br>Ile       | GCT<br>Ala       | ATG<br>Met        | GCT<br>Ala<br>130 | 440 |
| AAT<br>Asn                                                                      | CCT<br>Pro       | AAA<br>Lys<br>135 | CTA<br>Leu | GCC<br>Ala        | CCT<br>Pro        | TAT<br>Tyr       | GGA<br>Gly       | AAA<br>Lys<br>140 | GCC<br>Ala       | AGC<br>Ser        | ATG<br>Met       | GAA<br>Glu       | GTC<br>Val       | TTA<br>Leu<br>145 | GAG<br>Glu        | 488 |
| AAT                                                                             | TTA              | AAA               | CTC        | ACT               | CCC               | AGT              | CTT              | AAA               | TCT              | AAA               | ATC              | GTT              | TAT              | GGC               | GCT               | 536 |

[illegible]

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

|           |           |            |            |           |           |           |            |            |           |           |           |            |            |           |           |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Met<br>1  | Lys       | Asn        | Thr        | Phe<br>5  | Lys       | Ala       | Phe        | Ala        | Phe<br>10 | Leu       | Ile       | Val        | Phe        | Phe<br>15 | Ser       |
| Ser       | Ala       | Leu<br>20  | Leu        | Ala       | Gln       | Asp       | Leu        | Lys<br>25  | Ile       | Ala       | Ala       | Ala<br>30  | Ala        | Asn       | Leu       |
| Thr       | Arg       | Ala<br>35  | Leu        | Lys       | Ala       | Leu       | Val<br>40  | Lys        | Glu       | Phe       | Gln       | Lys<br>45  | Glu        | His       | Pro       |
| Lys       | Asp<br>50 | Thr        | Val        | Asn       | Ile       | Ser<br>55 | Phe        | Asn        | Ser       | Ser       | Gly<br>60 | Lys        | Leu        | Tyr       | Ala       |
| Gln<br>65 | Ile       | Ile        | Gln        | Asn       | Ala<br>70 | Pro       | Phe        | Asp        | Leu       | Phe<br>75 | Ile       | Ser        | Ala        | Asp       | Met<br>80 |
| Ile       | Arg       | Pro        | Lys        | Lys<br>85 | Leu       | Tyr       | Asp        | Lys        | Lys<br>90 | Ile       | Thr       | Pro        | Phe        | Lys<br>95 | Glu       |
| Glu       | Val       | Tyr        | Ala<br>100 | Lys       | Gly       | Val       | Leu        | Val<br>105 | Leu       | Trp       | Ser       | Glu        | Asp<br>110 | Leu       | Lys       |
| Met       | Asp       | Ser<br>115 | Leu        | Glu       | Ile       | Leu       | Lys<br>120 | Asn        | Pro       | Lys       | Ile       | Lys<br>125 | Arg        | Ile       | Ala       |

Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu Val  
130 135 140  
Leu Glu Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr  
145 150 155 160  
Gly Ala Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala  
165 170 175  
Gln Ile Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn  
180 185 190  
Leu Ser Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln  
195 200 205  
Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val  
210 215 220  
Phe Lys Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu  
225 230 235 240  
Tyr Gly Tyr Ile Val Asp  
245

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1406
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

|                                                                 |           |           |           |            |         |     |
|-----------------------------------------------------------------|-----------|-----------|-----------|------------|---------|-----|
| AGCCATTTTA                                                      | TGGCATTAA | AAAAGTTAA | AAATGTTAA | AAGGAATTTT | ATG TTA | 56  |
|                                                                 |           |           |           |            | Met Leu |     |
|                                                                 |           |           |           |            | 1       |     |
| AGG CTT TTG ATA GGA CTT CTT CTA ATG AGT TTT ATA AGC TTG CAA TCA |           |           |           |            |         | 104 |
| Arg Leu Leu Ile Gly Leu Leu Leu Met Ser Phe Ile Ser Leu Gln Ser |           |           |           |            |         |     |
| 5                                                               |           |           | 10        |            | 15      |     |
| GCC TCT TGG CAA GAA CCC TTA AGA GTG AGT ATA GAA TTT GTG GAT TTG |           |           |           |            |         | 152 |
| Ala Ser Trp Gln Glu Pro Leu Arg Val Ser Ile Glu Phe Val Asp Leu |           |           |           |            |         |     |
| 20                                                              |           | 25        |           | 30         |         |     |
| CCT AAA AAA ATC ATT CGT TTT CCG GCT CAT GAT TTG CAA GTG GGG GAG |           |           |           |            |         | 200 |
| Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val Gly Glu |           |           |           |            |         |     |
| 35                                                              |           | 40        |           | 45         | 50      |     |
| TTT GGT TTT GTC GTT ACT AAA CTT TCA GAT TAT GAA ATC GTT AAT TCT |           |           |           |            |         | 248 |
| Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val Asn Ser |           |           |           |            |         |     |
|                                                                 | 55        |           | 60        |            | 65      |     |
| GAA GTG GTC ATT ATT GCC GTT GAA AAT GGC GTC GCA ACG GCT AAA TTC |           |           |           |            |         | 296 |
| Glu Val Val Ile Ile Ala Val Glu Asn Gly Val Ala Thr Ala Lys Phe |           |           |           |            |         |     |















TAAACCTTG TATGATCGCT ATTTGTTAAA AGACGCTAAC AACAAACCTA TTGAATTGCC 540  
CCAACAC ATG TTT ATG AGC ATT GCG ATG TTT TTA GCA CAA AAC GAA CAA 589  
Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln  
1 5 10  
GAA CCC AAT AAA ATC GCC TTA GAA TTT TAT GAA GTT TTG AGC AAG TTT 637  
Glu Pro Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe  
15 20 25 30  
GAA GCG ATG TGC GCG ACC CCC ACT CTA GCG AAC GCC CGC ACC ACC AAA 685  
Glu Ala Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys  
35 40 45  
CAC CAG CTC AGC TCA TGC TAT ATT GGC AGC ACG CCG GAT AAT ATT GAG 733  
His Gln Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu  
50 55 60  
GGG ATT TTT GAC AGC TAT AAG GAA ATG GCG CTG TTG TCC AAA TAC GGC 781  
Gly Ile Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly  
65 70 75  
GGA GGG ATT GGC TGG GAT TTT TCT TTG GTG CGC TCT ATT GGG AGT TAT 829  
Gly Gly Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr  
80 85 90  
ATT GAT GGG CAT AAA AAT GCG AGC GCT GGC ACG ATC CCT TTT TTA AAA 877  
Ile Asp Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys  
95 100 105 110  
ATC GCT AAC GAT GTG GCG ATT GCG GTG GAT CAA TTA GGC ACA CGA AAG 925  
Ile Ala Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys  
115 120 125  
GGC GCG ATT GCG GTG TAT TTG GAA ATT TGG CAC ATT GAT GTG ATG GAG 973  
Gly Ala Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu  
130 135 140  
TTC ATT GAT TTA AGG AAA AAT AGC GGC GAT GAA AGG CGA AGA GCG CAT 1021  
Phe Ile Asp Leu Arg Lys Asn Ser Gly Asp Glu Arg Arg Arg Ala His  
145 150 155  
GAT TTA TTC CCG GCT CTT TGG GTG TGC GAT TTG TTT TTG AAA AGG GTT 1069  
Asp Leu Phe Pro Ala Leu Trp Val Cys Asp Leu Phe Leu Lys Arg Val  
160 165 170  
TTA GAA GAT GCG ATG TGG ACT TTA TTT GAC CCT TAT GAG TGT AAG GAT 1117  
Leu Glu Asp Ala Met Trp Thr Leu Phe Asp Pro Tyr Glu Cys Lys Asp  
175 180 185 190  
TTG ACT GAG CTT TAT GGG CAG GAT TTT GAA AAA CGC TAT TTA GAG TAT 1165  
Leu Thr Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr  
195 200 205  
GAA AAA GAT CCC AAG ATC ATT AAG GAA TAC ATT AAC GCT AAA GAT TTA 1213  
Glu Lys Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu  
210 215 220  
TGG AAA AAA ATC TTA ATG AAT TAT TTT GAA GCC GGT TTG CCT TTC TTA 1261

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Trp | Lys | Lys | Ile | Leu | Met | Asn | Tyr | Phe | Glu | Ala | Gly | Leu | Pro | Phe | Leu |      |
|     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |      |
| GCC | TTT | AAA | GAT | AAC | GCC | AAT | CGG | TGC | AAC | CCA | AAC | GCT | CAT | GCA | GGA | 1309 |
| Ala | Phe | Lys | Asp | Asn | Ala | Asn | Arg | Cys | Asn | Pro | Asn | Ala | His | Ala | Gly |      |
|     | 240 |     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     |      |
| ATC | ATT | CGA | TCC | AGC | AAT | CTA | TGC | ACG | GAG | ATT | TTC | CAA | AAT | ACC | GCG | 1357 |
| Ile | Ile | Arg | Ser | Ser | Asn | Leu | Cys | Thr | Glu | Ile | Phe | Gln | Asn | Thr | Ala |      |
| 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |      |
| CCT | AAC | CAC | TAC | TAC | ATG | CAA | ATA | GAA | TAC | ACC | GAC | GGC | ACC | ATA | GAG | 1405 |
| Pro | Asn | His | Tyr | Tyr | Met | Gln | Ile | Glu | Tyr | Thr | Asp | Gly | Thr | Ile | Glu |      |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |      |
| TTT | TTT | GAA | GAA | AAA | GAG | TTG | GTA | ACG | ACA | GAT | AGT | AAT | ATC | ACT | AAA | 1453 |
| Phe | Phe | Glu | Glu | Lys | Glu | Leu | Val | Thr | Thr | Asp | Ser | Asn | Ile | Thr | Lys |      |
|     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |      |
| TGC | GCT | AAC | AAG | CTC | ACT | AGC | ACC | GAT | ATT | CTA | AAG | GGC | AAG | CCA | ATC | 1501 |
| Cys | Ala | Asn | Lys | Leu | Thr | Ser | Thr | Asp | Ile | Leu | Lys | Gly | Lys | Pro | Ile |      |
|     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |      |
| TAT | ATC | GCT | ACT | AAA | GTC | GCT | AAA | GAC | GGG | CAA | ACG | GCG | GTG | TGC | AAT | 1549 |
| Tyr | Ile | Ala | Thr | Lys | Val | Ala | Lys | Asp | Gly | Gln | Thr | Ala | Val | Cys | Asn |      |
|     | 320 |     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     |      |
| CTG | GCG | AGC | ATC | AAT | TTA | AGC | AAA | ATC | AAC | ACT | GAA | GAA | GAC | ATT | AAA | 1597 |
| Leu | Ala | Ser | Ile | Asn | Leu | Ser | Lys | Ile | Asn | Thr | Glu | Glu | Asp | Ile | Lys |      |
| 335 |     |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |      |
| AGG | GTT | GTG | CCG | ATC | ATG | GTC | AGG | CTT | TTA | GAC | AAT | GTG | ATT | GAT | TTG | 1645 |
| Arg | Val | Val | Pro | Ile | Met | Val | Arg | Leu | Leu | Asp | Asn | Val | Ile | Asp | Leu |      |
|     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |      |
| AAT | TTC | TAC | CCT | AAC | CGC | AAA | GTC | AAA | GCC | ACT | AAT | TTA | CAA | AAT | AGG | 1693 |
| Asn | Phe | Tyr | Pro | Asn | Arg | Lys | Val | Lys | Ala | Thr | Asn | Leu | Gln | Asn | Arg |      |
|     |     |     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |      |
| GCC | ATA | GGG | TTA | GGG | GTT | ATG | GGT | GAA | GCG | CAA | ATG | CTC | GCA | GAA | CAC | 1741 |
| Ala | Ile | Gly | Leu | Gly | Val | Met | Gly | Glu | Ala | Gln | Met | Leu | Ala | Glu | His |      |
|     |     | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |      |
| CAA | ATC | GCT | TGG | GGG | TCT | AAA | GAG | CAT | TTA | GAA | AAA | ATT | GAC | GCT | TTA | 1789 |
| Gln | Ile | Ala | Trp | Gly | Ser | Lys | Glu | His | Leu | Glu | Lys | Ile | Asp | Ala | Leu |      |
|     | 400 |     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |      |
| ATG | GAG | CAA | ATC | AGC | TAC | CAT | GCG | ATT | GAC | ACG | AGC | GCG | AAT | TTA | GCG | 1837 |
| Met | Glu | Gln | Ile | Ser | Tyr | His | Ala | Ile | Asp | Thr | Ser | Ala | Asn | Leu | Ala |      |
| 415 |     |     |     |     | 420 |     |     |     |     | 425 |     |     |     | 430 |     |      |
| AAA | GAA | AAA | GGG | GTT | TAT | AAG | GAT | TTT | GAA | AAT | TCA | GAA | TGG | AGT | AAG | 1885 |
| Lys | Glu | Lys | Gly | Val | Tyr | Lys | Asp | Phe | Glu | Asn | Ser | Glu | Trp | Ser | Lys |      |
|     |     |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |      |
| GGG | ATT | TTC | CCC | ATT | GAT | AAA | GCC | AAT | AAT | GAA | GCC | TTA | AAG | CTC | ACC | 1933 |
| Gly | Ile | Phe | Pro | Ile | Asp | Lys | Ala | Asn | Asn | Glu | Ala | Leu | Lys | Leu | Thr |      |
|     |     |     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |      |



|                                                                   |      |
|-------------------------------------------------------------------|------|
| GAA AAA GGG CTT TTT AAT CAC GCT TGC GAT TGG CAA GGT TTG AGG GAA   | 1981 |
| Glu Lys Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu   |      |
| 465 470 475                                                       |      |
| AAA GTC AAA GCC AAT GGC ATG CGT AAT GGC TAT TTA ATG GCG ATC GCT   | 2029 |
| Lys Val Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala   |      |
| 480 485 490                                                       |      |
| CCC ACA AGC TCC ATT TCT ATT TTA GTA GGC ACA ACC CAA ACG ATT GAA   | 2077 |
| Pro Thr Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu   |      |
| 495 500 505 510                                                   |      |
| CCC ATT TAT AAG AAA AAA TGG TTT GAA GAA AAT TTG AGC GGG CTT ATT   | 2125 |
| Pro Ile Tyr Lys Lys Lys Trp Phe Glu Asn Leu Ser Gly Leu Ile       |      |
| 515 520 525                                                       |      |
| CCT GTT GTG GTG CCT AAT TTG AAT GTA GAA ACC TGG AAT TTT TAC ACA   | 2173 |
| Pro Val Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr   |      |
| 530 535 540                                                       |      |
| TCA GCC TAT GAT ATT GAC GCT AAA GAT TTG ATT AAA GCA GCG GCC GTG   | 2221 |
| Ser Ala Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val   |      |
| 545 550 555                                                       |      |
| CGC CAA AAG TGG ATT GAT CAA GGC CAA AGC CTT AAT GTG TTT TTA CGC   | 2269 |
| Arg Gln Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg   |      |
| 560 565 570                                                       |      |
| ATA GAA AAC GCC AGC GGT AAA ACC TTG CAT GAC ATC TAC ACG CTC GCT   | 2317 |
| Ile Glu Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala   |      |
| 575 580 585 590                                                   |      |
| TGG AAA TTA GGA CTC AAA TCC ACT TAT TAT TTG CGC AGC GAA AGC CCT   | 2365 |
| Trp Lys Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro   |      |
| 595 600 605                                                       |      |
| AGC ATA GAT GAA AAA AGC GTG TTG GAT CGA TCG GTG GAG TGT TTT AAT   | 2413 |
| Ser Ile Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn   |      |
| 610 615 620                                                       |      |
| TGC CAA TAATATAAGC TTAAATAAGC TAATCTTTGC TAAAATGAGA TTTAAAATTA TT | 2471 |
| Cys Gln                                                           |      |

TA 2473

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Met | Ser | Ile | Ala | Met | Phe | Leu | Ala | Gln | Asn | Glu | Gln | Glu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Lys | Ile | Ala | Leu | Glu | Phe | Tyr | Glu | Val | Leu | Ser | Lys | Phe | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Cys | Ala | Thr | Pro | Thr | Leu | Ala | Asn | Ala | Arg | Thr | Thr | Lys | His | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Ser | Cys | Tyr | Ile | Gly | Ser | Thr | Pro | Asp | Asn | Ile | Glu | Gly | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asp | Ser | Tyr | Lys | Glu | Met | Ala | Leu | Leu | Ser | Lys | Tyr | Gly | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Gly | Trp | Asp | Phe | Ser | Leu | Val | Arg | Ser | Ile | Gly | Ser | Tyr | Ile | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | His | Lys | Asn | Ala | Ser | Ala | Gly | Thr | Ile | Pro | Phe | Leu | Lys | Ile | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Asp | Val | Ala | Ile | Ala | Val | Asp | Gln | Leu | Gly | Thr | Arg | Lys | Gly | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Val | Tyr | Leu | Glu | Ile | Trp | His | Ile | Asp | Val | Met | Glu | Phe | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Leu | Arg | Lys | Asn | Ser | Gly | Asp | Glu | Arg | Arg | Ala | His | Asp | Leu |     |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Phe | Pro | Ala | Leu | Trp | Val | Cys | Asp | Leu | Phe | Leu | Lys | Arg | Val | Leu | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Ala | Met | Trp | Thr | Leu | Phe | Asp | Pro | Tyr | Glu | Cys | Lys | Asp | Leu | Thr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Glu | Leu | Tyr | Gly | Gln | Asp | Phe | Glu | Lys | Arg | Tyr | Leu | Glu | Tyr | Glu | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Pro | Lys | Ile | Ile | Lys | Glu | Tyr | Ile | Asn | Ala | Lys | Asp | Leu | Trp | Lys |
|     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |     |
| Lys | Ile | Leu | Met | Asn | Tyr | Phe | Glu | Ala | Gly | Leu | Pro | Phe | Leu | Ala | Phe |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Lys | Asp | Asn | Ala | Asn | Arg | Cys | Asn | Pro | Asn | Ala | His | Ala | Gly | Ile | Ile |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Arg | Ser | Ser | Asn | Leu | Cys | Thr | Glu | Ile | Phe | Gln | Asn | Thr | Ala | Pro | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Tyr | Tyr | Met | Gln | Ile | Glu | Tyr | Thr | Asp | Gly | Thr | Ile | Glu | Phe | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Glu | Lys | Glu | Leu | Val | Thr | Thr | Asp | Ser | Asn | Ile | Thr | Lys | Cys | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Lys | Leu | Thr | Ser | Thr | Asp | Ile | Leu | Lys | Gly | Lys | Pro | Ile | Tyr | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Thr | Lys | Val | Ala | Lys | Asp | Gly | Gln | Thr | Ala | Val | Cys | Asn | Leu | Ala |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ser | Ile | Asn | Leu | Ser | Lys | Ile | Asn | Thr | Glu | Glu | Asp | Ile | Lys | Arg | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Val | Pro | Ile | Met | Val | Arg | Leu | Leu | Asp | Asn | Val | Ile | Asp | Leu | Asn | Phe |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Tyr | Pro | Asn | Arg | Lys | Val | Lys | Ala | Thr | Asn | Leu | Gln | Asn | Arg | Ala | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | Leu | Gly | Val | Met | Gly | Glu | Ala | Gln | Met | Leu | Ala | Glu | His | Gln | Ile |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Trp | Gly | Ser | Lys | Glu | His | Leu | Glu | Lys | Ile | Asp | Ala | Leu | Met | Glu |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Gln | Ile | Ser | Tyr | His | Ala | Ile | Asp | Thr | Ser | Ala | Asn | Leu | Ala | Lys | Glu |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |
| Lys | Gly | Val | Tyr | Lys | Asp | Phe | Glu | Asn | Ser | Glu | Trp | Ser | Lys | Gly | Ile |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Phe | Pro | Ile | Asp | Lys | Ala | Asn | Asn | Glu | Ala | Leu | Lys | Leu | Thr | Glu | Lys |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu Lys Val  
 465 470 475 480  
 Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala Pro Thr  
 485 490 495  
 Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu Pro Ile  
 500 505 510  
 Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile Pro Val  
 515 520 525  
 Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr Ser Ala  
 530 535 540  
 Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val Arg Gln  
 545 550 555 560  
 Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg Ile Glu  
 565 570 575  
 Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala Trp Lys  
 580 585 590  
 Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro Ser Ile  
 595 600 605  
 Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn Cys Gln  
 610 615 620

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...1390
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GCAAAATTCT AGCCTTAAAT CTTTGATGAA ACGAAGTCAA ATTATAAGAT AAGGC ATG 58  
 Met  
 1  
 TTA AAA TTC CCT AAA ATG AGT TTA AGG ATT TTA ATG CTT TCT GTC ATC 106  
 Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val Ile  
 5 10 15  
 ATA CTG GCC GCT GGT AAA GGC ACT CGC ATG CGT TCT AGC CTG CCT AAA 154  
 Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro Lys  
 20 25 30  
 ACT TTA CAC ACC ATT TGT GGG GAG CCT ATG TTG TTT TAC ATT TTA GAA 202  
 Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu Glu  
 35 40 45  
 ACG GCT TTT TCA ATC AGC GAT GAT GTG CAT CTT ATC TTA CAC CAC CAA 250  
 Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His Gln

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| 50                |                   |                   |                   | 55                |                   |                   |                   | 60                |                   |                   |                   | 65                |                   |                   |                   |     |
| CAA<br>Gln        | GAA<br>Glu        | CGC<br>Arg        | ATT<br>Ile        | AAA<br>Lys<br>70  | GAA<br>Glu        | GCG<br>Ala        | GTG<br>Val        | TTG<br>Leu        | GAG<br>Glu<br>75  | CGT<br>Arg        | TTT<br>Phe        | AAG<br>Lys        | GGC<br>Gly        | GTC<br>Val<br>80  | ATT<br>Ile        | 298 |
| TTT<br>Phe        | CAC<br>His        | ACT<br>Thr        | CAA<br>Gln<br>85  | ATT<br>Ile        | GTG<br>Val        | GAA<br>Glu        | AAA<br>Lys        | TAT<br>Tyr<br>90  | TCA<br>Ser        | GGG<br>Gly        | ACA<br>Thr        | GGT<br>Gly<br>95  | GGG<br>Gly        | GCT<br>Ala        | ATC<br>Ile        | 346 |
| ATG<br>Met        | CAA<br>Gln        | AAA<br>Lys<br>100 | GAT<br>Asp        | AAA<br>Lys        | ACG<br>Thr        | CCT<br>Pro        | ATT<br>Ile<br>105 | TCT<br>Ser        | ACG<br>Thr        | AAA<br>Lys        | CAT<br>His        | GAG<br>Glu<br>110 | CGG<br>Arg        | GTT<br>Val        | TTG<br>Leu        | 394 |
| ATT<br>Ile        | TTG<br>Leu<br>115 | AAT<br>Asn        | GCG<br>Ala        | GAC<br>Asp        | ATG<br>Met        | CCT<br>Pro<br>120 | TTA<br>Leu        | ATC<br>Ile        | ACT<br>Thr        | AAA<br>Lys        | GAC<br>Asp<br>125 | GCT<br>Ala        | CTC<br>Leu        | GCC<br>Ala        | CCC<br>Pro        | 442 |
| TTA<br>Leu<br>130 | TTA<br>Leu        | GAA<br>Glu        | AGC<br>Ser        | AAG<br>Lys<br>135 | AAT<br>Asn<br>135 | AAC<br>Asn        | GCT<br>Ala        | ATA<br>Ile        | GGC<br>Gly<br>140 | TTA<br>Leu<br>140 | CTC<br>Leu        | CAT<br>His        | TTA<br>Leu        | GCT<br>Ala        | GAC<br>Asp<br>145 | 490 |
| CCT<br>Pro        | AAA<br>Lys        | GGT<br>Gly        | TAT<br>Tyr<br>150 | GGG<br>Gly<br>150 | CGC<br>Arg        | GTT<br>Val        | GTT<br>Val        | TTA<br>Leu        | GAA<br>Glu<br>155 | AAC<br>Asn        | CAT<br>His        | CAG<br>Gln        | GTT<br>Val<br>160 | AAA<br>Lys<br>160 | AAG<br>Lys        | 538 |
| ATT<br>Ile        | GTA<br>Val        | GAA<br>Glu        | GAA<br>Glu<br>165 | AAG<br>Lys        | GAC<br>Asp        | GCT<br>Ala        | AAT<br>Asn        | GAT<br>Asp<br>170 | GAA<br>Glu        | GAA<br>Glu        | AAA<br>Lys        | GAA<br>Glu<br>175 | ATT<br>Ile<br>175 | AAA<br>Lys        | AGC<br>Ser        | 586 |
| GTG<br>Val        | AAT<br>Asn        | GCT<br>Ala<br>180 | GGC<br>Gly        | GTG<br>Val        | TAT<br>Tyr        | GGG<br>Gly        | TTT<br>Phe<br>185 | GAA<br>Glu        | AGG<br>Arg        | GAT<br>Asp        | TTT<br>Phe        | TTA<br>Leu<br>190 | GAA<br>Glu        | AAA<br>Lys        | TAC<br>Tyr        | 634 |
| TTA<br>Leu        | CCC<br>Pro<br>195 | AAG<br>Lys        | CTC<br>Leu        | CAT<br>His        | GAC<br>Asp        | CAA<br>Gln<br>200 | AAC<br>Asn        | GCC<br>Ala        | CAA<br>Gln        | AAA<br>Lys        | GAA<br>Glu<br>205 | TAC<br>Tyr        | TAC<br>Tyr        | CTC<br>Leu        | ACG<br>Thr        | 682 |
| GAT<br>Asp<br>210 | TTA<br>Leu        | ATC<br>Ile        | GCT<br>Ala        | CTA<br>Leu        | GGG<br>Gly<br>215 | ATC<br>Ile        | AAT<br>Asn        | GAA<br>Glu        | AAC<br>Asn<br>220 | GAA<br>Glu<br>220 | ACA<br>Thr        | ATT<br>Ile        | GAC<br>Asp        | GCT<br>Ala<br>225 | ATT<br>Ile<br>225 | 730 |
| TTC<br>Phe        | TTA<br>Leu        | AAA<br>Lys        | GAA<br>Glu        | GAG<br>Glu<br>230 | TGT<br>Cys        | TTT<br>Phe        | TTA<br>Leu        | GGG<br>Gly        | GTG<br>Val<br>235 | AAT<br>Asn        | AGC<br>Ser        | CAA<br>Gln        | ACA<br>Thr        | GAA<br>Glu<br>240 | AGG<br>Arg        | 778 |
| GCG<br>Ala        | AAA<br>Lys        | GCT<br>Ala        | GAA<br>Glu<br>245 | GAA<br>Glu        | ATC<br>Ile        | ATG<br>Met        | CTA<br>Leu        | GAA<br>Glu<br>250 | AGA<br>Arg        | CTG<br>Leu        | CGC<br>Arg        | AAA<br>Lys        | AAC<br>Asn<br>255 | GCC<br>Ala        | ATG<br>Met        | 826 |
| GAC<br>Asp        | TTG<br>Leu        | GGG<br>Gly<br>260 | GTA<br>Val        | GTG<br>Val        | ATG<br>Met        | CAA<br>Gln        | TTG<br>Leu<br>265 | CCT<br>Pro        | AAT<br>Asn        | AGC<br>Ser        | ATT<br>Ile<br>270 | TAT<br>Tyr<br>270 | TTA<br>Leu        | GAA<br>Glu        | AAA<br>Lys        | 874 |
| GGC<br>Gly        | GTG<br>Val<br>275 | AGT<br>Ser        | TTT<br>Phe        | AAG<br>Lys        | GGG<br>Gly        | GAG<br>Glu<br>280 | TGC<br>Cys        | GTT<br>Val        | TTA<br>Leu        | GAG<br>Glu        | CAA<br>Gln<br>285 | GGG<br>Gly        | GTG<br>Val        | CGT<br>Arg        | TTG<br>Leu        | 922 |

[illegible]



[REDACTED]

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 771 base pairs

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(ix) FEATURE:

(B) LOCATION: 227...715

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

361

TTA TTG CAA GTG ATC AAG CAC CAA CAA GGC GTA TTT TCT ATG GTA AAA T 716  
 Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser Met Val Lys  
 150 155 160

AAGCCCTTTA ACATTGGATA GAACTCAAAA TAAAAGGATC AGTTTGAAAA AAGAG 771

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Met | Leu | Ala | Thr | Val | Ile | Asn | Ala | Val | Ala | Met | Gln | Glu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Glu | His | Ile | Gly | Leu | Asp | Thr | Arg | Val | Gln | Ser | Ala | Ile | Glu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Ile | Cys | Glu | Ser | Tyr | Ile | Tyr | Arg | Lys | Ala | Ile | Arg | His | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Lys | Gly | Arg | Val | Val | Ile | Phe | Gly | Ala | Gly | Thr | Gly | Asn | Pro | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Thr | Thr | Asp | Thr | Ala | Ala | Thr | Leu | Arg | Ala | Ile | Glu | Ile | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Leu | Ile | Ile | Lys | Ala | Thr | Lys | Val | Asp | Gly | Ile | Tyr | Asp | Lys | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Asn | Lys | Phe | Lys | Asp | Ala | Lys | Lys | Leu | Asp | Thr | Leu | Ser | Tyr | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Ala | Leu | Ile | Gly | Asp | Ile | Glu | Val | Met | Asp | Asp | Thr | Ala | Ile | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Lys | Asp | Asn | Lys | Leu | Pro | Ile | Val | Val | Cys | Asn | Met | Phe | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Gly | Asn | Leu | Leu | Gln | Val | Ile | Lys | His | Gln | Gln | Gly | Val | Phe | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Val | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...607
- (D) OTHER INFORMATION:



[illegible]

[REDACTED]

\_\_\_\_\_

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ala | Phe | Leu | Lys | Ile | Leu | Met | Val | Leu | Ile | Phe | Met | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Tyr | Ala | Lys | Asn | Pro | Ser | Thr | Leu | Ser | Lys | Glu | Glu | Glu | Val | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | His | Leu | Gln | Ser | Phe | Ser | Ala | His | Phe | Lys | Gln | Val | Leu | Lys | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Lys | Pro | Leu | Val | Tyr | Tyr | Gly | Val | Leu | Lys | Ala | Lys | Ala | Pro | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Ala | Leu | Trp | Val | Tyr | Glu | Lys | Pro | Leu | Lys | Lys | Glu | Ile | Tyr | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Asp | Lys | Glu | Val | Val | Ile | Tyr | Glu | Pro | Asn | Leu | Phe | Gln | Ala | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Thr | Pro | Leu | Lys | Asp | Lys | Thr | Asp | Phe | Phe | Thr | Ile | Leu | Lys | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Lys | Gln | Asp | Asp | Gly | Ser | Phe | Lys | Thr | Thr | Ile | Asn | Lys | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Tyr | Arg | Leu | Val | Phe | Lys | Asp | Gly | Lys | Pro | Phe | Ser | Leu | Glu | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Asp | Gly | Met | Asn | Asn | Leu | Val | Thr | Ile | Thr | Phe | Ser | Gln | Ala | Glu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Asn | Pro | Thr | Ile | Ala | Asn | Glu | Ile | Phe | Val | Phe | Lys | Pro | Lys | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Asn | Ile | Asp | Ile | Val | Arg | Gln |     |     |     |     |     |     |     |     |
|     |     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 729...2981
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAAACGATCG | CAGAAAGCAA | TGAAAGCACG | GTAGTAGCGG | AATTCATAG  | CAGTAATGAA | 60  |
| AAAAAAGCGC | TTATGAGAGC | GAAGCAGAGC | TAGAAAGGGC | GTTTATTAAG | CTTTTAGAAA | 120 |
| AACAAGGCTA | TGAATTAA   | AAAATCCACA | AAGAAGAAGA | ATTAAAAGAC | AATTTAAAG  | 180 |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CGC | ATT | TTA | GAT | AGC | GTT | AAA | ACG | CAT | GGG | AAT | ATC | GTG | TGT | TTT | AGG | 2066 |
| Arg | Ile | Leu | Asp | Ser | Val | Lys | Thr | His | Gly | Asn | Ile | Val | Cys | Phe | Arg |      |
|     |     |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |      |
| GAT | TTA | GAA | CAG | GAT | TTG | AAT | GAC | GCT | CTC | ATG | CTT | TTT | GGC | AAC | AAG | 2114 |
| Asp | Leu | Glu | Gln | Asp | Leu | Asn | Asp | Ala | Leu | Met | Leu | Phe | Gly | Asn | Lys |      |
|     |     |     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |      |
| GAC | GCT | CAA | TCT | ATT | GCG | CTG | TTA | AGA | AAA | TAT | GAA | GAT | TAT | TTG | AAA | 2162 |
| Asp | Ala | Gln | Ser | Ile | Ala | Leu | Leu | Arg | Lys | Tyr | Glu | Asp | Tyr | Leu | Lys |      |
|     |     | 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |      |
| GGC | TAC | ACG | GAT | AAC | AAC | AAA | GAA | TAC | GAG | GGC | TAT | GAG | GGT | TTG | ATT | 2210 |
| Gly | Tyr | Thr | Asp | Asn | Asn | Lys | Glu | Tyr | Glu | Gly | Tyr | Glu | Gly | Leu | Ile |      |
|     | 480 |     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |      |
| AAA | AGG | CTT | TTA | ACC | GAA | TTC | CCA | TTA | AAA | GAG | CCA | ATC | GTT | TCA | GAA | 2258 |
| Lys | Arg | Leu | Leu | Thr | Glu | Phe | Pro | Leu | Lys | Glu | Pro | Ile | Val | Ser | Glu |      |
|     | 495 |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |      |
| AGC | CAG | AAA | AAG | GAT | TTT | ATT | AAG | CTT | TTT | GGC | AAG | ATT | TTG | AAA | TTA | 2306 |
| Ser | Gln | Lys | Lys | Asp | Phe | Ile | Lys | Leu | Phe | Gly | Lys | Ile | Leu | Lys | Leu |      |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |      |
| GAA | AAT | ATT | TTA | AAC | AGC | TTT | GAA | AAT | TTC | AAA | AAA | GAC | GAT | TAC | ATC | 2354 |
| Glu | Asn | Ile | Leu | Asn | Ser | Phe | Glu | Asn | Phe | Lys | Lys | Asp | Asp | Tyr | Ile |      |
|     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |      |
| AAT | CCC | AGG | GAT | TTT | CAA | GAC | TAT | CAA | AGC | AAA | TAC | CTT | GAT | TTT | TAC | 2402 |
| Asn | Pro | Arg | Asp | Phe | Gln | Asp | Tyr | Gln | Ser | Lys | Tyr | Leu | Asp | Phe | Tyr |      |
|     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |      |
| GAT | GCA | ATG | AGA | TCA | GAA | AAA | GGG | AAG | GAT | AAA | GAA | GAG | ATT | AAT | GAT | 2450 |
| Asp | Ala | Met | Arg | Ser | Glu | Lys | Gly | Lys | Asp | Lys | Glu | Glu | Ile | Asn | Asp |      |
|     | 560 |     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     |      |
| GAT | TTG | ATT | TTT | GAA | ATT | GAA | CTC | ATC | AAA | CAA | GTG | GAA | GTC | AAT | ATT | 2498 |
| Asp | Leu | Ile | Phe | Glu | Ile | Glu | Leu | Ile | Lys | Gln | Val | Glu | Val | Asn | Ile |      |
|     | 575 |     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |      |
| GAC | TAT | ATT | TTG | AAT | TTG | ATT | GAA | GAG | TTC | GCT | AAA | GAG | CAT | GGG | GTG | 2546 |
| Asp | Tyr | Ile | Leu | Asn | Leu | Ile | Glu | Glu | Phe | Ala | Lys | Glu | His | Gly | Val |      |
|     |     |     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |      |
| GAA | ATC | CAA | GGC | GTT | AAA | ACC | AAA | ATA | GAG | CCA | ATC | ATC | AAC | TCC | AGC | 2594 |
| Glu | Ile | Gln | Gly | Val | Lys | Thr | Lys | Ile | Glu | Pro | Ile | Ile | Asn | Ser | Ser |      |
|     |     |     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |      |
| ATA | GAG | TTA | AGG | AAT | AAA | AAA | GAT | TTG | ATC | ATG | GAT | TTC | ATT | GAC | AAA | 2642 |
| Ile | Glu | Leu | Arg | Asn | Lys | Lys | Asp | Leu | Ile | Met | Asp | Phe | Ile | Asp | Lys |      |
|     |     | 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |      |
| TAC | AAC | AAA | GAC | CAA | GAA | GTC | CAT | GCG | CAT | TTT | CAA | GAT | TAT | ATC | CAC | 2690 |
| Tyr | Asn | Lys | Asp | Gln | Glu | Val | His | Ala | His | Phe | Gln | Asp | Tyr | Ile | His |      |
|     | 640 |     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     |      |
| CAA | AAA | AGA | GAA | GAG | GAA | TTC | CAA | AAT | ATC | ATA | GAA | GAA | AAC | CGC | TTG | 2738 |
| Gln | Lys | Arg | Glu | Glu | Glu | Phe | Gln | Asn | Ile | Ile | Glu | Glu | Asn | Arg | Leu |      |

| 655                                                             | 660 | 665 | 670 |      |
|-----------------------------------------------------------------|-----|-----|-----|------|
| AAT GAA GAA AAA GCC TAT TCG TTC ATG CAG CAT GCC TTT AAA GGG GGC |     |     |     | 2786 |
| Asn Glu Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly | 675 | 680 | 685 |      |
| GAA ATC AGT TTT AGT GGG ACG GAA TTC CCT AAA ATC ATT GAA GAA AAA |     |     |     | 2834 |
| Glu Ile Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys | 690 | 695 | 700 |      |
| CCC TCC ATG TTT GGT AAA AAT TCG CGC TAT CAA GAG GTG AAA GAA AAA |     |     |     | 2882 |
| Pro Ser Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys | 705 | 710 | 715 |      |
| GTC GCT GCA AGC CTT TCT CGT TTT TTC CAC CGC TTT TGT GAT CTC ACT |     |     |     | 2930 |
| Val Ala Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr | 720 | 725 | 730 |      |
| AGC GCT ATA TTT AAG AAA AAT GAG GTT AAA AAA GAT GAG GTT AAT GAA |     |     |     | 2978 |
| Ser Ala Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu | 735 | 740 | 745 | 750  |
| AAA TAGTTCATGA ACGCTTTTGC ATTAAGGCTC AAAAAAGCG CCGTTTAATG GATT  |     |     |     | 3035 |
| Lys                                                             |     |     |     |      |

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Ala | Lys | Ala | Phe | Phe | Ala | Lys | Arg | Ser | Leu | Leu | Asn | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Cys | Tyr | Cys | Val | Phe | Thr | Ser | Glu | Glu | Val | Leu | Leu | Val | Met |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Pro | Tyr | Gln | Ile | Val | Ala | Ala | Glu | Arg | Ile | Leu | Glu | Lys | Ile | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Gln | Asn | Ser | Lys | Thr | Lys | Asn | Gln | Ser | Lys | Gly | Tyr | Ile | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Thr | Thr | Gly | Ser | Gly | Lys | Thr | Leu | Thr | Ser | Phe | Lys | Ser | Ala | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ala | Lys | Glu | Leu | Glu | Ser | Val | Ser | Lys | Val | Leu | Phe | Val | Val | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Arg | Lys | Asp | Leu | Asp | Tyr | Gln | Thr | Met | Lys | Glu | Tyr | Asp | Lys | Phe | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Asp | Cys | Ala | Asn | Ser | Asn | Thr | Ser | Thr | Lys | Ile | Leu | Lys | Glu | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Glu | Asp | Ser | Asn | Ala | Lys | Ile | Ile | Ile | Thr | Thr | Ile | Gln | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Phe | Val | Lys | Ser | His | Lys | Gly | His | Ala | Ile | Phe | Asn | Glu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Val | Met | Ile | Phe | Asp | Glu | Cys | His | Arg | Ser | Gln | Leu | Gly | Ser | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Gln | Ala | Ile | Thr | Lys | Ala | Phe | Lys | Lys | Tyr | His | Leu | Phe | Gly | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Gly | Thr | Pro | Ile | Phe | Ala | Ala | Asn | Cys | Asp | Lys | Asn | Asn | Pro | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Thr | Thr | Glu | Gln | Lys | Phe | Gly | Lys | Cys | Leu | His | Gln | Tyr | Thr | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Asp | Ala | Ile | Arg | Asp | Lys | Asn | Val | Leu | Pro | Phe | Arg | Val | Glu | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| His | Asn | Thr | Ile | Lys | Ala | Lys | Glu | Asp | Ile | Lys | Asp | Asn | Lys | Val | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Val | Asp | Glu | Lys | Asn | Ala | Leu | Leu | Asp | Thr | Arg | Arg | Ile | Lys | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Thr | Lys | Cys | Ile | Leu | Glu | Arg | Phe | Asn | Gln | Ala | Thr | Lys | Asn | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Phe | Asn | Ser | Ile | Leu | Ala | Cys | Ser | Ser | Ile | Glu | Ala | Leu | Lys | Lys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Tyr | Gln | Ala | Phe | Lys | Glu | Glu | Lys | His | Asp | Leu | Lys | Ile | Ala | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ile | Phe | Ser | Tyr | Ser | Ala | Asn | Glu | Glu | Ile | Asp | Thr | Leu | Glu | Asp | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Asn | Glu | Ser | Ala | Cys | Arg | Leu | Asp | Lys | Ser | Ser | Arg | Asp | Phe | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Gly | Ala | Ile | Ala | Asp | Tyr | Asn | Gly | Met | Phe | Gly | Val | Ser | Phe | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Thr | Ser | Asp | Gln | Lys | Phe | Gln | Ser | Tyr | Tyr | Lys | Asp | Leu | Ser | Gln | Lys |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Met | Lys | Glu | Arg | Lys | Ile | Asp | Leu | Leu | Met | Val | Val | Asn | Met | Phe | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Gly | Phe | Asp | Ala | Thr | Arg | Leu | Asn | Thr | Leu | Trp | Val | Asp | Lys | Asn |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Lys | Tyr | His | Gly | Leu | Ile | Gln | Ala | Phe | Ser | Arg | Ala | Asn | Arg | Ile |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | Asp | Ser | Val | Lys | Thr | His | Gly | Asn | Ile | Val | Cys | Phe | Arg | Asp | Leu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Gln | Asp | Leu | Asn | Asp | Ala | Leu | Met | Leu | Phe | Gly | Asn | Lys | Asp | Ala |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gln | Ser | Ile | Ala | Leu | Leu | Arg | Lys | Tyr | Glu | Asp | Tyr | Leu | Lys | Gly | Tyr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |
| Thr | Asp | Asn | Asn | Lys | Glu | Tyr | Glu | Gly | Tyr | Glu | Gly | Leu | Ile | Lys | Arg |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Leu | Leu | Thr | Glu | Phe | Pro | Leu | Lys | Glu | Pro | Ile | Val | Ser | Glu | Ser | Gln |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Lys | Lys | Asp | Phe | Ile | Lys | Leu | Phe | Gly | Lys | Ile | Leu | Lys | Leu | Glu | Asn |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Ile | Leu | Asn | Ser | Phe | Glu | Asn | Phe | Lys | Lys | Asp | Asp | Tyr | Ile | Asn | Pro |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Arg | Asp | Phe | Gln | Asp | Tyr | Gln | Ser | Lys | Tyr | Leu | Asp | Phe | Tyr | Asp | Ala |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     | 560 |     |
| Met | Arg | Ser | Glu | Lys | Gly | Lys | Asp | Lys | Glu | Glu | Ile | Asn | Asp | Asp | Leu |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Ile | Phe | Glu | Ile | Glu | Leu | Ile | Lys | Gln | Val | Glu | Val | Asn | Ile | Asp | Tyr |
|     |     | 580 |     |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Ile | Leu | Asn | Leu | Ile | Glu | Glu | Phe | Ala | Lys | Glu | His | Gly | Val | Glu | Ile |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |

Gln Gly Val Lys Thr Lys Ile Glu Pro Ile Ile Asn Ser Ser Ile Glu  
610 615 620  
Leu Arg Asn Lys Lys Asp Leu Ile Met Asp Phe Ile Asp Lys Tyr Asn  
625 630 635 640  
Lys Asp Gln Glu Val His Ala His Phe Gln Asp Tyr Ile His Gln Lys  
645 650 655  
Arg Glu Glu Glu Phe Gln Asn Ile Ile Glu Glu Asn Arg Leu Asn Glu  
660 665 670  
Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly Glu Ile  
675 680 685  
Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys Pro Ser  
690 695 700  
Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys Val Ala  
705 710 715 720  
Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr Ser Ala  
725 730 735  
Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu Lys  
740 745 750

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

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ACCACTATTG TAGAAAAATA ACAAGAGGGT TTGCAAAAAC TCTCATTAAA AACAAGGAGC 60
AAAAAAG ATG AAA AAG GCG GGC TTT CTT TTT TTA GCG GTA ATG GCT ATC 109
 Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile
 1 5 10

GTT GTT ATG AGT TTA AAC GCT AAA GAT CCG AAT GTG TTG CGT AAG ATT 157
Val Val Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile
15 20 25 30

GTT TTT GAG AAA TGT CTG CCT AAT TAT GAG AAA AAT CAG AAT CCT TCG 205
Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser
 35 40 45

CCA TGC ATA GAA GTC AAA CCC GAT GCC GGC TAT GTG GTT TTA AAA GAT 253
Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp
 50 55 60

ATT AAC GGC CCG TTG CAA TAT TTG TTG ATG CCA ACA ACT CAC ATT AGC 301
Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser
65 70 75

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|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGT ATT GAA AGC CCT TTG TTA CTT GAT CCT TCT ACG CCT AAC TTT TTT   | 349 |
| Gly Ile Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe   |     |
| 80 85 90                                                          |     |
| TAT TTA TCC TGG CAA GCG CGT GAT TTT ATG AGT AAA AAA TAC GGC CAA   | 397 |
| Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln   |     |
| 95 100 105 110                                                    |     |
| CCC ATT CCT GAT TAT GCG ATT TCT TTG ACG ATT AAC TCT AGC AAA GGG   | 445 |
| Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly   |     |
| 115 120 125                                                       |     |
| CGA TCG CAA AAC CAT TTT CAT ATC CAT ATC TCT TGC ATT AGT CTT GAA   | 493 |
| Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu   |     |
| 130 135 140                                                       |     |
| GCA CGC AAA CAG CTG GAT AAT AAC CTA AAA AAA ATC AAC AGC CGT TGG   | 541 |
| Ala Arg Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp   |     |
| 145 150 155                                                       |     |
| TCG CCA TTA CCG GGC GGT TTG AAT GGG CAT AAA TAC TTG GCG CGT CGG   | 589 |
| Ser Pro Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg   |     |
| 160 165 170                                                       |     |
| GTA ACA GAG AGC GAG TTA GTG CAA AAA AGC CCG TTT GTC ATG CTT AAT   | 637 |
| Val Thr Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn   |     |
| 175 180 185 190                                                   |     |
| AAA GAA GTG CCT AAT GCG TAC AAA CGC ATG GGG GAC TAT GGC TTA GCG   | 685 |
| Lys Glu Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala   |     |
| 195 200 205                                                       |     |
| GTG GTG CAA CAA AGC GAT AAC TCC TTT GTC TTA TTA GCG ACA CAA TTT   | 733 |
| Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe   |     |
| 210 215 220                                                       |     |
| AAC CCA TTG ACT TTA AAT CGC GCT TCA GCC GAA GAG ATT CAA GAT CAT   | 781 |
| Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His   |     |
| 225 230 235                                                       |     |
| GAA TGC GCG ATT TTG CAC TAAAGCGAGT TAGATTCTTA AGCTTGAGCG ATAACCTT | 837 |
| Glu Cys Ala Ile Leu His                                           |     |
| 240                                                               |     |
| TAAAAAGCGT TAT                                                    | 850 |

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile Val Val  
 1 5 10 15  
 Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val Phe  
 20 25 30  
 Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys  
 35 40 45  
 Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn  
 50 55 60  
 Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile  
 65 70 75 80  
 Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu  
 85 90 95  
 Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile  
 100 105 110  
 Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser  
 115 120 125  
 Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu Ala Arg  
 130 135 140  
 Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro  
 145 150 155 160  
 Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr  
 165 170 175  
 Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn Lys Glu  
 180 185 190  
 Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val  
 195 200 205  
 Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro  
 210 215 220  
 Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys  
 225 230 235 240  
 Ala Ile Leu His

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 57...929
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GTCCTATTTT TTCATTCATT CAACGAATTT AAAAATTACA ATAAAGAGTT ATAGTT ATG 59  
 Met  
 1  
 AAA CGA AGG GAT TTT ATT AAA ACG ACT ACT TTA GGC GCT ACA GGT GCT 107  
 Lys Arg Arg Asp Phe Ile Lys Thr Thr Thr Leu Gly Ala Thr Gly Ala

|                   |                   |                   | 5                 |                   |                   |                   | 10                |                   |                   |                   | 15                |                   |                   |                   |                   |     |  |  |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|--|--|
| GTT<br>Val        | TTA<br>Leu        | GGA<br>Gly<br>20  | GCA<br>Ala        | CAG<br>Gln        | ATT<br>Ile        | TTG<br>Leu        | CAG<br>Gln<br>25  | GCA<br>Ala        | GAA<br>Glu        | GAA<br>Glu        | AGT<br>Ser        | AAA<br>Lys<br>30  | GGG<br>Gly        | AGT<br>Ser        | GTT<br>Val        | 155 |  |  |
| GCA<br>Ala        | AAA<br>Lys<br>35  | TAT<br>Tyr        | AAA<br>Lys        | ATA<br>Ile        | GAA<br>Glu        | GCT<br>Ala<br>40  | CAA<br>Gln        | TAC<br>Tyr        | AGC<br>Ser        | ATT<br>Ile        | GAT<br>Asp<br>45  | TTT<br>Phe        | GAT<br>Asp        | TCT<br>Ser        | GCA<br>Ala        | 203 |  |  |
| GAA<br>Glu<br>50  | CAC<br>His        | ACT<br>Thr        | TCA<br>Ser        | CTT<br>Leu        | TTC<br>Phe<br>55  | ATT<br>Ile        | CCC<br>Pro        | ATG<br>Met        | CCG<br>Pro        | AGT<br>Ser<br>60  | GTT<br>Val        | GTA<br>Val        | GCG<br>Ala        | AGC<br>Ser        | AAT<br>Asn<br>65  | 251 |  |  |
| GTG<br>Val        | CAT<br>His        | TTA<br>Leu        | CAA<br>Gln        | GGC<br>Gly<br>70  | AAT<br>Asn        | CAT<br>His        | GCT<br>Ala        | AGC<br>Ser        | TAT<br>Tyr<br>75  | AAA<br>Lys        | AGC<br>Ser        | ATG<br>Met        | CTC<br>Leu        | AAT<br>Asn<br>80  | TTT<br>Phe        | 299 |  |  |
| GGA<br>Gly        | GTG<br>Val        | CCT<br>Pro        | TAT<br>Tyr<br>85  | TTG<br>Leu        | CAA<br>Gln        | GTG<br>Val        | GAT<br>Asp<br>90  | TTT<br>Phe        | TTA<br>Leu        | AAA<br>Lys        | AGC<br>Ser        | ACT<br>Thr        | CAA<br>Gln<br>95  | AAA<br>Lys        | AAG<br>Lys        | 347 |  |  |
| CAA<br>Gln        | GTC<br>Val        | CAT<br>His<br>100 | TTG<br>Leu        | TCT<br>Ser        | TAT<br>Tyr        | GAG<br>Glu        | ATC<br>Ile<br>105 | GCT<br>Ala        | AGC<br>Ser        | TAT<br>Tyr        | CAA<br>Gln<br>110 | TTG<br>Leu        | AAT<br>Asn        | GAG<br>Glu        | CGT<br>Arg        | 395 |  |  |
| TTG<br>Leu        | TTT<br>Phe<br>115 | GAA<br>Glu        | ACG<br>Thr        | AGC<br>Ser        | GAT<br>Asp        | TTT<br>Phe<br>120 | GTA<br>Val        | GCA<br>Ala        | ATG<br>Met        | GGG<br>Gly        | CGT<br>Arg<br>125 | TAT<br>Tyr        | GAA<br>Glu        | AGA<br>Arg        | GAC<br>Asp        | 443 |  |  |
| GAT<br>Asp<br>130 | GCG<br>Ala        | AGC<br>Ser        | GTG<br>Val        | GCT<br>Ala        | AAC<br>Asn<br>135 | ATT<br>Ile        | GCC<br>Ala        | AAC<br>Asn        | CAG<br>Gln        | CTT<br>Leu<br>140 | AAG<br>Lys        | GGA<br>Gly        | ACA<br>Thr        | ACC<br>Thr        | CCT<br>Pro<br>145 | 491 |  |  |
| AAA<br>Lys        | GAA<br>Glu        | AGC<br>Ser        | GTT<br>Val        | CGC<br>Arg<br>150 | AAT<br>Asn        | TTT<br>Phe        | TAT<br>Tyr        | GCG<br>Ala        | TTC<br>Phe<br>155 | ATC<br>Ile        | AAG<br>Lys        | CAT<br>His        | GAG<br>Glu        | ATG<br>Met<br>160 | CCT<br>Pro        | 539 |  |  |
| AAG<br>Lys        | AGA<br>Arg        | CAG<br>Gln        | AAG<br>Lys<br>165 | GCT<br>Ala        | TTA<br>Leu        | GAG<br>Glu        | GGT<br>Gly<br>170 | AAA<br>Lys        | GAA<br>Glu        | AAT<br>Asn        | TTA<br>Leu        | CCT<br>Pro        | AAG<br>Lys<br>175 | CGT<br>Arg        | GAG<br>Glu        | 587 |  |  |
| AGT<br>Ser        | TTG<br>Leu        | CCC<br>Pro<br>180 | TGG<br>Trp        | TTT<br>Phe        | GCA<br>Ala        | ACC<br>Thr<br>185 | ATT<br>Ile        | TCA<br>Ser        | AAA<br>Lys        | GAG<br>Glu        | AGC<br>Ser        | ATG<br>Met<br>190 | TTT<br>Phe        | GTG<br>Val        | TCC<br>Ser        | 635 |  |  |
| TTA<br>Leu        | TGC<br>Cys<br>195 | CAT<br>His        | GCG<br>Ala        | TGC<br>Cys        | GGG<br>Gly        | ATT<br>Ile<br>200 | AAA<br>Lys        | AGC<br>Ser        | GCT<br>Ala        | GAA<br>Glu        | GTG<br>Val<br>205 | CAA<br>Gln        | GGC<br>Gly        | TTG<br>Leu        | AAA<br>Lys        | 683 |  |  |
| CTG<br>Leu<br>210 | GGT<br>Gly        | CAA<br>Gln        | AAC<br>Asn        | AGC<br>Ser        | GTG<br>Val<br>215 | GTG<br>Val        | AAA<br>Lys        | AAC<br>Asn        | GCT<br>Ala        | CCT<br>Pro<br>220 | AGA<br>Arg        | GTG<br>Val        | GAA<br>Glu        | GTG<br>Val        | TAT<br>Tyr<br>225 | 731 |  |  |
| TTG<br>Leu        | AAA<br>Lys        | GAT<br>Asp        | TCA<br>Ser        | TTT<br>Phe<br>230 | CTA<br>Leu        | GCG<br>Ala        | TTT<br>Phe        | GAT<br>Asp<br>235 | TTT<br>Phe        | CAA<br>Gln        | AAT<br>Asn        | AAT<br>Asn        | CAC<br>His        | AAG<br>Lys<br>240 | GAA<br>Glu        | 779 |  |  |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

```
(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

374

Tyr Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys  
 225 230 235 240  
 Glu Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser  
 245 250 255  
 Ala Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg  
 260 265 270  
 Asp Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr  
 275 280 285  
 Thr Ile Val  
 290

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 82...633
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TGTGATTAAA CAAAATCAAA AACTTTTTTAA CTATAATCAA ACCTAAATTA AAGTTCAAGG | 60  |
| AGTGGCATT TT TGTTTAAAAG A ATG GTT TTA ATC GCT CTT TTA GGG GTG TTT  | 111 |
| Met Val Leu Ile Ala Leu Leu Gly Val Phe                            |     |
| 1 5 10                                                             |     |
| TCA AGC GTT TCA TTA AGC GCT AAG AGT CTT TTA AGA GAT GAT GGG ATT    | 159 |
| Ser Ser Val Ser Leu Ser Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile    |     |
| 15 20 25                                                           |     |
| TTA GTC TCT GAT TTA AAG GGC ATG AAA TCA GAA CTA TCT GAT GCT CCT    | 207 |
| Leu Val Ser Asp Leu Lys Gly Met Lys Ser Glu Leu Ser Asp Ala Pro    |     |
| 30 35 40                                                           |     |
| GCT TGG GTT TTT GAA GAC GCT AAA GCC CCC TAC GAA GAA ATG GGC GTG    | 255 |
| Ala Trp Val Phe Glu Asp Ala Lys Ala Pro Tyr Glu Glu Met Gly Val    |     |
| 45 50 55                                                           |     |
| GCG TAT ATC CCT GTT AAT AAT AAA TAT TTA GGG ATT GAG CAA GCG ACC    | 303 |
| Ala Tyr Ile Pro Val Asn Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr    |     |
| 60 65 70                                                           |     |
| TTA AAC GCT AAA TTG AGT CTG ATC GTG GTT TTT CAT GAA ATC ATG ATG    | 351 |
| Leu Asn Ala Lys Leu Ser Leu Ile Val Val Phe His Glu Ile Met Met    |     |
| 75 80 85 90                                                        |     |
| AAG TAT AAA AAA CGC TTC ATG GAG CAA TTC CAT GAG TCC GAG CAG ACG    | 399 |
| Lys Tyr Lys Lys Arg Phe Met Glu Gln Phe His Glu Ser Glu Gln Thr    |     |
| 95 100 105                                                         |     |

ACT ACG AAT ATC AGT TAC GCT ATC TAT AAT TAT CTA GCG ACT AAG ATC 447  
 Thr Thr Asn Ile Ser Tyr Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile  
 110 115 120  
 CAG GTA TCC AAC ACC TAC ACG AAT TTA AAA TCG GAG GTG GCG GTG GTG 495  
 Gln Val Ser Asn Thr Tyr Thr Asn Leu Lys Ser Glu Val Ala Val Val  
 125 130 135  
 AAA ATC AAG CTA GTG GGT TGT CAG ATT GAG CAA ATC AAA AGG TAT TTA 543  
 Lys Ile Lys Leu Val Gly Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu  
 140 145 150  
 AAA GCG AGC GTT GAA AAC CTT AAC GAT AAT GAA ATC GCT TAC ATC GCT 591  
 Lys Ala Ser Val Glu Asn Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala  
 155 160 165 170  
 AAG GTC GCT CAA AAA GAA TTT GGT AGC GTT TGT GCG TTA AGG TAGTTTTAT 642  
 Lys Val Ala Gln Lys Glu Phe Gly Ser Val Cys Ala Leu Arg  
 175 180  
 AGCATTCTAG CGAGCATGTT TAAGGCATGC TCTACGCTTT TATT 686

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Val Leu Ile Ala Leu Leu Gly Val Phe Ser Ser Val Ser Leu Ser  
 1 5 10 15  
 Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile Leu Val Ser Asp Leu Lys  
 20 25 30  
 Gly Met Lys Ser Glu Leu Ser Asp Ala Pro Ala Trp Val Phe Glu Asp  
 35 40 45  
 Ala Lys Ala Pro Tyr Glu Glu Met Gly Val Ala Tyr Ile Pro Val Asn  
 50 55 60  
 Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr Leu Asn Ala Lys Leu Ser  
 65 70 75 80  
 Leu Ile Val Val Phe His Glu Ile Met Met Lys Tyr Lys Lys Arg Phe  
 85 90 95  
 Met Glu Gln Phe His Glu Ser Glu Gln Thr Thr Thr Asn Ile Ser Tyr  
 100 105 110  
 Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile Gln Val Ser Asn Thr Tyr  
 115 120 125  
 Thr Asn Leu Lys Ser Glu Val Ala Val Val Lys Ile Lys Leu Val Gly  
 130 135 140  
 Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu Lys Ala Ser Val Glu Asn  
 145 150 155 160  
 Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala Lys Val Ala Gln Lys Glu  
 165 170 175  
 Phe Gly Ser Val Cys Ala Leu Arg

180

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 112...252
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
ATGCCTGCCA TTTCATAGCC TAAATTTTCT TTAGAGCCGA ATTGATAAGC GGCTTTTAAG 60
ACTTCTTTTT GCTTAGCGTT AAAATCTTTA ATATTGTCGC AATTGGTCAT C ATG ACT 117
 Met Thr
 1

TTA GTA ACG GGC GAT TTG GGC TTG TTT TTA ACC CCT TTA GCG GGC TTA 165
Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala Gly Leu
 5 10 15

GGC TCT GTT TTA GTG GGG CTT TCT GTT GCG GCT AAA CTT AAA GAT GCA 213
Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys Asp Ala
 20 25 30

CTT AAG GCT GTG CCT AGC CAT AAG GCT TTA AAG ATG GTG TGAGTGAGTG GG 264
Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
 35 40 45

GTTAAATGTT TCAAAACGCC TACCTTTTGT ATTAAGAAAT AAAC TA 310
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
Met Thr Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala
 1 5 10 15
Gly Leu Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys
 20 25 30
Asp Ala Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
```

35

40

45

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 145...579
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GCGTTCAATA GAATGCTTTA GTTAGGAAGC TCCTTGCTTT AGCAAGGNGT GGTTCCTACTG | 60  |
| AAAGAGAGTA AGAAATTTGA AGAAAGGGTT TATCTTTTTT TAGATGAATT TGTGCGTTTT  | 120 |
| GGTAAATTGC CTTTTTTATT AGAA ATG CCA GCA TTA AGT AGG AGC TAT GGT     | 171 |
| Met Pro Ala Leu Ser Arg Ser Tyr Gly                                |     |
| 1 5                                                                |     |
| GTG GTT TTA ATT TTT ATC ACG CAA TCC AAC GCT CTT ATT GAA AAA TAT    | 219 |
| Val Val Leu Ile Phe Ile Thr Gln Ser Asn Ala Leu Ile Glu Lys Tyr    |     |
| 10 15 20 25                                                        |     |
| TAC GGC AGA GAA GAT GCA AGA ATT GTT AAT AGC ACC GTG GCT TAC AAA    | 267 |
| Tyr Gly Arg Glu Asp Ala Arg Ile Val Asn Ser Thr Val Ala Tyr Lys    |     |
| 30 35 40                                                           |     |
| ATA ATT TTC AAA ATG GAT GAT TTA GAA TAC GCT AAA CAG GTG AGC GAA    | 315 |
| Ile Ile Phe Lys Met Asp Asp Leu Glu Tyr Ala Lys Gln Val Ser Glu    |     |
| 45 50 55                                                           |     |
| GAA GTC GGT AAG ATG ACT AGA AAA ACA CGA AGC CAC TCT ACA GAA AAA    | 363 |
| Glu Val Gly Lys Met Thr Arg Lys Thr Arg Ser His Ser Thr Glu Lys    |     |
| 60 65 70                                                           |     |
| GGA CAA CTC ATT ACC GGA GGG ACT TCT AGT ATA GGT AAA GAG GCG TGG    | 411 |
| Gly Gln Leu Ile Thr Gly Gly Thr Ser Ser Ile Gly Lys Glu Ala Trp    |     |
| 75 80 85                                                           |     |
| GAC TTA TTG AGC GCG CAA GAT ATT ATG AAT ATT GAT AAA GAT GAA GTG    | 459 |
| Asp Leu Leu Ser Ala Gln Asp Ile Met Asn Ile Asp Lys Asp Glu Val    |     |
| 90 95 100 105                                                      |     |
| ATC GTT TTA GTA AGC GGT CAT AAG GCT AAA CCC TTA AAA TTA AAA GCG    | 507 |
| Ile Val Leu Val Ser Gly His Lys Ala Lys Pro Leu Lys Leu Lys Ala    |     |
| 110 115 120                                                        |     |
| AAT TAT TAT TTC AAA AAC AAA GAA TTA CTC TCT CGT ATT AAC TGG GAA    | 555 |
| Asn Tyr Tyr Phe Lys Asn Lys Glu Leu Leu Ser Arg Ile Asn Trp Glu    |     |
| 125 130 135                                                        |     |



GTC AAG CCC AAT GAA GAA GTG TTT TGATGGATTA AAAAAGTTTG CATGAGTATT 609  
 Val Lys Pro Asn Glu Glu Val Phe  
 140 145

TTTTAATTGC TTTTTTAAAA AT 631

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ala | Leu | Ser | Arg | Ser | Tyr | Gly | Val | Val | Leu | Ile | Phe | Ile | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ser | Asn | Ala | Leu | Ile | Glu | Lys | Tyr | Tyr | Gly | Arg | Glu | Asp | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Val | Asn | Ser | Thr | Val | Ala | Tyr | Lys | Ile | Ile | Phe | Lys | Met | Asp | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | Tyr | Ala | Lys | Gln | Val | Ser | Glu | Glu | Val | Gly | Lys | Met | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Thr | Arg | Ser | His | Ser | Thr | Glu | Lys | Gly | Gln | Leu | Ile | Thr | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Ser | Ser | Ile | Gly | Lys | Glu | Ala | Trp | Asp | Leu | Leu | Ser | Ala | Gln | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Met | Asn | Ile | Asp | Lys | Asp | Glu | Val | Ile | Val | Leu | Val | Ser | Gly | His |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Ala | Lys | Pro | Leu | Lys | Leu | Lys | Ala | Asn | Tyr | Tyr | Phe | Lys | Asn | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Glu | Leu | Leu | Ser | Arg | Ile | Asn | Trp | Glu | Val | Lys | Pro | Asn | Glu | Glu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 106...237
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TAAGGGCTTA CGCATAAAAT CGCATCCGCG CCGATTTTTT GAGCGAACTT TGCTAAAGAA 60  
 AGGGACTCGC TCGTGGCGTT ACTGCCCACG CCGGCTAACA CTTTC ATG CGC GAA TTT 117  
 Met Arg Glu Phe  
 1

GAG GGC GTT TTA GTG TTT TTG CAA GTT TCT ATG GCG ATT TCA ATG CAA 165  
 Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala Ile Ser Met Gln  
 5 10 15 20

CGC ATG TGC TCT TTG TGG GTG AGC GTG GCG GAT TCT CCT GTC GTG CCA 213  
 Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser Pro Val Val Pro  
 25 30 35

ACA GGC ACG CAT GCG TCC ATG CCC TGAAAAATTT GGCGCTTGAT CAAGGTTTCA 267  
 Thr Gly Thr His Ala Ser Met Pro  
 40

TAAGCGGCCT CATCAACGCT CAA 290

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met Arg Glu Phe Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala  
 1 5 10 15  
 Ile Ser Met Gln Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser  
 20 25 30  
 Pro Val Val Pro Thr Gly Thr His Ala Ser Met Pro  
 35 40

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...369
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

$$\frac{1}{\Gamma(\alpha)} \int_0^t (t-\tau)^{\alpha-1} f(\tau) d\tau = I^\alpha f(t), \quad t \geq 0, \quad (1)$$

85  
Ser Tyr Asp Phe Asp Asp Gly Lys  
100

90

95

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...617
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GTTTAGAAAA GCGTTTGAAC GCTATAAAAA ATGCAGAGTG GCTTTAAGGC ATG AAA  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| AAG ATT GCA TTT TTT ATT TTT GTC ATT TTG TTT TCG GTA GGG ATT TAT | 104 |
| Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly Ile Tyr |     |
| 5 10 15                                                         |     |
| TTA ATT TGG CAT GTT TTA TTG GAA AAA GCC CTA GAA TTG AAA TTA GCA | 152 |
| Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys Leu Ala |     |
| 20 25 30                                                        |     |
| ACC TCA GCT AAT GAT TTG CTT TTA AAA TTG TTG GCA ATT CTT GGC GTT | 200 |
| Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu Gly Val |     |
| 35 40 45 50                                                     |     |
| TTT TCA ATG TTA GTG CTT TTT CAA GGC ATT ATT TCT TCG TAT AAG AAG | 248 |
| Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr Lys Lys |     |
| 55 60 65                                                        |     |
| CGC CAA CTC AAA CGC ATT TTA CAA AAA ATA GAC GCC ATG AAC GGC TTT | 296 |
| Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn Gly Phe |     |
| 70 75 80                                                        |     |
| GAA TTT GAA GAA TAT TCC AAA ATC TTT TTC ACT TCA AAG GGT TTT GAA | 344 |
| Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly Phe Glu |     |
| 85 90 95                                                        |     |
| GTG AGC ATC ACG CAA AAA AGC GGC GAT TAT GGA GCG GAT TTG ATT ATA | 392 |
| Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu Ile Ile |     |
| 100 105 110                                                     |     |
| GAA AAA GAC GGC ATC AAG TGG GCG GTT CAA GTC AAA CGC TAC TCG CAT | 440 |
| Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr Ser His |     |
| 115 120 125 130                                                 |     |

|            |                   |                   |                   |                   |            |                   |                   |            |                   |            |            |                   |                   |                   |            |     |     |
|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|------------|-------------------|------------|------------|-------------------|-------------------|-------------------|------------|-----|-----|
| AAA<br>Lys | GTT<br>Val        | TCG<br>Ser        | CCC<br>Pro        | AAA<br>Lys<br>135 | GCC<br>Ala | ATT<br>Ile        | CAA<br>Gln        | GAG<br>Glu | GTG<br>Val<br>140 | GTC<br>Val | TCT<br>Ser | TCT<br>Ser        | AAA<br>Lys        | GCT<br>Ala<br>145 | TAT<br>Tyr | 488 |     |
| TAC<br>Tyr | GCT<br>Ala        | TGC<br>Cys        | GAA<br>Glu<br>150 | AAA<br>Lys        | GCT<br>Ala | TGC<br>Cys        | GTG<br>Val<br>155 | ATC<br>Ile | ACC<br>Thr        | AAC<br>Asn | AGC<br>Ser | TAT<br>Tyr        | TTC<br>Phe<br>160 | ACG<br>Thr        | CAA<br>Gln | 536 |     |
| GCC<br>Ala | GCT<br>Ala        | CAA<br>Gln<br>165 | AAA<br>Lys        | CTG<br>Leu        | GCT<br>Ala | CAA<br>Gln<br>170 | GCT<br>Ala        | AAC<br>Asn | GAA<br>Glu        | GTG<br>Val | CTC<br>Leu | TTG<br>Leu<br>175 | ATT<br>Ile        | GAC<br>Asp        | AGA<br>Arg | 584 |     |
| GAC<br>Asp | GAA<br>Glu<br>180 | TGG<br>Trp        | GTC<br>Val        | AGG<br>Arg        | TTT<br>Phe | TTG<br>Leu<br>185 | AAC<br>Asn        | GAA<br>Glu | AAG<br>Lys        | AGA<br>Arg | TGAACCGATC |                   |                   | CCATCAGATC        |            | 637 |     |
| GTTTGTTC   |                   |                   | AAGTTCTTTT        |                   |            | AAAAATTTTGT       |                   |            | CGT               |            |            |                   |                   |                   |            |     | 670 |

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:296:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Lys        | Lys        | Ile        | Ala<br>5   | Phe        | Phe        | Ile        | Phe        | Val<br>10  | Ile        | Leu        | Phe        | Ser        | Val<br>15 | Gly        |
| Ile        | Tyr        | Leu        | Ile<br>20  | Trp        | His        | Val        | Leu        | Leu<br>25  | Glu        | Lys        | Ala        | Leu        | Glu<br>30  | Leu       | Lys        |
| Leu        | Ala        | Thr<br>35  | Ser        | Ala        | Asn        | Asp        | Leu<br>40  | Leu        | Leu        | Lys        | Leu        | Leu<br>45  | Ala        | Ile       | Leu        |
| Gly        | Val<br>50  | Phe        | Ser        | Met        | Leu        | Val<br>55  | Leu        | Phe        | Gln        | Gly        | Ile<br>60  | Ile        | Ser        | Ser       | Tyr        |
| Lys<br>65  | Lys        | Arg        | Gln        | Leu        | Lys<br>70  | Arg        | Ile        | Leu        | Gln        | Lys<br>75  | Ile        | Asp        | Ala        | Met       | Asn<br>80  |
| Gly        | Phe        | Glu        | Phe        | Glu<br>85  | Glu        | Tyr        | Ser        | Lys        | Ile<br>90  | Phe        | Phe        | Thr        | Ser<br>95  | Lys       | Gly        |
| Phe        | Glu        | Val        | Ser<br>100 | Ile        | Thr        | Gln        | Lys        | Ser<br>105 | Gly        | Asp        | Tyr        | Gly        | Ala<br>110 | Asp       | Leu        |
| Ile        | Ile        | Glu<br>115 | Lys        | Asp        | Gly        | Ile        | Lys<br>120 | Trp        | Ala        | Val        | Gln        | Val<br>125 | Lys        | Arg       | Tyr        |
| Ser        | His<br>130 | Lys        | Val        | Ser        | Pro        | Lys<br>135 | Ala        | Ile        | Gln        | Glu        | Val<br>140 | Val        | Ser        | Ser       | Lys        |
| Ala<br>145 | Tyr        | Tyr        | Ala        | Cys        | Glu<br>150 | Lys        | Ala        | Cys        | Val        | Ile<br>155 | Thr        | Asn        | Ser        | Tyr       | Phe<br>160 |
| Thr        | Gln        | Ala        | Ala        | Gln<br>165 | Lys        | Leu        | Ala        | Gln        | Ala<br>170 | Asn        | Glu        | Val        | Leu<br>175 | Leu       | Ile        |
| Asp        | Arg        | Asp        | Glu<br>180 | Trp        | Val        | Arg        | Phe        | Leu<br>185 | Asn        | Glu        | Lys        | Arg        |            |           |            |

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 125...538
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```
CAAAGAGTGG GATAAAATCA CAGAAATTTG TAAGAGAGCG CTAGCTTTAA GATAACAAAA 60
AGATCATGGC ATTTTGTATT TGCTTAATAA CACTATAATA AAATTTTTAA TAAGGAGATA 120
CATC ATG TTA GAA AAT GTC AAA AAG TCC TTT TTT AGG GTT TTG TGC TTG 169
Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu
 1 5 10 15

GGT GCG TTG TGT TTA GGG GGG CTA ATG GCA GAG CAA GAC CCT AAA GAG 217
Gly Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu
 20 25 30

CTT GTG GGT TTG GGG GCA AAG AGC TAC AAA GAG AAA GAT TTC ACT CAA 265
Leu Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln
 35 40 45

GCG AAG AAA TAT TTT GAG AAA GCG TGC GAT TTG AAA GAA AAT AGC GGG 313
Ala Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly
 50 55 60

TGT TTT AAT TTA GGG GTG CTT TAT TAT CAA GGG CAA GGG GTG GAA AAG 361
Cys Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys
 65 70 75

AAC TTG AAA AAA GCC GCC TCC TTT TAC GCT AAA GCT TGC GAT TTG AAT 409
Asn Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn
 80 85 90 95

TAC AGC AAT GGG TGT CAT TTG CTA GGG AAT TTA TAT TAC AGC GGG CAA 457
Tyr Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln
 100 105 110

GGC GTG TCC CAA AAC ACC AAT AAA GCC CTA CAA TAC TAC TCT AAA GCG 505
Gly Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala
 115 120 125

TGC GAT TTG AAA TAC GCT GAA GGG TGC GCG ACT TAGGGGGGAT TTATCATGAT 558
Cys Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
 130 135

GGTAAAGTGG TAACTAGGGA TTTTAAAAAA GCGGTGGAAT AT 600
```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu Gly
 1 5 10 15
Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu Leu
 20 25 30
Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln Ala
 35 40 45
Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly Cys
 50 55 60
Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys Asn
 65 70 75 80
Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn Tyr
 85 90 95
Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln Gly
 100 105 110
Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala Cys
 115 120 125
Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
 130 135

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...826
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

TTTTAAGATT GGTAGCCATT GGCATTATGT TTGATCTTAT TAAAGCAGAG GAGTAACA 58

ATG GGA TAC GCA AGC AAA TTA GCC TTG AAG ATT TGT TTG GCA AGT TTA 106
Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
 1 5 10 15

TGT TTA TTT AGC GCT CTT GGT GCA GAA CAC CTT GAA CAA AAA AGG AAC 154
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn

```

| 20                                                                                                                                                    | 25 | 30 |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|-----|
| TAT ATT TAT AAM GGG GAG GAA GCC TAT AAT AAT AAG GAA TAT GAG CGG<br>Tyr Ile Tyr Xaa Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg<br>35 40 45        |    |    | 202 |
| GCG GCT TCT TTT TAT AAG AGC GCG ATT AAA AAT GGC GAG CCG CTT GCT<br>Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala<br>50 55 60        |    |    | 250 |
| TAT GTT CTT TTA GGG ATC ATG TAT GAA AAT GGT AGG GGT GTG CCT AAA<br>Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys<br>65 70 75 80     |    |    | 298 |
| GAT GAA AAG AAA GCG GCT GAA TAT TTT CAA AAA GCG GTT GAT AAC GAT<br>Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp<br>85 90 95        |    |    | 346 |
| ATA CCT AGA GGG TAT AAC AAT TTA GGC GTG ATG TAT AAA GAG GGT AGA<br>Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg<br>100 105 110     |    |    | 394 |
| GGT GTG CCT AAA GAT GAA AAG AAA GCC GTG GAG TAT TTT AGA ATA GCT<br>Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala<br>115 120 125     |    |    | 442 |
| ACC GAG AAG GGC TAT ACT AAC GCC TAT ATA AAC TTA GGC ATC ATG TAT<br>Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr<br>130 135 140     |    |    | 490 |
| ATG GAG GGT AGG GGA GTT CCA AGC AAC TAT GTG AAA GCG ACA GAG TGC<br>Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys<br>145 150 155 160 |    |    | 538 |
| TTT AGA AAA GCG ATG CAT AAG GGT AAT GTA GAA GCT TAT ATC CTT TTA<br>Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu<br>165 170 175     |    |    | 586 |
| GGG GAT ATT TAT TAT AGT GGG AAT GAT CAA TTG GGT ATT GAG CCA GAC<br>Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp<br>180 185 190     |    |    | 634 |
| AAA GAT AAG GCG ATT GTC TAT TAT AAA ATG GCG GCT GAT ATG AGC TCT<br>Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser<br>195 200 205     |    |    | 682 |
| TCT AGA GCT TAT GAA GGG TTA GCA GAG TCT TAT CAG TAT GGG TTA GGC<br>Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly<br>210 215 220     |    |    | 730 |
| GTG GAA AAA GAT AAG AAA AAG GCT GAA GAA TAC ATG CAA AAA GCA TGC<br>Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys<br>225 230 235 240 |    |    | 778 |
| GAT TTT GAC ATT GAT AAA AAT TGT AAG AAA AAG AAC ACT TCA AGC CGA<br>Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg<br>245 250 255     |    |    | 826 |



TAAGTCTCAA ACTTGGGCTT GATTAGGATT TTTGTTTTAT TTTAAGTAGC ATG

879

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Tyr | Ala | Ser | Lys | Leu | Ala | Leu | Lys | Ile | Cys | Leu | Ala | Ser | Leu | 1   | 5   | 10  | 15  |
| Cys | Leu | Phe | Ser | Ala | Leu | Gly | Ala | Glu | His | Leu | Glu | Gln | Lys | Arg | Asn | 20  | 25  | 30  |     |
| Tyr | Ile | Tyr | Xaa | Gly | Glu | Glu | Ala | Tyr | Asn | Asn | Lys | Glu | Tyr | Glu | Arg | 35  | 40  | 45  |     |
| Ala | Ala | Ser | Phe | Tyr | Lys | Ser | Ala | Ile | Lys | Asn | Gly | Glu | Pro | Leu | Ala | 50  | 55  | 60  |     |
| Tyr | Val | Leu | Leu | Gly | Ile | Met | Tyr | Glu | Asn | Gly | Arg | Gly | Val | Pro | Lys | 65  | 70  | 75  | 80  |
| Asp | Glu | Lys | Lys | Ala | Ala | Glu | Tyr | Phe | Gln | Lys | Ala | Val | Asp | Asn | Asp | 85  | 90  | 95  |     |
| Ile | Pro | Arg | Gly | Tyr | Asn | Asn | Leu | Gly | Val | Met | Tyr | Lys | Glu | Gly | Arg | 100 | 105 | 110 |     |
| Gly | Val | Pro | Lys | Asp | Glu | Lys | Lys | Ala | Val | Glu | Tyr | Phe | Arg | Ile | Ala | 115 | 120 | 125 |     |
| Thr | Glu | Lys | Gly | Tyr | Thr | Asn | Ala | Tyr | Ile | Asn | Leu | Gly | Ile | Met | Tyr | 130 | 135 | 140 |     |
| Met | Glu | Gly | Arg | Gly | Val | Pro | Ser | Asn | Tyr | Val | Lys | Ala | Thr | Glu | Cys | 145 | 150 | 155 | 160 |
| Phe | Arg | Lys | Ala | Met | His | Lys | Gly | Asn | Val | Glu | Ala | Tyr | Ile | Leu | Leu | 165 | 170 | 175 |     |
| Gly | Asp | Ile | Tyr | Tyr | Ser | Gly | Asn | Asp | Gln | Leu | Gly | Ile | Glu | Pro | Asp | 180 | 185 | 190 |     |
| Lys | Asp | Lys | Ala | Ile | Val | Tyr | Tyr | Lys | Met | Ala | Ala | Asp | Met | Ser | Ser | 195 | 200 | 205 |     |
| Ser | Arg | Ala | Tyr | Glu | Gly | Leu | Ala | Glu | Ser | Tyr | Gln | Tyr | Gly | Leu | Gly | 210 | 215 | 220 |     |
| Val | Glu | Lys | Asp | Lys | Lys | Lys | Ala | Glu | Glu | Tyr | Met | Gln | Lys | Ala | Cys | 225 | 230 | 235 | 240 |
| Asp | Phe | Asp | Ile | Asp | Lys | Asn | Cys | Lys | Lys | Lys | Asn | Thr | Ser | Ser | Arg | 245 | 250 | 255 |     |

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

THE UNIVERSITY OF CHICAGO PRESS

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[illegible]

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 66...1058  
(D) OTHER INFORMATION:

|            |        |      |             |            |         |     |            |     |     |     |     |     |     |     |     |     |
|------------|--------|------|-------------|------------|---------|-----|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAAAACTAGA | GAGTGT | TATA | AAGAAAAACAG | AAGAGTGGAT | GTCAAAT | TAA | TGAAGTAATT | 60  |     |     |     |     |     |     |     |     |
| CTAGG      | ATG    | AAA  | AGG         | CTT        | TTT     | TTT | ATC        | CCT | TTT | ATC | GCT | CCC | TTT | TTT | CTC | 110 |
| Met        | Lys    | Arg  | Leu         | Phe        | Phe     | Ile | Pro        | Phe | Ile | Ala | Pro | Phe | Phe | Leu |     |     |
| 1          |        |      |             | 5          |         |     |            |     | 10  |     |     |     |     | 15  |     |     |
| AAT        | GGG    | GAG  | CCT         | TCA        | GCG     | TTT | GAT        | TTG | CAA | AGT | GGG | GCT | ACC | AAA | AAA | 158 |
| Asn        | Gly    | Glu  | Pro         | Ser        | Ala     | Phe | Asp        | Leu | Gln | Ser | Gly | Ala | Thr | Lys | Lys |     |
|            |        |      | 20          |            |         |     |            | 25  |     |     |     |     |     | 30  |     |     |
| GAA        | CTC    | AAG  | CAG         | TTG        | CAA     | ATC | AAT        | AGT | AAG | AAT | TTT | TCT | AAT | ATT | TTG | 206 |
| Glu        | Leu    | Lys  | Gln         | Leu        | Gln     | Ile | Asn        | Ser | Lys | Asn | Phe | Ser | Asn | Ile | Leu |     |
|            |        |      | 35          |            |         |     |            | 40  |     |     |     |     | 45  |     |     |     |
| ACC        | AAA    | ATC  | CAT         | TCG        | CAA     | GTA | GAG        | GCT | AAC | ACT | CAA | GCT | CAA | GAG | GGT | 254 |
| Thr        | Lys    | Ile  | His         | Ser        | Gln     | Val | Glu        | Ala | Asn | Thr | Gln | Ala | Gln | Glu | Gly |     |
|            |        | 50   |             |            |         |     | 55         |     |     |     |     | 60  |     |     |     |     |
| TTG        | AGA    | AGC  | GTT         | TAT        | GAG     | GGG | CAG        | GCT | AAT | AAG | ATT | AAA | GAT | CTC | AAT | 302 |
| Leu        | Arg    | Ser  | Val         | Tyr        | Glu     | Gly | Gln        | Ala | Asn | Lys | Ile | Lys | Asp | Leu | Asn |     |
|            | 65     |      |             |            |         | 70  |            |     |     |     | 75  |     |     |     |     |     |
| AAC        | GCT    | ATC  | CTT         | TCC        | CAA     | GAA | GAA        | TCC | TTA | CGA | GCC | TTA | AAA | GCT | TCG | 350 |
| Asn        | Ala    | Ile  | Leu         | Ser        | Gln     | Glu | Glu        | Ser | Leu | Arg | Ala | Leu | Lys | Ala | Ser |     |
| 80         |        |      |             |            | 85      |     |            |     |     | 90  |     |     |     |     | 95  |     |
| CAA        | GAA    | GTG  | CAG         | GCT        | AAC     | ACG | CTT        | AAG | CAG | CAA | TCG | CAA | ACT | TTA | GAG | 398 |
| Gln        | Glu    | Val  | Gln         | Ala        | Asn     | Thr | Leu        | Lys | Gln | Gln | Ser | Gln | Thr | Leu | Glu |     |
|            |        |      | 100         |            |         |     |            | 105 |     |     |     |     |     | 110 |     |     |
| GAT        | TTG    | AGG  | AAT         | GAG        | ATT     | CAC | GCT        | AAC | CAG | CAA | GCT | ATC | CAG | CAG | TTA | 446 |
| Asp        | Leu    | Arg  | Asn         | Glu        | Ile     | His | Ala        | Asn | Gln | Gln | Ala | Ile | Gln | Gln | Leu |     |
|            |        |      | 115         |            |         |     |            | 120 |     |     |     |     | 125 |     |     |     |
| GAC        | AAG    | CAA  | AAT         | AAA        | GAG     | ATG | AGT        | GAA | TTA | TTG | ACC | AAG | TTA | AGC | CAG | 494 |
| Asp        | Lys    | Gln  | Asn         | Lys        | Glu     | Met | Ser        | Glu | Leu | Leu | Thr | Lys | Leu | Ser | Gln |     |
|            |        | 130  |             |            |         |     | 135        |     |     |     |     | 140 |     |     |     |     |
| GAT        | TTG    | GTT  | TCA         | CAA        | ATC     | GCC | TTA        | ATC | CAA | AAA | GCT | CTC | AAA | GAA | CAA | 542 |
| Asp        | Leu    | Val  | Ser         | Gln        | Ile     | Ala | Leu        | Ile | Gln | Lys | Ala | Leu | Lys | Glu | Gln |     |
|            | 145    |      |             |            |         | 150 |            |     |     |     | 155 |     |     |     |     |     |
| GAG        | GAA    | AAA  | GCT         | GAA        | AAG     | CCG | CTC        | AAA | TCA | AAC | GCT | CCG | GCT | AAT | AAA | 590 |

[illegible]

(2) INFORMATION FOR SEO ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

[illegible]

[REDACTED]

(A) LENGTH: 531 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- 391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AACAAATGCG AGTTTCAAAT ATTTTGTAGG ATTTTAGGAA AGAAATAGGT T ATG AAT  | 57  |
| Met Asn                                                           |     |
| 1                                                                 |     |
| ATA TCG GTT AAC CCC TAT TTA ATG GCG GTC GTT TTT GTG GTG TTT GTG   | 105 |
| Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val Phe Val   |     |
| 5 10 15                                                           |     |
| TTA TTG TTA TGG GCG ATG AAT GTT TGG GTG TAT AGG CCT TTG TTG GCT   | 153 |
| Leu Leu Leu Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu Leu Ala   |     |
| 20 25 30                                                          |     |
| TTT ATG GAT AAC AGA CAG GCA GAG ATA AAG GAT AGC TTG GCT AAA ATC   | 201 |
| Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala Lys Ile   |     |
| 35 40 45 50                                                       |     |
| AAA ACG GAT AAT GCC CAA AGT GTG GAG ATT GGC CAT CAA ATT GAG GCT   | 249 |
| Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile Glu Ala   |     |
| 55 60 65                                                          |     |
| CTT CTT AAA GAA GCG GCT GAA AAA CGC AGA GAA ATA ATA GCA GAA GCG   | 297 |
| Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala Glu Ala   |     |
| 70 75 80                                                          |     |
| ATT CAA AAA GCC ACA GAG TCC TAT GAC GCT GTG ATC AAG CAA AAA GAG   | 345 |
| Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln Lys Glu   |     |
| 85 90 95                                                          |     |
| AAC GAA CTC AAT CAA GAG TTT GAA GCG TTT GCG AAG CAA TTA CAA AAT   | 393 |
| Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu Gln Asn   |     |
| 100 105 110                                                       |     |
| GAA AAG CAA GCG CTA AAA GAG CAG TTG CAA GCG CAA ATG CCG GTA TTT   | 441 |
| Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro Val Phe   |     |
| 115 120 125 130                                                   |     |
| GAA GAC GAG TTA AAC AAG CGT GTG GCT ATG GGT TTA GGG AGT TGATGAATG | 492 |
| Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser           |     |
| 135 140                                                           |     |
| TTTGTAGTTA AAATGGTGTG AGGGTTTTTG ATCCTTTTA                        | 531 |

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Asn Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val  
1 5 10 15  
Phe Val Leu Leu Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu  
20 25 30  
Leu Ala Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala  
35 40 45  
Lys Ile Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile  
50 55 60  
Glu Ala Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala  
65 70 75 80  
Glu Ala Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln  
85 90 95  
Lys Glu Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu  
100 105 110  
Gln Asn Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro  
115 120 125  
Val Phe Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 387...5777
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAGCTTGATA TGGAGCATTT TGATCGCTTG ACCATGCTCA ATAGAGAAGA ATTGTTGCGC | 60  |
| GTTACTCGCT CCTTTCTCAA GCGATTTTAT AAGAGCCTTT CAGCCATAAC GGCAAGGATT | 120 |
| ATAAAGAAGG CGATCAAATC CCTAAAGAAG AAATCGCTTC AATCAACCGC TTCACCTTGG | 180 |
| CTAGTTTGGT CAAAAAGTAT TCTAAAGAAG TGCAAAACCA CTATGAAATC ACTAAAAACA | 240 |
| ATTTCTTAGA GCAAAGAAA GTTTTGGGCG AAGAGCATGA AGAAAAGCTT TCTATTTTAG  | 300 |
| AAAAAGATGA TATTTTGCCT AATGGCGTGA TCAAAAAGT CAAGCTCTAT ATCGCTACAA  | 360 |
| AACGAAAGCT TAAAGTGGGC GATAAA ATG GCA GGA AGG CAT GGG AAT AAA GGG  | 413 |
| Met Ala Gly Arg His Gly Asn Lys Gly                               |     |
| 1 5                                                               |     |
| ATT GTG TCT AAT ATC GTG CCG GTT GCG GAT ATG CCT TAT ACC GCT GAT   | 461 |
| Ile Val Ser Asn Ile Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp   |     |
| 10 15 20 25                                                       |     |
| GGC GAG CCT GTA GAT ATT GTT TTA AAC CCT TTA GGC GTG CCA AGC CGC   | 509 |
| Gly Glu Pro Val Asp Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg   |     |
| 30 35 40                                                          |     |
| ATG AAT ATC GGG CAG ATT TTA GAA ATG CAT TTA GGC TTA GTG GGG AAA   | 557 |
| Met Asn Ile Gly Gln Ile Leu Glu Met His Leu Gly Leu Val Gly Lys   |     |

| 45  |     |     |     |     |     |     |     |     |     | 50  |     |     |     |     |     |      |  |  |  | 55 |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|----|--|--|--|--|--|--|--|--|--|--|
| GAA | TTT | GGG | AAG | CAA | ATC | GCT | CGC | ATG | CTA | GAG | GAT | AAA | ACC | AAA | GAT | 605  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Glu | Phe | Gly | Lys | Gln | Ile | Ala | Arg | Met | Leu | Glu | Asp | Lys | Thr | Lys | Asp |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 60  |     |     |     |     |     |     |     |     |     | 70  |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| TTT | GCC | AAA | GAA | TTG | CGT | GCT | AAA | ATG | CTA | GAA | AWC | GCT | AAC | GCT | ATT | 653  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Phe | Ala | Lys | Glu | Leu | Arg | Ala | Lys | Met | Leu | Glu | Xaa | Ala | Asn | Ala | Ile |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 75  |     |     |     |     |     |     |     |     |     | 85  |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| AAT | GAA | AAA | GAC | CCC | TTG | ACA | ATC | CAT | GCG | CTT | GAG | AAT | TGT | TCT | GAT | 701  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Asn | Glu | Lys | Asp | Pro | Leu | Thr | Ile | His | Ala | Leu | Glu | Asn | Cys | Ser | Asp |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 90  |     |     |     |     |     |     |     |     |     | 105 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| GAA | GAG | CTT | TTG | GAA | TAC | GCA | AAA | GAT | TGG | AGC | AAG | GGC | GTT | AAG | ATG | 749  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Glu | Glu | Leu | Leu | Glu | Tyr | Ala | Lys | Asp | Trp | Ser | Lys | Gly | Val | Lys | Met |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 110 |     |     |     |     |     |     |     |     |     | 120 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| GCT | ATC | CCT | GTG | TTT | GAA | GGC | ATC | TCG | CAA | GAA | AAA | TTT | TAT | AAG | CTA | 797  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Ala | Ile | Pro | Val | Phe | Glu | Gly | Ile | Ser | Gln | Glu | Lys | Phe | Tyr | Lys | Leu |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 125 |     |     |     |     |     |     |     |     |     | 135 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| TTT | GAA | TTA | GCT | AAG | ATC | GCT | ATG | GAT | GGC | AAA | ATG | GAT | CTG | TAT | GAC | 845  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Phe | Glu | Leu | Ala | Lys | Ile | Ala | Met | Asp | Gly | Lys | Met | Asp | Leu | Tyr | Asp |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 140 |     |     |     |     |     |     |     |     |     | 150 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| GGA | CGC | ACA | GGC | GAG | AAA | ATG | AGG | GAG | CGC | GTG | AAT | GTG | GGC | TAC | ATG | 893  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Gly | Arg | Thr | Gly | Glu | Lys | Met | Arg | Glu | Arg | Val | Asn | Val | Gly | Tyr | Met |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 155 |     |     |     |     |     |     |     |     |     | 165 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| TAT | ATG | ATC | AAA | CTC | CAC | CAT | TTA | GTG | GAT | GAA | AAA | GTC | CAT | GCC | AGA | 941  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Tyr | Met | Ile | Lys | Leu | His | His | Leu | Val | Asp | Glu | Lys | Val | His | Ala | Arg |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 170 |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| AGC | ACA | GGC | CCT | TAT | AGC | TTA | GTA | ACG | CAC | CAG | CCC | GTG | GGG | GGT | AAA | 989  |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Ser | Thr | Gly | Pro | Tyr | Ser | Leu | Val | Thr | His | Gln | Pro | Val | Gly | Gly | Lys |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 190 |     |     |     |     |     |     |     |     |     | 200 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| GCG | CTC | TTT | GGG | GGT | CAA | AGG | TTT | GGG | GAA | ATG | GAA | GTG | TGG | GCC | TTG | 1037 |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Ala | Leu | Phe | Gly | Gly | Gln | Arg | Phe | Gly | Glu | Met | Glu | Val | Trp | Ala | Leu |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 205 |     |     |     |     |     |     |     |     |     | 215 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| GAA | GCT | TAT | GGC | GCA | GCG | CAC | ACT | CTA | AAA | GAA | ATG | CTC | ACC | ATT | AAA | 1085 |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Glu | Ala | Tyr | Gly | Ala | Ala | His | Thr | Leu | Lys | Glu | Met | Leu | Thr | Ile | Lys |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 220 |     |     |     |     |     |     |     |     |     | 230 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| TCC | GAT | GAT | ATT | AGA | GGC | AGA | GAG | AAC | GCT | TAT | AGG | GCT | ATC | GCT | AAA | 1133 |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Ser | Asp | Asp | Ile | Arg | Gly | Arg | Glu | Asn | Ala | Tyr | Arg | Ala | Ile | Ala | Lys |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 235 |     |     |     |     |     |     |     |     |     | 245 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| GGT | GAG | CAA | GTG | GGC | GAG | AGT | GAA | ATC | CCT | GAG | ACT | TTC | TAT | GTT | TTG | 1181 |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Gly | Glu | Gln | Val | Gly | Glu | Ser | Glu | Ile | Pro | Glu | Thr | Phe | Tyr | Val | Leu |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 250 |     |     |     |     |     |     |     |     |     | 265 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| ACT | AAA | GAA | TTG | CAA | TCG | CTC | GCT | TTG | GAT | ATT | AAT | ATT | TTT | GGG | GAC | 1229 |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| Thr | Lys | Glu | Leu | Gln | Ser | Leu | Ala | Leu | Asp | Ile | Asn | Ile | Phe | Gly | Asp |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |
| 270 |     |     |     |     |     |     |     |     |     | 280 |     |     |     |     |     |      |  |  |  |    |  |  |  |  |  |  |  |  |  |  |



|                                                                 |      |
|-----------------------------------------------------------------|------|
| GAT GTG GAT GAG GAT GGA GCA CCT AAA CCC ATT GTC ATT AAA GAA GAT | 1277 |
| Asp Val Asp Glu Asp Gly Ala Pro Lys Pro Ile Val Ile Lys Glu Asp |      |
| 285 290 295                                                     |      |
| GAC AGG CCT AAA GAC TTT AGC TCT TTC CAG CTC ACA CTA GCT AGC CCT | 1325 |
| Asp Arg Pro Lys Asp Phe Ser Ser Phe Gln Leu Thr Leu Ala Ser Pro |      |
| 300 305 310                                                     |      |
| GAA AAA ATC CAT TCT TGG AGT TAT GGG GAA GTT AAA AAG CCA GAA ACG | 1373 |
| Glu Lys Ile His Ser Trp Ser Tyr Gly Glu Val Lys Lys Pro Glu Thr |      |
| 315 320 325                                                     |      |
| ATC AAT TAT CGC ACC CTA AAA CCT GAA CGA GAC GGC TTG TTT TGC ATG | 1421 |
| Ile Asn Tyr Arg Thr Leu Lys Pro Glu Arg Asp Gly Leu Phe Cys Met |      |
| 330 335 340 345                                                 |      |
| AAA ATC TTT GGC CCC ACT AAA GAT TAT GAA TGC TTG TGC GGC AAA TAC | 1469 |
| Lys Ile Phe Gly Pro Thr Lys Asp Tyr Glu Cys Leu Cys Gly Lys Tyr |      |
| 350 355 360                                                     |      |
| AAA AAG CCT CGC TTC AAA GAC ATT GGC ACA TGC GAA AAA TGC GGC GTG | 1517 |
| Lys Lys Pro Arg Phe Lys Asp Ile Gly Thr Cys Glu Lys Cys Gly Val |      |
| 365 370 375                                                     |      |
| GCG ATC ACG CAC TCC AAA GTC AGG CGT TTT AGA ATG GGC CAT ATT GAA | 1565 |
| Ala Ile Thr His Ser Lys Val Arg Arg Phe Arg Met Gly His Ile Glu |      |
| 380 385 390                                                     |      |
| TTG GCC ACT CCT GTA GCG CAT ATC TGG TAT GTT AAT TCC TTG CCT AGC | 1613 |
| Leu Ala Thr Pro Val Ala His Ile Trp Tyr Val Asn Ser Leu Pro Ser |      |
| 395 400 405                                                     |      |
| CGT ATC GGC ACG CTT TTA GGC GTT AAG ATG AAA GAC TTA GAG CGC GTG | 1661 |
| Arg Ile Gly Thr Leu Leu Gly Val Lys Met Lys Asp Leu Glu Arg Val |      |
| 410 415 420 425                                                 |      |
| TTG TAT TAT GAA GCT TAT ATC GTT AAA GAA CCA GGC GAA GCC GCT TAT | 1709 |
| Leu Tyr Tyr Glu Ala Tyr Ile Val Lys Glu Pro Gly Glu Ala Ala Tyr |      |
| 430 435 440                                                     |      |
| GAC AAT GAA GGC ACT AAG CTT GTG ATG AAA TAC GAT ATT TTG AAT GAA | 1757 |
| Asp Asn Glu Gly Thr Lys Leu Val Met Lys Tyr Asp Ile Leu Asn Glu |      |
| 445 450 455                                                     |      |
| GAG CAG TAT CAA AAT ATC TCA CGA AGA TAC GAA GAC AGG GGC TTT GTA | 1805 |
| Glu Gln Tyr Gln Asn Ile Ser Arg Arg Tyr Glu Asp Arg Gly Phe Val |      |
| 460 465 470                                                     |      |
| GCG CAA ATG GGC GGT GAA GCG ATC AAG GAT TTG TTA GAA GAA ATT GAT | 1853 |
| Ala Gln Met Gly Gly Glu Ala Ile Lys Asp Leu Leu Glu Glu Ile Asp |      |
| 475 480 485                                                     |      |
| TTG ATC ACC TTA TTG CAG AGT TTG AAA GAA GAA GTG AAA GAC ACC AAT | 1901 |
| Leu Ile Thr Leu Leu Gln Ser Leu Lys Glu Glu Val Lys Asp Thr Asn |      |
| 490 495 500 505                                                 |      |
| TCT GAT GCG AAA AAG AAA AAA CTC ATT AAG CGT TTG AAA GTG GTA GAA | 1949 |
| Ser Asp Ala Lys Lys Lys Lys Leu Ile Lys Arg Leu Lys Val Val Glu |      |

| 510 |     |     |     |     |     |     |     |     |     | 515 |     |     |     |     | 520 |      |  |  |  |     |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|-----|--|--|--|--|--|
| AGC | TTT | TTA | AAT | TCT | GGT | AAT | AGG | CCT | GAA | TGG | ATG | ATG | CTC | ACG | GTT | 1997 |  |  |  |     |  |  |  |  |  |
| Ser | Phe | Leu | Asn | Ser | Gly | Asn | Arg | Pro | Glu | Trp | Met | Met | Leu | Thr | Val |      |  |  |  |     |  |  |  |  |  |
| 525 |     |     |     |     |     |     |     |     |     | 530 |     |     |     |     | 535 |      |  |  |  |     |  |  |  |  |  |
| TTA | CCG | GTA | TTG | CCA | CCG | GAT | TTA | AGG | CCT | TTA | GTC | GCG | CTA | GAT | GGC | 2045 |  |  |  |     |  |  |  |  |  |
| Leu | Pro | Val | Leu | Pro | Pro | Asp | Leu | Arg | Pro | Leu | Val | Ala | Leu | Asp | Gly |      |  |  |  |     |  |  |  |  |  |
| 540 |     |     |     |     |     |     |     |     |     | 545 |     |     |     |     | 550 |      |  |  |  |     |  |  |  |  |  |
| GGG | AAG | TTT | GCA | GTC | AGC | GAT | GTG | AAT | GAA | TTG | TAT | CGT | CGT | GTC | ATC | 2093 |  |  |  |     |  |  |  |  |  |
| Gly | Lys | Phe | Ala | Val | Ser | Asp | Val | Asn | Glu | Leu | Tyr | Arg | Arg | Val | Ile |      |  |  |  |     |  |  |  |  |  |
| 555 |     |     |     |     |     |     |     |     |     | 560 |     |     |     |     | 565 |      |  |  |  |     |  |  |  |  |  |
| AAT | CGT | AAC | CAA | CGC | TTG | AAA | CGC | TTA | ATG | GAG | CTT | GGA | GCG | CCA | GAA | 2141 |  |  |  |     |  |  |  |  |  |
| Asn | Arg | Asn | Gln | Arg | Leu | Lys | Arg | Leu | Met | Glu | Leu | Gly | Ala | Pro | Glu |      |  |  |  |     |  |  |  |  |  |
| 570 |     |     |     |     |     |     |     |     |     | 575 |     |     |     |     | 580 |      |  |  |  | 585 |  |  |  |  |  |
| ATC | ATT | GTG | CGC | AAT | GAA | AAA | AGG | ATG | TTG | CAA | GAA | GCC | GTG | GAT | GTG | 2189 |  |  |  |     |  |  |  |  |  |
| Ile | Ile | Val | Arg | Asn | Glu | Lys | Arg | Met | Leu | Gln | Glu | Ala | Val | Asp | Val |      |  |  |  |     |  |  |  |  |  |
| 590 |     |     |     |     |     |     |     |     |     | 595 |     |     |     |     | 600 |      |  |  |  |     |  |  |  |  |  |
| CTT | TTT | GAT | AAC | GGC | CGC | AGC | ACT | AAT | GCG | GTT | AAA | GGG | GCT | AAC | AAA | 2237 |  |  |  |     |  |  |  |  |  |
| Leu | Phe | Asp | Asn | Gly | Arg | Ser | Thr | Asn | Ala | Val | Lys | Gly | Ala | Asn | Lys |      |  |  |  |     |  |  |  |  |  |
| 605 |     |     |     |     |     |     |     |     |     | 610 |     |     |     |     | 615 |      |  |  |  |     |  |  |  |  |  |
| CGC | CCT | TTA | AAA | TCG | CTC | AGT | GAA | ATC | ATT | AAA | GGC | AAG | CAG | GGG | CGT | 2285 |  |  |  |     |  |  |  |  |  |
| Arg | Pro | Leu | Lys | Ser | Leu | Ser | Glu | Ile | Ile | Lys | Gly | Lys | Gln | Gly | Arg |      |  |  |  |     |  |  |  |  |  |
| 620 |     |     |     |     |     |     |     |     |     | 625 |     |     |     |     | 630 |      |  |  |  |     |  |  |  |  |  |
| TTC | AGG | CAA | AAC | CTT | TTA | GGT | AAG | CGC | GTG | GAT | TTT | TCA | GGC | AGA | AGC | 2333 |  |  |  |     |  |  |  |  |  |
| Phe | Arg | Gln | Asn | Leu | Leu | Gly | Lys | Arg | Val | Asp | Phe | Ser | Gly | Arg | Ser |      |  |  |  |     |  |  |  |  |  |
| 635 |     |     |     |     |     |     |     |     |     | 640 |     |     |     |     | 645 |      |  |  |  |     |  |  |  |  |  |
| GTG | ATT | GTG | GTT | GGG | CCT | AAT | CTC | AAA | ATG | GAT | GAA | TGC | GGG | TTG | CCT | 2381 |  |  |  |     |  |  |  |  |  |
| Val | Ile | Val | Val | Gly | Pro | Asn | Leu | Lys | Met | Asp | Glu | Cys | Gly | Leu | Pro |      |  |  |  |     |  |  |  |  |  |
| 650 |     |     |     |     |     |     |     |     |     | 655 |     |     |     |     | 660 |      |  |  |  | 665 |  |  |  |  |  |
| AAA | AAC | ATG | GCG | TTA | GAA | CTC | TTC | AAA | CCG | CAT | TTG | TTA | TCC | AAG | CTT | 2429 |  |  |  |     |  |  |  |  |  |
| Lys | Asn | Met | Ala | Leu | Glu | Leu | Phe | Lys | Pro | His | Leu | Leu | Ser | Lys | Leu |      |  |  |  |     |  |  |  |  |  |
| 670 |     |     |     |     |     |     |     |     |     | 675 |     |     |     |     | 680 |      |  |  |  |     |  |  |  |  |  |
| GAA | GAG | AGA | GGC | TAT | GCC | ACC | ACG | CTC | AAA | CAG | GCT | AAA | CGC | ATG | ATT | 2477 |  |  |  |     |  |  |  |  |  |
| Glu | Glu | Arg | Gly | Tyr | Ala | Thr | Thr | Leu | Lys | Gln | Ala | Lys | Arg | Met | Ile |      |  |  |  |     |  |  |  |  |  |
| 685 |     |     |     |     |     |     |     |     |     | 690 |     |     |     |     | 695 |      |  |  |  |     |  |  |  |  |  |
| GAG | CAA | AAA | AGC | AAT | GAA | GTA | TGG | GAG | TGC | TTG | CAA | GAA | ATC | ACA | GAG | 2525 |  |  |  |     |  |  |  |  |  |
| Glu | Gln | Lys | Ser | Asn | Glu | Val | Trp | Glu | Cys | Leu | Gln | Glu | Ile | Thr | Glu |      |  |  |  |     |  |  |  |  |  |
| 700 |     |     |     |     |     |     |     |     |     | 705 |     |     |     |     | 710 |      |  |  |  |     |  |  |  |  |  |
| GGG | TAT | CCG | GTG | CTA | CTC | AAC | CGC | GCT | CCT | ACC | TTG | CAC | AAG | CAA | TCC | 2573 |  |  |  |     |  |  |  |  |  |
| Gly | Tyr | Pro | Val | Leu | Leu | Asn | Arg | Ala | Pro | Thr | Leu | His | Lys | Gln | Ser |      |  |  |  |     |  |  |  |  |  |
| 715 |     |     |     |     |     |     |     |     |     | 720 |     |     |     |     | 725 |      |  |  |  |     |  |  |  |  |  |
| ATT | CAA | GCG | TTC | CAT | CCA | AAG | CTG | ATT | GAC | GGC | AAA | GCG | ATC | CAA | TTG | 2621 |  |  |  |     |  |  |  |  |  |
| Ile | Gln | Ala | Phe | His | Pro | Lys | Leu | Ile | Asp | Gly | Lys | Ala | Ile | Gln | Leu |      |  |  |  |     |  |  |  |  |  |
| 730 |     |     |     |     |     |     |     |     |     | 735 |     |     |     |     | 740 |      |  |  |  | 745 |  |  |  |  |  |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CAC CCG TTA GTG TGT TCA GCG TTC AAC GCC GAT TTT GAC GGG GAC CAA | 2669 |
| His Pro Leu Val Cys Ser Ala Phe Asn Ala Asp Phe Asp Gly Asp Gln |      |
| 750 755 760                                                     |      |
| ATG GCG GTG CAT GTG CCT TTA AGC CAG GAA GCG ATC GCT GAA TGC AAG | 2717 |
| Met Ala Val His Val Pro Leu Ser Gln Glu Ala Ile Ala Glu Cys Lys |      |
| 765 770 775                                                     |      |
| GTG CTG ATG CTA AGC TCT ATG AAT ATC CTT TTG CCT GCT AGC GGT AAG | 2765 |
| Val Leu Met Leu Ser Ser Met Asn Ile Leu Leu Pro Ala Ser Gly Lys |      |
| 780 785 790                                                     |      |
| GCC GTA GCC ATT CCT AGC CAA GAT ATG GTT TTA GGG CTT TAT TAT CTT | 2813 |
| Ala Val Ala Ile Pro Ser Gln Asp Met Val Leu Gly Leu Tyr Tyr Leu |      |
| 795 800 805                                                     |      |
| TCT TTA GAA AAG AGC GGG GTC AAG GGC GAG CAT AAG CTT TTT TCT AGC | 2861 |
| Ser Leu Glu Lys Ser Gly Val Lys Gly Glu His Lys Leu Phe Ser Ser |      |
| 810 815 820 825                                                 |      |
| GTG AAT GAA ATC ATC ACC GCC ATT GAC ACG AAA GAA TTA GAC ATC CAC | 2909 |
| Val Asn Glu Ile Ile Thr Ala Ile Asp Thr Lys Glu Leu Asp Ile His |      |
| 830 835 840                                                     |      |
| GCA AAG ATT AGG GTT TTA GAT CAA GGG AAT ATT ATC GCT ACG AGT GCA | 2957 |
| Ala Lys Ile Arg Val Leu Asp Gln Gly Asn Ile Ile Ala Thr Ser Ala |      |
| 845 850 855                                                     |      |
| GGG CGC ATG ATC ATT AAG TCC ATT TTG CCT GAT TTT ATC CCT ACG GAT | 3005 |
| Gly Arg Met Ile Ile Lys Ser Ile Leu Pro Asp Phe Ile Pro Thr Asp |      |
| 860 865 870                                                     |      |
| TTG TGG AAC AGA CCC ATG AAG AAA AAA GAT ATT GGC GTG CTT GTG GAT | 3053 |
| Leu Trp Asn Arg Pro Met Lys Lys Lys Asp Ile Gly Val Leu Val Asp |      |
| 875 880 885                                                     |      |
| TAT GTG CAT AAA GTT GGC GGT ATC GGT ATT ACT GCA ACC TTT TTG GAT | 3101 |
| Tyr Val His Lys Val Gly Gly Ile Gly Ile Thr Ala Thr Phe Leu Asp |      |
| 890 895 900 905                                                 |      |
| AAT TTA AAA ACG CTT GGC TTT AGG TAT GCG ACT AAG GCT GGT ATT TCT | 3149 |
| Asn Leu Lys Thr Leu Gly Phe Arg Tyr Ala Thr Lys Ala Gly Ile Ser |      |
| 910 915 920                                                     |      |
| ATC TCT ATG GAG GAT ATT ATC ACG CCA AAA GAC AAG CAA AAA ATG GTG | 3197 |
| Ile Ser Met Glu Asp Ile Ile Thr Pro Lys Asp Lys Gln Lys Met Val |      |
| 925 930 935                                                     |      |
| GAA AAA GCC AAA GTA GAG GTT AAA AAA ATC CAG CAA CAA TAC GAT CAA | 3245 |
| Glu Lys Ala Lys Val Glu Val Lys Lys Ile Gln Gln Gln Tyr Asp Gln |      |
| 940 945 950                                                     |      |
| GGG CTG CTC ACT GAC CAA GAG CGT TAC AAT AAG ATC ATT GAC ACT TGG | 3293 |
| Gly Leu Leu Thr Asp Gln Glu Arg Tyr Asn Lys Ile Ile Asp Thr Trp |      |
| 955 960 965                                                     |      |
| ACT GAA GTC AAT GAC AAA ATG AGT AAA GAA ATG ATG ACC GCT ATC GCG | 3341 |
| Thr Glu Val Asn Asp Lys Met Ser Lys Glu Met Met Thr Ala Ile Ala |      |

| 970                                                             | 975  | 980  | 985  |      |
|-----------------------------------------------------------------|------|------|------|------|
| CAA GAT AAA GAG GGC TTT AAC TCT ATT TAT ATG ATG GCA GAT AGC GGC |      |      |      | 3389 |
| Gln Asp Lys Glu Gly Phe Asn Ser Ile Tyr Met Met Ala Asp Ser Gly | 990  | 995  | 1000 |      |
| GCA AGG GGT AGC GCG GCG CAA ATC CGT CAG CTT TCA GCG ATG AGG GGT |      |      |      | 3437 |
| Ala Arg Gly Ser Ala Ala Gln Ile Arg Gln Leu Ser Ala Met Arg Gly | 1005 | 1010 | 1015 |      |
| CTT ATG ACA AAG CCG GAC GGC AGT ATC ATT GAA ACG CCC ATT ATT TCT |      |      |      | 3485 |
| Leu Met Thr Lys Pro Asp Gly Ser Ile Ile Glu Thr Pro Ile Ile Ser | 1020 | 1025 | 1030 |      |
| AAC TTT AAA GAG GGG TTG AAT GTC TTA GAA TAC TTC AAT TCC ACG CAT |      |      |      | 3533 |
| Asn Phe Lys Glu Gly Leu Asn Val Leu Glu Tyr Phe Asn Ser Thr His | 1035 | 1040 | 1045 |      |
| GGC GCT AGA AAG GGC TTA GCG GAT ACA GCG CTA AAA ACA GCC AAT GCG |      |      |      | 3581 |
| Gly Ala Arg Lys Gly Leu Ala Asp Thr Ala Leu Lys Thr Ala Asn Ala | 1050 | 1055 | 1060 | 1065 |
| GGG TAT TTG ACC AGA AAG CTC ATT GAT GTT TCG CAA AAT GTC AAG GTG |      |      |      | 3629 |
| Gly Tyr Leu Thr Arg Lys Leu Ile Asp Val Ser Gln Asn Val Lys Val | 1070 | 1075 | 1080 |      |
| GTG TCT GAT GAT TGC GGC ACG CAT GAA GGG ATT GAA ATC ACG GAT ATT |      |      |      | 3677 |
| Val Ser Asp Asp Cys Gly Thr His Glu Gly Ile Glu Ile Thr Asp Ile | 1085 | 1090 | 1095 |      |
| GCG GTG GGG AGT GAG CTG ATT GAA CCT TTA GAA GAG CGT ATT TTT GGG |      |      |      | 3725 |
| Ala Val Gly Ser Glu Leu Ile Glu Pro Leu Glu Glu Arg Ile Phe Gly | 1100 | 1105 | 1110 |      |
| CGC GTT TTA TTA GAA GAT GTG ATC GAT CCC ATT ACG AAT GAA ATC TTG |      |      |      | 3773 |
| Arg Val Leu Leu Glu Asp Val Ile Asp Pro Ile Thr Asn Glu Ile Leu | 1115 | 1120 | 1125 |      |
| CTT TAT GCG GAC ACT TTG ATT GAT GAA GAG GGT GCT AAA AAG GTG GTT |      |      |      | 3821 |
| Leu Tyr Ala Asp Thr Leu Ile Asp Glu Glu Gly Ala Lys Lys Val Val | 1130 | 1135 | 1140 | 1145 |
| GAA GCC GGG ATT AAA TCC ATT ACG ATC CGC ACC CCA GTA ACT TGT AAA |      |      |      | 3869 |
| Glu Ala Gly Ile Lys Ser Ile Thr Ile Arg Thr Pro Val Thr Cys Lys | 1150 | 1155 | 1160 |      |
| GCG CCA AAG GGC GTG TGC GCG AAA TGC TAT GGC TTG AAT TTG GGC GAA |      |      |      | 3917 |
| Ala Pro Lys Gly Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu Gly Glu | 1165 | 1170 | 1175 |      |
| GGC AAG ATG AGT TAT CCG GGT GAA GCG GTG GGC GTG GTA GCC GCG CAA |      |      |      | 3965 |
| Gly Lys Met Ser Tyr Pro Gly Glu Ala Val Gly Val Val Ala Ala Gln | 1180 | 1185 | 1190 |      |
| TCT ATT GGG GAG CCT GGA ACG CAG CTC ACT TTA AGG ACT TTC CAT GTG |      |      |      | 4013 |
| Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Leu Arg Thr Phe His Val | 1195 | 1200 | 1205 |      |

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GGC GGG ACA GCG AGC AGG AGT CAG GAT GAG CGC GAA ATC GTA GCG AGC<br>Gly Gly Thr Ala Ser Arg Ser Gln Asp Glu Arg Glu Ile Val Ala Ser<br>1210 1215 1220 1225 | 4061 |
| AAA GAA GGT TTT GTG CGT TTT TAC AAC CTT AGG ACT TAC ACG AAT AAA<br>Lys Glu Gly Phe Val Arg Phe Tyr Asn Leu Arg Thr Tyr Thr Asn Lys<br>1230 1235 1240      | 4109 |
| GAG GGT AAA AAC ATT ATC GCT AAC CGC CGT AAC GCT TCT ATT TTA GTG<br>Glu Gly Lys Asn Ile Ile Ala Asn Arg Arg Asn Ala Ser Ile Leu Val<br>1245 1250 1255      | 4157 |
| GTA GAG CCT AAG ATT AAA GCG CCT TTT GAT GGG GAA TTA CGC ATT GAA<br>Val Glu Pro Lys Ile Lys Ala Pro Phe Asp Gly Glu Leu Arg Ile Glu<br>1260 1265 1270      | 4205 |
| ACG GTT TAT GAA GAA GTC GTT GTG AGC GTG AAA AAT GGC GAT CAA GAA<br>Thr Val Tyr Glu Glu Val Val Ser Val Lys Asn Gly Asp Gln Glu<br>1275 1280 1285          | 4253 |
| GCT AAA TTT GTT TTA AGG AGA AGC GAT ATT GTC AAG CCA AGC GAA TTA<br>Ala Lys Phe Val Leu Arg Arg Ser Asp Ile Val Lys Pro Ser Glu Leu<br>1290 1295 1300 1305 | 4301 |
| GCC GGC GTT GGC GGT AAG ATT GAG GGG AAA GTG TAT TTG CCT TAT GCT<br>Ala Gly Val Gly Gly Lys Ile Glu Gly Lys Val Tyr Leu Pro Tyr Ala<br>1310 1315 1320      | 4349 |
| AGT GGG CAT AAG GTG CAT AAG GGG GGA AGT ATC GCT GAT ATT ATC CAA<br>Ser Gly His Lys Val His Lys Gly Gly Ser Ile Ala Asp Ile Ile Gln<br>1325 1330 1335      | 4397 |
| GAG GGC TGG AAT GTG CCT AAT CGC ATC CCT TAT GCG AGC GAA TTG CTA<br>Glu Gly Trp Asn Val Pro Asn Arg Ile Pro Tyr Ala Ser Glu Leu Leu<br>1340 1345 1350      | 4445 |
| GTC AAG GAT AAT GAC CCT ATT GCG CAA GAT GTG TAT GCC AAA GAA AAA<br>Val Lys Asp Asn Asp Pro Ile Ala Gln Asp Val Tyr Ala Lys Glu Lys<br>1355 1360 1365      | 4493 |
| GGC GTA ATC AAA TAC TAT GTT TTA GAG GCT AAC CAT TTA GAG CGC ACC<br>Gly Val Ile Lys Tyr Tyr Val Leu Glu Ala Asn His Leu Glu Arg Thr<br>1370 1375 1380 1385 | 4541 |
| CAT GGG ATC AAA AAG GGC GAT ATG GTG AGT GAA AAA GGC TTG TTT GCG<br>His Gly Ile Lys Lys Gly Asp Met Val Ser Glu Lys Gly Leu Phe Ala<br>1390 1395 1400      | 4589 |
| GTG ATA GCT GAT GAT AAT GGT AGG GAA GCC GCT CGC CAT TAT ATC GCT<br>Val Ile Ala Asp Asp Asn Gly Arg Glu Ala Ala Arg His Tyr Ile Ala<br>1405 1410 1415      | 4637 |
| AGG GGT TCT GAG ATC TTG ATT GAT GAT AAT AGT GAA GTG AGC ACT AAT<br>Arg Gly Ser Glu Ile Leu Ile Asp Asp Asn Ser Glu Val Ser Thr Asn<br>1420 1425 1430      | 4685 |
| AGC GTG ATT TCT AAA CCC ACG ACT AAC ACT TTC AAA ACG ATT GCC ACA<br>Ser Val Ile Ser Lys Pro Thr Thr Asn Thr Phe Lys Thr Ile Ala Thr                        | 4733 |

| 1435                                                                                                                                                      | 1440 | 1445 |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|
| TGG GAT CCT TAC AAC ACC CCT ATC ATT GCG GAC TTT AAA GGT AAG GTG<br>Trp Asp Pro Tyr Asn Thr Pro Ile Ile Ala Asp Phe Lys Gly Lys Val<br>1450 1455 1460 1465 |      |      | 4781 |
| GGT TTT GTG GAT GTT ATC GCA GGG GTT ACG GTC GCT GAA AAA GAA GAC<br>Gly Phe Val Asp Val Ile Ala Gly Val Thr Val Ala Glu Lys Glu Asp<br>1470 1475 1480      |      |      | 4829 |
| GAA AAT ACC GGT ATC ACA AGC TTA GTG GTG AAT GAT TAC ATT CCA AGC<br>Glu Asn Thr Gly Ile Thr Ser Leu Val Val Asn Asp Tyr Ile Pro Ser<br>1485 1490 1495      |      |      | 4877 |
| GGA TAC AAA CCA AGC TTG TTT TTA GAG GGG GCT AAT GGC GAA GAG ATG<br>Gly Tyr Lys Pro Ser Leu Phe Leu Glu Gly Ala Asn Gly Glu Glu Met<br>1500 1505 1510      |      |      | 4925 |
| CGT TAT TTC CTA GAG CCA AAA ACC TCT ATC GCC ATT AGC GAT GGC TCT<br>Arg Tyr Phe Leu Glu Pro Lys Thr Ser Ile Ala Ile Ser Asp Gly Ser<br>1515 1520 1525      |      |      | 4973 |
| AGC GTG GAG CAA GCT GAA GTG TTA GCG AAA ATC CCT AAA GCG ACC GTT<br>Ser Val Glu Gln Ala Glu Val Leu Ala Lys Ile Pro Lys Ala Thr Val<br>1530 1535 1540 1545 |      |      | 5021 |
| AAA TCT AGG GAT ATT ACC GGG GGT CTC CCA AGG GTT TCG GAA CTC TTT<br>Lys Ser Arg Asp Ile Thr Gly Gly Leu Pro Arg Val Ser Glu Leu Phe<br>1550 1555 1560      |      |      | 5069 |
| GAA GCG AGA AAA CCC AAG CCT AAA GAT GTG GCG ATC CTT TCT GAA GTT<br>Glu Ala Arg Lys Pro Lys Pro Lys Asp Val Ala Ile Leu Ser Glu Val<br>1565 1570 1575      |      |      | 5117 |
| GAT GGG ATT GTG AGT TTT GGC AAA CCC ATT CGC AAT AAA GAA CAC ATC<br>Asp Gly Ile Val Ser Phe Gly Lys Pro Ile Arg Asn Lys Glu His Ile<br>1580 1585 1590      |      |      | 5165 |
| ATC GTA ACT TCT AAA GAT GGC CGT TCC ATG GAT TAT TTT GTG GAT AAA<br>Ile Val Thr Ser Lys Asp Gly Arg Ser Met Asp Tyr Phe Val Asp Lys<br>1595 1600 1605      |      |      | 5213 |
| GGC AAG CAA ATT TTA GTG CAT GCC GAT GAA TTT GTG CAT GCG GGA GAA<br>Gly Lys Gln Ile Leu Val His Ala Asp Glu Phe Val His Ala Gly Glu<br>1610 1615 1620 1625 |      |      | 5261 |
| GCG ATG ACG GAC GGA GTA ATT TCA AGC CAT GAT ATT TTA AGG ATC AGT<br>Ala Met Thr Asp Gly Val Ile Ser Ser His Asp Ile Leu Arg Ile Ser<br>1630 1635 1640      |      |      | 5309 |
| GGC GAA AAA GAG CTT TAT AAA TAC ATT GTG AGC GAA GTC CAG CAA GTG<br>Gly Glu Lys Glu Leu Tyr Lys Tyr Ile Val Ser Glu Val Gln Gln Val<br>1645 1650 1655      |      |      | 5357 |
| TAT CGC AGG CAG GGG GTG AGC ATT GCG GAC AAG CAC ATT GAA ATC ATT<br>Tyr Arg Arg Gln Gly Val Ser Ile Ala Asp Lys His Ile Glu Ile Ile<br>1660 1665 1670      |      |      | 5405 |



402



403



1475                      1480                      1485  
 Leu Val Val Asn Asp Tyr Ile Pro Ser Gly Tyr Lys Pro Ser Leu Phe  
 1490                      1495                      1500  
 Leu Glu Gly Ala Asn Gly Glu Glu Met Arg Tyr Phe Leu Glu Pro Lys  
 505                      1510                      1515                      1520  
 Thr Ser Ile Ala Ile Ser Asp Gly Ser Ser Val Glu Gln Ala Glu Val  
                     1525                      1530                      1535  
 Leu Ala Lys Ile Pro Lys Ala Thr Val Lys Ser Arg Asp Ile Thr Gly  
                     1540                      1545                      1550  
 Gly Leu Pro Arg Val Ser Glu Leu Phe Glu Ala Arg Lys Pro Lys Pro  
                     1555                      1560                      1565  
 Lys Asp Val Ala Ile Leu Ser Glu Val Asp Gly Ile Val Ser Phe Gly  
 1570                      1575                      1580  
 Lys Pro Ile Arg Asn Lys Glu His Ile Ile Val Thr Ser Lys Asp Gly  
 585                      1590                      1595                      1600  
 Arg Ser Met Asp Tyr Phe Val Asp Lys Gly Lys Gln Ile Leu Val His  
                     1605                      1610                      1615  
 Ala Asp Glu Phe Val His Ala Gly Glu Ala Met Thr Asp Gly Val Ile  
                     1620                      1625                      1630  
 Ser Ser His Asp Ile Leu Arg Ile Ser Gly Glu Lys Glu Leu Tyr Lys  
                     1635                      1640                      1645  
 Tyr Ile Val Ser Glu Val Gln Gln Val Tyr Arg Arg Gln Gly Val Ser  
 1650                      1655                      1660  
 Ile Ala Asp Lys His Ile Glu Ile Ile Val Ser Gln Met Leu Arg Gln  
 665                      1670                      1675                      1680  
 Val Arg Ile Leu Asp Ser Gly Asp Ser Lys Phe Ile Glu Gly Asp Leu  
                     1685                      1690                      1695  
 Val Ser Lys Lys Leu Phe Lys Glu Glu Asn Ala Arg Val Ile Ala Leu  
                     1700                      1705                      1710  
 Lys Gly Glu Pro Ala Ile Ala Glu Pro Val Leu Leu Gly Ile Thr Arg  
                     1715                      1720                      1725  
 Ala Ala Ile Gly Ser Asp Ser Ile Ile Ser Ala Ala Ser Phe Gln Glu  
                     1730                      1735                      1740  
 Thr Thr Lys Val Leu Thr Glu Ala Ser Ile Ala Met Lys Lys Asp Phe  
 745                      1750                      1755                      1760  
 Leu Glu Asp Leu Lys Glu Asn Val Val Leu Gly Arg Met Ile Pro Val  
                     1765                      1770                      1775  
 Gly Thr Gly Met Tyr Lys Asn Lys Lys Ile Val Leu Arg Ala Leu Glu  
                     1780                      1785                      1790  
 Asp Asn Ser Lys Phe  
 1795

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 65...640
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

TAAGCGATTT GCTCTGTGTG GTGATTGACC CTAGGATTGA TTTTGAAAAG CGTTGAGGGT 60  
AGGA ATG AAA ACT GAG ATG AAA TCT TCT TTA AAA CTT TTT ATG CGG CCT 109  
Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro  
1 5 10 15

TTG TTG GTG GTT TTA GCG TTC ATG TTG TTG TAT GCT TTA GTG CAT GCT 157  
Leu Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala  
20 25 30

GCG CTT GGT TTT TAT GTA AAA AAA GAC AGC GCT CCA ATA AGC CCA AAT 205  
Ala Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn  
35 40 45

GTA GAA AAA ACC GAG ACA GAG CGT CAA AAC GGC GTG CTT TCG CCC AAA 253  
Val Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys  
50 55 60

CAA GAA GAA GCC AAC GCA ACC ACA ACT GCC ACA GAA GAA AGC CCC ACC 301  
Gln Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr  
65 70 75

AAA GAC ACA GCG CCG CCT TTA GAC ACA GCC GCG CAA AAA CAA GAA ACT 349  
Lys Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr  
80 85 90 95

AAA CAA GAG CAA GAA AAA GAA AAC GAG CCT AAA CAA GAT AGC GTC CCG 397  
Lys Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro  
100 105 110

CCC GTT CAA AAC AAT CAA AAA ACC CCT ACA ACC CCC TTA ATG GGA AAA 445  
Pro Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys  
115 120 125

AAA CCT TTA GAG TAT AAA GTC GCA GTC AGT GGC GTG AAT GTG CGC GCT 493  
Lys Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala  
130 135 140

TTT CCC AGC ACA AAA GGT AAA ATC TTG GGA TTG CTT TTA AAA AAT AAA 541  
Phe Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Leu Lys Asn Lys  
145 150 155

AGC GTG AAA GTT TTA GAA ATC CAA AAC GAT TGG GCT GAA ATT GAA TTT 589  
Ser Val Lys Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe  
160 165 170 175

TCT CAC GAA ACA AAG GGC TAT GTG TTT TTA AAA CTT TTA AAA AAG GCT 637  
Ser His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala  
180 185 190

GAA TGAAAGAATA ATGAAATTAA AATCTTTTGG GGT'TTTTGGGA AATCCCATTA 690  
Glu

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Glu | Met | Lys | Ser | Ser | Leu | Lys | Leu | Phe | Met | Arg | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Val | Leu | Ala | Phe | Met | Leu | Leu | Tyr | Ala | Leu | Val | His | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Phe | Tyr | Val | Lys | Lys | Asp | Ser | Ala | Pro | Ile | Ser | Pro | Asn | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Lys | Thr | Glu | Thr | Glu | Arg | Gln | Asn | Gly | Val | Leu | Ser | Pro | Lys | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Ala | Asn | Ala | Thr | Thr | Thr | Ala | Thr | Glu | Glu | Ser | Pro | Thr | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Thr | Ala | Pro | Pro | Leu | Asp | Thr | Ala | Ala | Gln | Lys | Gln | Glu | Thr | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Glu | Gln | Glu | Lys | Glu | Asn | Glu | Pro | Lys | Gln | Asp | Ser | Val | Pro | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Gln | Asn | Asn | Gln | Lys | Thr | Pro | Thr | Thr | Pro | Leu | Met | Gly | Lys | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Glu | Tyr | Lys | Val | Ala | Val | Ser | Gly | Val | Asn | Val | Arg | Ala | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Ser | Thr | Lys | Gly | Lys | Ile | Leu | Gly | Leu | Leu | Lys | Asn | Lys | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Lys | Val | Leu | Glu | Ile | Gln | Asn | Asp | Trp | Ala | Glu | Ile | Glu | Phe | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| His | Glu | Thr | Lys | Gly | Tyr | Val | Phe | Leu | Lys | Leu | Leu | Lys | Lys | Ala | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...1502
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTATGACTTT TACTAAACCT TTTTSTAAGC TATAATCCAA AAATCTAAAA TAAAAAGGAA | 60  |
| TAAGC ATG AAA AAA TCC CTT TGT CTG TCT TTC TTT CTG ACT TTC TCT AAC | 110 |
| Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn       |     |

| 1                                                               | 5                                                               | 10  | 15 |  |
|-----------------------------------------------------------------|-----------------------------------------------------------------|-----|----|--|
| CCT CTT CAA GCC CTT GTG ATC GAG CTT TTA GAA GAA ATC AAA ACT TCG | Pro Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser | 158 |    |  |
|                                                                 | 20 25 30                                                        |     |    |  |
| CCG CAT AAA GGC ACT TTT AAG GCT AAA GTC CTT GAT TCT AAA AAA CCA | Pro His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Lys Pro | 206 |    |  |
|                                                                 | 35 40 45                                                        |     |    |  |
| AGA CAA GTT TTA GGC GTT TAT AAT ATC TCC CCA CAC AAA AAA CTC ACG | Arg Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr | 254 |    |  |
|                                                                 | 50 55 60                                                        |     |    |  |
| CTC ACT ATC ACC CAC ATA TCC ACT GCA ATC GTC TAT CAA CCC CTT GAT | Leu Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp | 302 |    |  |
|                                                                 | 65 70 75                                                        |     |    |  |
| GAA AAA CTT TCT TTA GAA ACA ACC TTA AAC CCT AAC CGC CCT ACT ATC | Glu Lys Leu Ser Leu Glu Thr Thr Leu Asn Pro Asn Arg Pro Thr Ile | 350 |    |  |
|                                                                 | 80 85 90 95                                                     |     |    |  |
| CCT AGA AAC ACC CAG ATT GTT TTT TCT TCA AAA GAA TTG AAA GAG TCG | Pro Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Ser | 398 |    |  |
|                                                                 | 100 105 110                                                     |     |    |  |
| CAC CCG CAC CAA ATG CCT TCT TTA AAC GCG CCC ATG CAA AAA CCA CAA | His Pro His Gln Met Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln | 446 |    |  |
|                                                                 | 115 120 125                                                     |     |    |  |
| AAC AAA CCC CAT TCA TCG CAA CAA CCT TCT CAA AAC TTT TCT TAC CCA | Asn Lys Pro His Ser Ser Gln Gln Pro Ser Gln Asn Phe Ser Tyr Pro | 494 |    |  |
|                                                                 | 130 135 140                                                     |     |    |  |
| GAG CCC AAA CTA GGC TCT AAA AAC TCT AAA AAC AGC CTT TTA CAG CCT | Glu Pro Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro | 542 |    |  |
|                                                                 | 145 150 155                                                     |     |    |  |
| TTA GCA ATT CCT AGC AAA ATA AGT CCC ACT AAC GAA ACT CAA ACG CCA | Leu Ala Ile Pro Ser Lys Ile Ser Pro Thr Asn Glu Thr Gln Thr Pro | 590 |    |  |
|                                                                 | 160 165 170 175                                                 |     |    |  |
| ACA AAC GAC ACT AAA CCC CCT TTA AAG CAT TCT TCA GAA GAT CAA GAA | Thr Asn Asp Thr Lys Pro Pro Leu Lys His Ser Ser Glu Asp Gln Glu | 638 |    |  |
|                                                                 | 180 185 190                                                     |     |    |  |
| AGC AAC CTC TTT ATA ACG CCA CCC ACT GAA AAA ACG CTC CCT AAC AAC | Ser Asn Leu Phe Ile Thr Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn | 686 |    |  |
|                                                                 | 195 200 205                                                     |     |    |  |
| ACC TCT AAC GCT GAT ATT AGT GAA AAC AAT GAA AGC AAT GAG AAT AAA | Thr Ser Asn Ala Asp Ile Ser Glu Asn Asn Glu Ser Asn Glu Asn Lys | 734 |    |  |
|                                                                 | 210 215 220                                                     |     |    |  |
| GAT AAT GTG GAA AAA CAA GCC ATT AGA GAT GCT AAT ATT AAA GAA TTT | Asp Asn Val Glu Lys Gln Ala Ile Arg Asp Ala Asn Ile Lys Glu Phe | 782 |    |  |
|                                                                 | 225 230 235                                                     |     |    |  |



465

470

475

AAGATGGTGG CTTGAGGCGG AATCGAACCA CCGACACGAA GATTTTC

1550

## (2) INFORMATION FOR SEQ ID NO:312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ser | Leu | Cys | Leu | Ser | Phe | Phe | Leu | Thr | Phe | Ser | Asn | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gln | Ala | Leu | Val | Ile | Glu | Leu | Leu | Glu | Glu | Ile | Lys | Thr | Ser | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Lys | Gly | Thr | Phe | Lys | Ala | Lys | Val | Leu | Asp | Ser | Lys | Lys | Pro | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Val | Leu | Gly | Val | Tyr | Asn | Ile | Ser | Pro | His | Lys | Lys | Leu | Thr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ile | Thr | His | Ile | Ser | Thr | Ala | Ile | Val | Tyr | Gln | Pro | Leu | Asp | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Leu | Ser | Leu | Glu | Thr | Thr | Leu | Asn | Pro | Asn | Arg | Pro | Thr | Ile | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Asn | Thr | Gln | Ile | Val | Phe | Ser | Ser | Lys | Glu | Leu | Lys | Glu | Ser | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | His | Gln | Met | Pro | Ser | Leu | Asn | Ala | Pro | Met | Gln | Lys | Pro | Gln | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Pro | His | Ser | Ser | Gln | Gln | Pro | Ser | Gln | Asn | Phe | Ser | Tyr | Pro | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Lys | Leu | Gly | Ser | Lys | Asn | Ser | Lys | Asn | Ser | Leu | Leu | Gln | Pro | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Ile | Pro | Ser | Lys | Ile | Ser | Pro | Thr | Asn | Glu | Thr | Gln | Thr | Pro | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Asp | Thr | Lys | Pro | Pro | Leu | Lys | His | Ser | Ser | Glu | Asp | Gln | Glu | Ser |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asn | Leu | Phe | Ile | Thr | Pro | Pro | Thr | Glu | Lys | Thr | Leu | Pro | Asn | Asn | Thr |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Asn | Ala | Asp | Ile | Ser | Glu | Asn | Asn | Glu | Ser | Asn | Glu | Asn | Lys | Asp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Val | Glu | Lys | Gln | Ala | Ile | Arg | Asp | Ala | Asn | Ile | Lys | Glu | Phe | Ala |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Cys | Gly | Lys | Trp | Val | Tyr | Asp | Asp | Glu | Asn | Leu | Gln | Ala | Tyr | Arg | Pro |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ser | Ile | Leu | Lys | Arg | Val | Asp | Glu | Asp | Lys | Gln | Thr | Ala | Thr | Asp | Ile |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| Thr | Pro | Cys | Asp | Tyr | Ser | Thr | Ala | Glu | Asn | Lys | Ser | Gly | Lys | Ile | Ile |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Thr | Pro | Tyr | Thr | Lys | Ile | Ser | Val | His | Lys | Thr | Glu | Pro | Leu | Glu | Glu |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Pro | Gln | Thr | Phe | Glu | Ala | Lys | Asn | Asn | Phe | Ala | Ile | Leu | Gln | Ala | Arg |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Ser | Ser | Thr | Glu | Lys | Cys | Lys | Arg | Ala | Arg | Ala | Arg | Lys | Asp | Gly | Thr |



325 330 335  
 Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp Glu  
 340 345 350  
 Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu Arg  
 355 360 365  
 Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser Glu  
 370 375 380  
 Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu Leu  
 385 390 395 400  
 Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly His  
 405 410 415  
 Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp Val  
 420 425 430  
 Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu Ile  
 435 440 445  
 Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn Ser  
 450 455 460  
 Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val  
 465 470 475

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...568
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TGTAAAATAG GGATTTGCTA GGCCTTTAGT CGTTAAAAGG TAATTATCAT TAAGGAGTTT | 60  |
| TTTAATC ATG GCA GAT ATT CAA AGG CGT GAT TTT TTA GGA ATG AGC CTT   | 109 |
| Met Ala Asp Ile Gln Arg Arg Asp Phe Leu Gly Met Ser Leu           |     |
| 1 5 10                                                            |     |
| GCT AGT GTT ACA GCT ATA GGG GCT ATA GCG AGT CTG GTA GCG ATG AAA   | 157 |
| Ala Ser Val Thr Ala Ile Gly Ala Ile Ala Ser Leu Val Ala Met Lys   |     |
| 15 20 25 30                                                       |     |
| AAG ACT TGG GAT CCG CTT CCA AGC GTT GTT TCA GCC GGT TTT ACG ACC   | 205 |
| Lys Thr Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr   |     |
| 35 40 45                                                          |     |
| ATA GAT GTG GCG AAT ATG CAA GAA GGG CAG TTT TCC ACC GTG GAA TGG   | 253 |
| Ile Asp Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp   |     |
| 50 55 60                                                          |     |
| CGT GGG AAA CCG GTC TAT ATC CTC AAG CGT TCT AAA AAA GAG GGC TTT   | 301 |
| Arg Gly Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe   |     |



130 135 140  
 Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala Glu Tyr  
 145 150 155 160  
 Lys Lys Met Met Ala Lys Ala  
 165

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1167
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TTATAATCAA AGCTATTTTA AAAGCTGAAT AGCTATAGTT ATTAGGATGC G ATG TCA | 57  |
| Met Ser                                                          |     |
| 1                                                                |     |
| AAA AGA ATG AAG TGT TTT AGT CAA AAA TGG TTG GTT TTT TTT GTT ACC  | 105 |
| Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe Val Thr  |     |
| 5 10 15                                                          |     |
| CTT TTA TTG GCT TCT TTA GGC CAT GCG AAA ATG GCT TTT GAA TCC GAT  | 153 |
| Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu Ser Asp  |     |
| 20 25 30                                                         |     |
| ATT GAC ACC AAA GCG CTA GAG GCT TTT GGG GTT AAT GCG GGC TTT TTA  | 201 |
| Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly Phe Leu  |     |
| 35 40 45 50                                                      |     |
| TCC CAA ATG CCC AAC GCT TTA AAA AAA ATG AAT AAA GAA GAA GAA TGG  | 249 |
| Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu Glu Trp  |     |
| 55 60 65                                                         |     |
| AAG AGA CTT GTC AAA AGA TTT GAT GTG AAT TAC CAG TTC ATC CCC ATC  | 297 |
| Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile Pro Ile  |     |
| 70 75 80                                                         |     |
| ATT AAA AAC ATG CTC ATA GAA GCG AGC GTG CCG CAA GAA TTT TTA TTT  | 345 |
| Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe Leu Phe  |     |
| 85 90 95                                                         |     |
| TTA GCC ATG GCC GAG TCT AAA TTT TCA TCA AGG GCT TAT AGC AGG AAA  | 393 |
| Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser Arg Lys  |     |
| 100 105 110                                                      |     |
| AAA GCG GTA GGG ATT TGG CAA TTC ATG CCA AGC ACG GCT AAA GAA TTA  | 441 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Lys | Ala | Val | Gly | Ile | Trp | Gln | Phe | Met | Pro | Ser | Thr | Ala | Lys | Glu | Leu |      |
| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |      |
| GGG | CTT | AAG | GTC | AAT | CAT | TAC | ATT | GAT | GAA | AGA | AGA | GAT | CCC | ATT | AAA | 489  |
| Gly | Leu | Lys | Val | Asn | His | Tyr | Ile | Asp | Glu | Arg | Arg | Asp | Pro | Ile | Lys |      |
|     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |      |
| AGC | ACT | CAA | GCG | GCG | ATC | ACT | TAT | TTG | AAA | CGG | CTC | TAC | AAG | CAA | ACC | 537  |
| Ser | Thr | Gln | Ala | Ala | Ile | Thr | Tyr | Leu | Lys | Arg | Leu | Tyr | Lys | Gln | Thr |      |
|     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |      |
| GGA | GAG | TGG | TAT | TTG | GTC | GCT | ATG | GCG | TAT | AAT | TAC | GGC | TTA | CGC | AAG | 585  |
| Gly | Glu | Trp | Tyr | Leu | Val | Ala | Met | Ala | Tyr | Asn | Tyr | Gly | Leu | Arg | Lys |      |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |      |
| GTT | CAA | AAC | GCT | ATT | AAA | GCC | GCC | GGC | ACT | TCG | GAC | ATT | AAA | ATT | TTG | 633  |
| Val | Gln | Asn | Ala | Ile | Lys | Ala | Ala | Gly | Thr | Ser | Asp | Ile | Lys | Ile | Leu |      |
|     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |      |
| TTG | GAT | GAA | GAT | AAG | AAA | TAC | CTC | CCT | AAA | GAA | ACA | CGA | GAG | TAT | ATC | 681  |
| Leu | Asp | Glu | Asp | Lys | Lys | Tyr | Leu | Pro | Lys | Glu | Thr | Arg | Glu | Tyr | Ile |      |
| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |      |
| CGC | TCC | ATT | CTA | AGC | CTA | GCG | TTA | AAA | TTC | AAC | AGC | CTA | GAC | AAC | CTC | 729  |
| Arg | Ser | Ile | Leu | Ser | Leu | Ala | Leu | Lys | Phe | Asn | Ser | Leu | Asp | Asn | Leu |      |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |      |
| AAA | GAT | AAA | GAA | TAT | CTG | CTC | AAT | CGT | GGG | GCG | AGG | GTG | AGT | TTA | GTG | 777  |
| Lys | Asp | Lys | Glu | Tyr | Leu | Leu | Asn | Arg | Gly | Ala | Arg | Val | Ser | Leu | Val |      |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |     |     |      |
| GGC | GTC | CCG | TTT | AAA | AGG | CGT | GCT | TCT | TTA | GTC | CAA | GTA | GCC | AAA | AAT | 825  |
| Gly | Val | Pro | Phe | Lys | Arg | Arg | Ala | Ser | Leu | Val | Gln | Val | Ala | Lys | Asn |      |
|     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |      |
| TTG | AAT | TTG | AGT | TTG | GAA | ACC | TTA | AAA | TCC | TAC | AAC | CAC | CAA | TTC | CGT | 873  |
| Leu | Asn | Leu | Ser | Leu | Glu | Thr | Leu | Lys | Ser | Tyr | Asn | His | Gln | Phe | Arg |      |
|     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |      |
| TAT | AAC | ATT | CTG | CCT | TCT | AAA | GAC | CCC | ACT | TAT | ACC | ATT | TAT | ATC | CCT | 921  |
| Tyr | Asn | Ile | Leu | Pro | Ser | Lys | Asp | Pro | Thr | Tyr | Thr | Ile | Tyr | Ile | Pro |      |
| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |      |
| TAT | GAA | AAA | CTC | GCT | CTT | TTC | AAA | CAA | CGC | CAG | ATC | AAA | CAA | AAT | AAA | 969  |
| Tyr | Glu | Lys | Leu | Ala | Leu | Phe | Lys | Gln | Arg | Gln | Ile | Lys | Gln | Asn | Lys |      |
|     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |      |
| AAC | ATT | CAA | GCC | AGT | TCA | AAA | AGC | CCT | TTT | ATC | ACC | CAT | GTG | GTC | TTA | 1017 |
| Asn | Ile | Gln | Ala | Ser | Ser | Lys | Ser | Pro | Phe | Ile | Thr | His | Val | Val | Leu |      |
|     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |      |
| CCT | AAA | GAA | ACC | CTA | TCT | TCT | ATC | GCT | AAA | CGC | TAT | CAA | GTC | AGT | ATT | 1065 |
| Pro | Lys | Glu | Thr | Leu | Ser | Ser | Ile | Ala | Lys | Arg | Tyr | Gln | Val | Ser | Ile |      |
|     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |     |      |
| TCC | AAT | ATC | CAA | TTA | GCC | AAT | GAT | CTC | AAA | GAT | TCT | AAT | ATT | TTT | ATC | 1113 |
| Ser | Asn | Ile | Gln | Leu | Ala | Asn | Asp | Leu | Lys | Asp | Ser | Asn | Ile | Phe | Ile |      |
|     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |      |



275                      280                      285  
 Ile Pro Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln  
 290                      295                      300  
 Asn Lys Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val  
 305                      310                      315                      320  
 Val Leu Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val  
 325                      330                      335  
 Ser Ile Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile  
 340                      345                      350  
 Phe Ile His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala  
 355                      360                      365  
 Thr Arg Glu Phe  
 370

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...510
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAATGAGCTA AAATGAGCGT TTCATTTGAC AAATAAAGGG ATTGA ATG GCT TTT AAG | 57  |
| Met Ala Phe Lys                                                   |     |
| 1                                                                 |     |
| GTG GTG CAA ATT TGC GGA GGG CTT GGG AAT CAA ATG TTT CAA TAC GCT   | 105 |
| Val Val Gln Ile Cys Gly Gly Leu Gly Asn Gln Met Phe Gln Tyr Ala   |     |
| 5 10 15 20                                                        |     |
| TTC GCT AAA AGT TTG CAA AAA CAC TCT AAT ACG CCT GTG CTG TTA GAT   | 153 |
| Phe Ala Lys Ser Leu Gln Lys His Ser Asn Thr Pro Val Leu Leu Asp   |     |
| 25 30 35                                                          |     |
| ATC ACT TCT TTT GAT TGG AGC GAT AGG AAA ATG CAA TTA GAA CTT TTC   | 201 |
| Ile Thr Ser Phe Asp Trp Ser Asp Arg Lys Met Gln Leu Glu Leu Phe   |     |
| 40 45 50                                                          |     |
| CCT ATT GAT TTG CCC TAT GCG AGC GCG AAA GAA ATC GCT ATA GCT AAA   | 249 |
| Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile Ala Ile Ala Lys   |     |
| 55 60 65                                                          |     |
| ATG CAA CAC CTC CCC AAG CTA GTA AGA GAC GCG CTC AAA TGC ATG GGA   | 297 |
| Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu Lys Cys Met Gly   |     |
| 70 75 80                                                          |     |
| TTT GAT AGG GTG AGT CAA GAA ATC GTT TTT GAA TAC GAG CCT AAA TTG   | 345 |







|            |            |            |     |     |     |     |     |     |     |     |            |            |     |     |     |      |
|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|------------|------------|-----|-----|-----|------|
| Pro        | Leu        | Asp        | Gly | Tyr | Tyr | Phe | Gly | Ala | Ala | Lys | Asp        | Phe        | Ala | Ser | Asp |      |
| 155        |            |            |     |     |     | 160 |     |     |     |     | 165        |            |     |     |     |      |
| AAA        | AGC        | CCT        | AAA | CAT | TTT | CAA | ATA | GTG | CGA | GAA | AAA        | GAC        | CCT | CGT | CAA | 640  |
| Lys        | Ser        | Pro        | Lys | His | Phe | Gln | Ile | Val | Arg | Glu | Lys        | Asp        | Pro | Arg | Gln |      |
| 170        |            |            |     |     | 175 |     |     |     |     | 180 |            |            |     |     | 185 |      |
| GCC        | TTT        | TCC        | CTT | TAT | GAG | CAT | TAC | CTT | AAT | GAA | AGC        | GAT        | ATG | CAA | ATC | 688  |
| Ala        | Phe        | Ser        | Leu | Tyr | Glu | His | Tyr | Leu | Asn | Glu | Ser        | Asp        | Met | Gln | Ile |      |
|            |            |            |     | 190 |     |     |     |     | 195 |     |            |            |     | 200 |     |      |
| ATC        | TAT        | GAA        | AGC | AAT | TAT | AAC | GCC | GGG | TTT | TTA | GTC        | GTG        | AAT | TTA | AAG | 736  |
| Ile        | Tyr        | Glu        | Ser | Asn | Tyr | Asn | Ala | Gly | Phe | Leu | Val        | Val        | Asn | Leu | Lys |      |
|            |            |            | 205 |     |     |     |     | 210 |     |     |            |            | 215 |     |     |      |
| CTG        | TGG        | CGT        | GCT | GAT | CAT | TTA | GAA | GAG | CGC | TTA | CTC        | AAT        | TTA | ACC | CAT | 784  |
| Leu        | Trp        | Arg        | Ala | Asp | His | Leu | Glu | Glu | Arg | Leu | Leu        | Asn        | Leu | Thr | His |      |
|            |            | 220        |     |     |     |     | 225 |     |     |     |            | 230        |     |     |     |      |
| CAA        | AAA        | GGC        | CAG | TGC | GTG | TTT | TAC | CCT | GAA | CAG | GAC        | CTT        | TTA | ACG | CTC | 832  |
| Gln        | Lys        | Gly        | Gln | Cys | Val | Phe | Tyr | Pro | Glu | Gln | Asp        | Leu        | Leu | Thr | Leu |      |
|            | 235        |            |     |     |     | 240 |     |     |     |     | 245        |            |     |     |     |      |
| GCA        | TGC        | TAT        | CAA | AAA | GTT | TTA | ATC | TTG | CCT | TAT | ATT        | TAT        | AAC | ACC | CAC | 880  |
| Ala        | Cys        | Tyr        | Gln | Lys | Val | Leu | Ile | Leu | Pro | Tyr | Ile        | Tyr        | Asn | Thr | His |      |
| 250        |            |            |     |     | 255 |     |     |     |     | 260 |            |            |     |     | 265 |      |
| CCT        | TTC        | ATG        | GCC | AAT | CAA | AAA | CGC | TTC | ATC | CCT | GAC        | AAA        | AAA | GAA | ATC | 928  |
| Pro        | Phe        | Met        | Ala | Asn | Gln | Lys | Arg | Phe | Ile | Pro | Asp        | Lys        | Lys | Glu | Ile |      |
|            |            |            |     | 270 |     |     |     | 275 |     |     |            |            |     | 280 |     |      |
| GTC        | ATG        | CTG        | CAT | TTT | TAT | TTT | GTA | GGA | AAA | CCT | TGG        | GTT        | TTA | CCT | ACT | 976  |
| Val        | Met        | Leu        | His | Phe | Tyr | Phe | Val | Gly | Lys | Pro | Trp        | Val        | Leu | Pro | Thr |      |
|            |            |            | 285 |     |     |     |     | 290 |     |     |            |            | 295 |     |     |      |
| TTT        | TCA        | TAT        | TCT | AAA | GAA | TGG | CAT | GAG | ACT | CTT | TTA        | AAA        | ACC | CCT | TTT | 1024 |
| Phe        | Ser        | Tyr        | Ser | Lys | Glu | Trp | His | Glu | Thr | Leu | Leu        | Lys        | Thr | Pro | Phe |      |
|            |            | 300        |     |     |     |     | 305 |     |     |     |            | 310        |     |     |     |      |
| TAT        | GCT        | GAA        | TAT | TCC | GTG | AAA | TTC | CTT | AAA | CAA | ATG        | ACA        | GAA | TGT | TTA | 1072 |
| Tyr        | Ala        | Glu        | Tyr | Ser | Val | Lys | Phe | Leu | Lys | Gln | Met        | Thr        | Glu | Cys | Leu |      |
|            | 315        |            |     |     |     | 320 |     |     |     |     | 325        |            |     |     |     |      |
| AGC        | CTT        | AAA        | GAC | AAA | CAA | AAA | ACC | TTT | GAA | TTT | CTT        | GCC        | CCC | CTA | CTC | 1120 |
| Ser        | Leu        | Lys        | Asp | Lys | Gln | Lys | Thr | Phe | Glu | Phe | Leu        | Ala        | Pro | Leu | Leu |      |
| 330        |            |            |     |     | 335 |     |     |     |     | 340 |            |            |     | 345 |     |      |
| AAT        | AAA        | AAA        | ACC | CTT | TTA | GAA | TAC | GTC | TTT | TTT | AGA        | TTG        | AAT | AGG | ATT | 1168 |
| Asn        | Lys        | Lys        | Thr | Leu | Leu | Glu | Tyr | Val | Phe | Phe | Arg        | Leu        | Asn | Arg | Ile |      |
|            |            |            | 350 |     |     |     |     | 355 |     |     |            |            |     | 360 |     |      |
| TTC        | AAA        | CGC        | TTA | AAA | GAA | AAA | TTT | TTT | AAC | TCT | TAGCGTTCTC | GTTTGGGCAA |     |     |     | 1221 |
| Phe        | Lys        | Arg        | Leu | Lys | Glu | Lys | Phe | Phe | Asn | Ser |            |            |     |     |     |      |
|            |            |            | 365 |     |     |     |     | 370 |     |     |            |            |     |     |     |      |
| CACGCTATAG | GCGAATTTGA | CATAAATCGC |     |     |     |     |     |     |     |     |            |            |     |     |     | 1251 |

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Ile | Ile | Pro | Ile | Val | Ile | Ala | Phe | Asp | Asn | His | Tyr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Pro | Ala | Gly | Val | Ser | Leu | Tyr | Ser | Met | Leu | Ala | Cys | Ala | Lys | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | His | Pro | Gln | Ser | Gln | Asn | Asp | Ser | Glu | Lys | Leu | Phe | Tyr | Lys | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Cys | Leu | Val | Asp | Asn | Leu | Ser | Leu | Glu | Asn | Gln | Ser | Lys | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Thr | Leu | Ala | Pro | Phe | Ser | Ala | Phe | Ser | Ser | Leu | Glu | Phe | Leu | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ile | Ser | Thr | Pro | Asn | Leu | His | Ala | Thr | Pro | Ile | Glu | Pro | Ser | Ala | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Lys | Ile | Asn | Glu | Ala | Phe | Leu | Gln | Leu | Asn | Ile | Tyr | Ala | Lys | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Phe | Ser | Lys | Met | Val | Met | Cys | Arg | Leu | Phe | Leu | Ala | Ser | Leu | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gln | Tyr | Asp | Lys | Ile | Ile | Met | Phe | Asp | Ala | Asp | Thr | Leu | Phe | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asn | Asp | Val | Ser | Glu | Ser | Phe | Phe | Ile | Pro | Leu | Asp | Gly | Tyr | Tyr | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Ala | Ala | Lys | Asp | Phe | Ala | Ser | Asp | Lys | Ser | Pro | Lys | His | Phe | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Val | Arg | Glu | Lys | Asp | Pro | Arg | Gln | Ala | Phe | Ser | Leu | Tyr | Glu | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Leu | Asn | Glu | Ser | Asp | Met | Gln | Ile | Ile | Tyr | Glu | Ser | Asn | Tyr | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Gly | Phe | Leu | Val | Val | Asn | Leu | Lys | Leu | Trp | Arg | Ala | Asp | His | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Glu | Arg | Leu | Leu | Asn | Leu | Thr | His | Gln | Lys | Gly | Gln | Cys | Val | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Pro | Glu | Gln | Asp | Leu | Leu | Thr | Leu | Ala | Cys | Tyr | Gln | Lys | Val | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Leu | Pro | Tyr | Ile | Tyr | Asn | Thr | His | Pro | Phe | Met | Ala | Asn | Gln | Lys |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Arg | Phe | Ile | Pro | Asp | Lys | Lys | Glu | Ile | Val | Met | Leu | His | Phe | Tyr | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Val | Gly | Lys | Pro | Trp | Val | Leu | Pro | Thr | Phe | Ser | Tyr | Ser | Lys | Glu | Trp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| His | Glu | Thr | Leu | Leu | Lys | Thr | Pro | Phe | Tyr | Ala | Glu | Tyr | Ser | Val | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Leu | Lys | Gln | Met | Thr | Glu | Cys | Leu | Ser | Leu | Lys | Asp | Lys | Gln | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | Phe | Glu | Phe | Leu | Ala | Pro | Leu | Leu | Asn | Lys | Lys | Thr | Leu | Leu | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Tyr | Val | Phe | Phe | Arg | Leu | Asn | Arg | Ile | Phe | Lys | Arg | Leu | Lys | Glu | Lys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| Phe | Phe | Asn | Ser |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...2193
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| CAAGAAGCCA TAGAAGCTGA TGGGAAATTC CACAAAGAAT AAGGGTAGAA A ATG AAA | 57  |
| Met Lys                                                          |     |
| 1                                                                |     |
| ATA ACA TAT TGT GAT GCG CTA ATT ATT GGA GGC GGA CTA GCT GGG TTA  | 105 |
| Ile Thr Tyr Cys Asp Ala Leu Ile Ile Gly Gly Gly Leu Ala Gly Leu  |     |
| 5 10 15                                                          |     |
| AGG GCT AGT ATC GCA TGC AAA CAA AAG GGT TTA AAC ACC ATC GTT TTA  | 153 |
| Arg Ala Ser Ile Ala Cys Lys Gln Lys Gly Leu Asn Thr Ile Val Leu  |     |
| 20 25 30                                                         |     |
| AGC CTA GTG CCT GTC AGG CGT TCG CAC TCT GCA GCC GCT CAA GGG GGC  | 201 |
| Ser Leu Val Pro Val Arg Arg Ser His Ser Ala Ala Ala Gln Gly Gly  |     |
| 35 40 45 50                                                      |     |
| ATG CAA GCG AGC CTT GCG AAC GCT AAA AAA AGC GAG GGC GAT AAT GAA  | 249 |
| Met Gln Ala Ser Leu Ala Asn Ala Lys Lys Ser Glu Gly Asp Asn Glu  |     |
| 55 60 65                                                         |     |
| GAT TTA CAC TTT TTA GAC ACG GTT AAG GGG AGC GAT TGG GGG TGC GAT  | 297 |
| Asp Leu His Phe Leu Asp Thr Val Lys Gly Ser Asp Trp Gly Cys Asp  |     |
| 70 75 80                                                         |     |
| CAG CAA GTG GCT AGG ATG TTT GTA ACC ACT GCT CCT AAA GCC ATT AGG  | 345 |
| Gln Gln Val Ala Arg Met Phe Val Thr Thr Ala Pro Lys Ala Ile Arg  |     |
| 85 90 95                                                         |     |
| GAA TTG GCC AGT TGG GGG GTG CCT TGG ACT AGG ATT AAA AAG GGC GAT  | 393 |
| Glu Leu Ala Ser Trp Gly Val Pro Trp Thr Arg Ile Lys Lys Gly Asp  |     |
| 100 105 110                                                      |     |
| AGG CCT GCG GTC GTC AAT GGT GAG CAT GTA ACT ATC ACT GAA AGA GAC  | 441 |
| Arg Pro Ala Val Val Asn Gly Glu His Val Thr Ile Thr Glu Arg Asp  |     |
| 115 120 125 130                                                  |     |
| GAC AGG CAT GGT TAT ATC TTA AGC CGT GAT TTT GGC GGC ACT AAA AAA  | 489 |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| Asp               | Arg               | His               | Gly               | Tyr<br>135        | Ile               | Leu               | Ser               | Arg               | Asp<br>140        | Phe               | Gly               | Gly               | Thr               | Lys<br>145        | Lys               |      |
| TGG<br>Trp        | CGC<br>Arg        | ACA<br>Thr        | TGC<br>Cys<br>150 | TTT<br>Phe        | ACG<br>Thr        | GCT<br>Ala        | GAT<br>Asp        | GCC<br>Ala<br>155 | ACA<br>Thr        | GGG<br>Gly        | CAT<br>His        | ACC<br>Thr<br>160 | ATG<br>Met<br>160 | CTT<br>Leu        | TAT<br>Tyr        | 537  |
| GCG<br>Ala        | GTC<br>Val        | GCT<br>Ala<br>165 | AAT<br>Asn        | GAA<br>Glu        | GCC<br>Ala        | TTA<br>Leu        | CAC<br>His<br>170 | CAC<br>His        | AAA<br>Lys        | GTG<br>Val        | GAT<br>Asp<br>175 | ATT<br>Ile<br>175 | CAA<br>Gln        | GAC<br>Asp        | AGA<br>Arg        | 585  |
| AAG<br>Lys        | GAC<br>Asp<br>180 | ATG<br>Met        | CTC<br>Leu        | GCT<br>Ala        | TTC<br>Phe        | ATT<br>Ile<br>185 | CAT<br>His        | CAT<br>His        | GAT<br>Asp        | AAT<br>Asn<br>190 | AAA<br>Lys<br>190 | TGC<br>Cys        | TAT<br>Tyr        | GGG<br>Gly        | GCG<br>Ala        | 633  |
| GTG<br>Val<br>195 | GTA<br>Val        | AGG<br>Arg        | GAT<br>Asp        | TTG<br>Leu        | ATC<br>Ile<br>200 | ACA<br>Thr        | GGC<br>Gly        | GAA<br>Glu        | ATT<br>Ile<br>205 | TCA<br>Ser<br>205 | GCG<br>Ala        | TAT<br>Tyr        | GTT<br>Val        | TCT<br>Ser        | AAA<br>Lys<br>210 | 681  |
| GGC<br>Gly        | ACG<br>Thr        | CTT<br>Leu        | TTA<br>Leu        | GCT<br>Ala<br>215 | ACC<br>Thr        | GGA<br>Gly        | GGT<br>Gly        | TAT<br>Tyr<br>220 | GGG<br>Gly<br>220 | CGC<br>Arg        | GTG<br>Val        | TAT<br>Tyr        | AAA<br>Lys        | CAC<br>His<br>225 | ACC<br>Thr        | 729  |
| ACT<br>Thr        | AAC<br>Asn        | GCT<br>Ala<br>230 | GTG<br>Val        | ATT<br>Ile        | TGC<br>Cys        | GAT<br>Asp        | GGA<br>Gly        | GCC<br>Ala<br>235 | GGG<br>Gly        | GCT<br>Ala        | GCA<br>Ala        | AGC<br>Ser<br>240 | GCC<br>Ala<br>240 | TTA<br>Leu        | GAA<br>Glu        | 777  |
| ACC<br>Thr        | GGC<br>Gly        | GTG<br>Val<br>245 | GCT<br>Ala        | AAA<br>Lys        | TTG<br>Leu        | GGC<br>Gly        | AAC<br>Asn<br>250 | ATG<br>Met        | GAA<br>Glu        | GCG<br>Ala        | GTG<br>Val        | CAA<br>Gln<br>255 | TTC<br>Phe        | CAC<br>His        | CCT<br>Pro        | 825  |
| ACC<br>Thr<br>260 | GCT<br>Ala        | TTA<br>Leu        | GTG<br>Val        | CCA<br>Pro        | AGC<br>Ser        | GGG<br>Gly<br>265 | ATT<br>Ile        | TTA<br>Leu        | ATG<br>Met        | ACC<br>Thr<br>270 | GAA<br>Glu<br>270 | GGT<br>Gly        | TGC<br>Cys        | AGG<br>Arg        | GGC<br>Gly        | 873  |
| GAT<br>Asp<br>275 | GGC<br>Gly        | GGT<br>Gly        | GTT<br>Val        | TTA<br>Leu        | AGA<br>Arg<br>280 | GAC<br>Asp        | AAG<br>Lys        | TTT<br>Phe        | GGC<br>Gly        | AGA<br>Arg<br>285 | CGC<br>Arg        | TTC<br>Phe        | ATG<br>Met        | CCC<br>Pro        | GCT<br>Ala<br>290 | 921  |
| TAT<br>Tyr        | GAG<br>Glu        | CCG<br>Pro        | GAG<br>Glu        | AAA<br>Lys<br>295 | AAA<br>Lys        | GAG<br>Glu        | CTT<br>Leu        | GCA<br>Ala<br>300 | AGC<br>Ser<br>300 | AGA<br>Arg        | GAT<br>Asp        | GTG<br>Val        | GTC<br>Val<br>305 | TCA<br>Ser<br>305 | AGG<br>Arg        | 969  |
| CGG<br>Arg        | ATT<br>Ile        | TTA<br>Leu        | GAG<br>Glu<br>310 | CAT<br>His        | ATC<br>Ile        | CAA<br>Gln        | AAA<br>Lys        | GGC<br>Gly<br>315 | TAT<br>Tyr        | GGA<br>Gly        | GCC<br>Ala        | AAA<br>Lys<br>320 | TCG<br>Ser<br>320 | CCT<br>Pro        | TAT<br>Tyr        | 1017 |
| GGG<br>Gly        | GAT<br>Asp        | CAT<br>His<br>325 | GTG<br>Val        | TGG<br>Trp        | CTG<br>Leu        | GAT<br>Asp        | ATT<br>Ile<br>330 | GCT<br>Ala        | ATT<br>Ile        | TTA<br>Leu        | GGG<br>Gly        | CGT<br>Arg<br>335 | AAC<br>Asn        | CAT<br>His        | GTG<br>Val        | 1065 |
| GAA<br>Glu        | AAA<br>Lys<br>340 | AAC<br>Asn        | TTA<br>Leu        | AGG<br>Arg        | GAT<br>Asp        | GTG<br>Val<br>345 | CGC<br>Arg        | GAT<br>Asp        | ATA<br>Ile        | GCC<br>Ala        | ATG<br>Met<br>350 | ACT<br>Thr        | TTT<br>Phe        | GCG<br>Ala        | GGC<br>Gly        | 1113 |
| ATT<br>Ile<br>355 | GAT<br>Asp        | CCG<br>Pro        | GCT<br>Ala        | GAT<br>Asp<br>360 | AGC<br>Ser        | AAG<br>Lys        | GAA<br>Glu        | CAA<br>Gln        | ACC<br>Thr<br>365 | AAA<br>Lys<br>365 | GAC<br>Asp        | AAC<br>Asn        | ATG<br>Met        | CAA<br>Gln<br>370 | GGA<br>Gly<br>370 | 1161 |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GTG CCC GCA AAT GAG CCT GAA TAC GGG CAA GCG ATG GCC AAG CAA AAA | 1209 |
| Val Pro Ala Asn Glu Pro Glu Tyr Gly Gln Ala Met Ala Lys Gln Lys |      |
| 375 380 385                                                     |      |
| GGC TGG ATC CCC ATA AAA CCC ATG CAA CAC TAT TCT ATG GGT GGG GTT | 1257 |
| Gly Trp Ile Pro Ile Lys Pro Met Gln His Tyr Ser Met Gly Gly Val |      |
| 390 395 400                                                     |      |
| AGG ACA AAC CCT AAA GGC GAA ACC CAT TTA AAA GGC TTG TTT TGC GCG | 1305 |
| Arg Thr Asn Pro Lys Gly Glu Thr His Leu Lys Gly Leu Phe Cys Ala |      |
| 405 410 415                                                     |      |
| GGT GAA GCG GCA TGC TGG GAT TTG CAT GGG TTT AAC CGC TTG GGG GGT | 1353 |
| Gly Glu Ala Ala Cys Trp Asp Leu His Gly Phe Asn Arg Leu Gly Gly |      |
| 420 425 430                                                     |      |
| AAT TCT GTG AGT GAA GCG GTG GTC GCT GGC ATG ATC ATT GGG GAT TAT | 1401 |
| Asn Ser Val Ser Glu Ala Val Val Ala Gly Met Ile Ile Gly Asp Tyr |      |
| 435 440 445 450                                                 |      |
| TTT GCC TCG CAT TGT TTA GAA GCG CAA ATT GAA ATC AAC ACG CAA AAA | 1449 |
| Phe Ala Ser His Cys Leu Glu Ala Gln Ile Glu Ile Asn Thr Gln Lys |      |
| 455 460 465                                                     |      |
| GTT GAA GCT TTC ATT AAA GAA AGC CAA GAC TAT ATG CAT TTT TTA TTG | 1497 |
| Val Glu Ala Phe Ile Lys Glu Ser Gln Asp Tyr Met His Phe Leu Leu |      |
| 470 475 480                                                     |      |
| CAT AAT GAA GGC AAA GAA GAT GTG TAT GAA ATT AGA GAG CGC ATG AAA | 1545 |
| His Asn Glu Gly Lys Glu Asp Val Tyr Glu Ile Arg Glu Arg Met Lys |      |
| 485 490 495                                                     |      |
| GAA GTC ATG GAT GAA AAA GTG GGC GTT TTT AGA GAA GGC AAA AGG CTA | 1593 |
| Glu Val Met Asp Glu Lys Val Gly Val Phe Arg Glu Gly Lys Arg Leu |      |
| 500 505 510                                                     |      |
| GAA GAA GCC CTT AAA GAA TTG CAA GAG CTT TAT GCA CGC TCC AAA AAC | 1641 |
| Glu Glu Ala Leu Lys Glu Leu Gln Glu Leu Tyr Ala Arg Ser Lys Asn |      |
| 515 520 525 530                                                 |      |
| ATT TGC GTG AAA AAC AAG GTT TTA CAC AAT AAC CCT GAA TTA GAA GAC | 1689 |
| Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu Glu Asp |      |
| 535 540 545                                                     |      |
| GCT TAC CGC ACC AAA AAA ATG CTC AAA CTC GCG CTT TGT ATC ACT CAA | 1737 |
| Ala Tyr Arg Thr Lys Lys Met Leu Lys Leu Ala Leu Cys Ile Thr Gln |      |
| 550 555 560                                                     |      |
| GGA GCG TTA CTG CGC ACT GAA AGC AGA GGG GCT CAC ACA AGG ATT GAC | 1785 |
| Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg Ile Asp |      |
| 565 570 575                                                     |      |
| TAC CCT AAA AGA GAC GAT GAA AAA TGG CTT AAT CGG ACT CTA GCG AGC | 1833 |
| Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu Ala Ser |      |
| 580 585 590                                                     |      |
| TGG CCT AGC GCT GAG CAA GAC ATG CCC ACG ATT GAA TAC GAA GAA TTA | 1881 |
| Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu Glu Leu |      |

[illegible]

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

```
(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

|           |           |           |           |           |     |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Met<br>1  | Lys       | Ile       | Thr       | Tyr<br>5  | Cys | Asp       | Ala       | Leu       | Ile<br>10 | Ile       | Gly       | Gly       | Gly       | Leu<br>15 | Ala       |
| Gly       | Leu       | Arg       | Ala<br>20 | Ser       | Ile | Ala       | Cys       | Lys<br>25 | Gln       | Lys       | Gly       | Leu       | Asn<br>30 | Thr       | Ile       |
| Val       | Leu       | Ser<br>35 | Leu       | Val       | Pro | Val       | Arg<br>40 | Arg       | Ser       | His       | Ser       | Ala<br>45 | Ala       | Ala       | Gln       |
| Gly       | Gly<br>50 | Met       | Gln       | Ala       | Ser | Leu<br>55 | Ala       | Asn       | Ala       | Lys       | Lys<br>60 | Ser       | Glu       | Gly       | Asp       |
| Asn<br>65 | Glu       | Asp       | Leu       | His<br>70 | Phe | Leu       | Asp       | Thr       | Val       | Lys<br>75 | Gly       | Ser       | Asp       | Trp       | Gly<br>80 |
| Cys       | Asp       | Gln       | Gln       | Val<br>85 | Ala | Arg       | Met       | Phe       | Val<br>90 | Thr       | Thr       | Ala       | Pro       | Lys<br>95 | Ala       |
| Ile       | Arg       | Glu       | Leu       | Ala       | Ser | Trp       | Gly       | Val       | Pro       | Trp       | Thr       | Arg       | Ile       | Lys       | Lys       |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asp | Arg | Pro | Ala | Val | Val | Asn | Gly | Glu | His | Val | Thr | Ile | Thr | Glu |
| 115 |     |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Arg | Asp | Asp | Arg | His | Gly | Tyr | Ile | Leu | Ser | Arg | Asp | Phe | Gly | Gly | Thr |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Lys | Trp | Arg | Thr | Cys | Phe | Thr | Ala | Asp | Ala | Thr | Gly | His | Thr | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Tyr | Ala | Val | Ala | Asn | Glu | Ala | Leu | His | His | Lys | Val | Asp | Ile | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Asp | Arg | Lys | Asp | Met | Leu | Ala | Phe | Ile | His | His | Asp | Asn | Lys | Cys | Tyr |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |
| Gly | Ala | Val | Val | Arg | Asp | Leu | Ile | Thr | Gly | Glu | Ile | Ser | Ala | Tyr | Val |
|     |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Lys | Gly | Thr | Leu | Leu | Ala | Thr | Gly | Gly | Tyr | Gly | Arg | Val | Tyr | Lys |
| 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| His | Thr | Thr | Asn | Ala | Val | Ile | Cys | Asp | Gly | Ala | Gly | Ala | Ala | Ser | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Glu | Thr | Gly | Val | Ala | Lys | Leu | Gly | Asn | Met | Glu | Ala | Val | Gln | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |
| His | Pro | Thr | Ala | Leu | Val | Pro | Ser | Gly | Ile | Leu | Met | Thr | Glu | Gly | Cys |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Gly | Asp | Gly | Gly | Val | Leu | Arg | Asp | Lys | Phe | Gly | Arg | Arg | Phe | Met |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Ala | Tyr | Glu | Pro | Glu | Lys | Lys | Glu | Leu | Ala | Ser | Arg | Asp | Val | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Arg | Arg | Ile | Leu | Glu | His | Ile | Gln | Lys | Gly | Tyr | Gly | Ala | Lys | Ser |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Tyr | Gly | Asp | His | Val | Trp | Leu | Asp | Ile | Ala | Ile | Leu | Gly | Arg | Asn |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| His | Val | Glu | Lys | Asn | Leu | Arg | Asp | Val | Arg | Asp | Ile | Ala | Met | Thr | Phe |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Gly | Ile | Asp | Pro | Ala | Asp | Ser | Lys | Glu | Gln | Thr | Lys | Asp | Asn | Met |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gln | Gly | Val | Pro | Ala | Asn | Glu | Pro | Glu | Tyr | Gly | Gln | Ala | Met | Ala | Lys |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gln | Lys | Gly | Trp | Ile | Pro | Ile | Lys | Pro | Met | Gln | His | Tyr | Ser | Met | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Val | Arg | Thr | Asn | Pro | Lys | Gly | Glu | Thr | His | Leu | Lys | Gly | Leu | Phe |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Cys | Ala | Gly | Glu | Ala | Ala | Cys | Trp | Asp | Leu | His | Gly | Phe | Asn | Arg | Leu |
|     |     |     |     | 420 |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Gly | Gly | Asn | Ser | Val | Ser | Glu | Ala | Val | Val | Ala | Gly | Met | Ile | Ile | Gly |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Asp | Tyr | Phe | Ala | Ser | His | Cys | Leu | Glu | Ala | Gln | Ile | Glu | Ile | Asn | Thr |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gln | Lys | Val | Glu | Ala | Phe | Ile | Lys | Glu | Ser | Gln | Asp | Tyr | Met | His | Phe |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Leu | His | Asn | Glu | Gly | Lys | Glu | Asp | Val | Tyr | Glu | Ile | Arg | Glu | Arg |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Met | Lys | Glu | Val | Met | Asp | Glu | Lys | Val | Gly | Val | Phe | Arg | Glu | Gly | Lys |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Arg | Leu | Glu | Glu | Ala | Leu | Lys | Glu | Leu | Gln | Glu | Leu | Tyr | Ala | Arg | Ser |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Lys | Asn | Ile | Cys | Val | Lys | Asn | Lys | Val | Leu | His | Asn | Asn | Pro | Glu | Leu |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Glu | Asp | Ala | Tyr | Arg | Thr | Lys | Lys | Met | Leu | Lys | Leu | Ala | Leu | Cys | Ile |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Thr | Gln | Gly | Ala | Leu | Leu | Arg | Thr | Glu | Ser | Arg | Gly | Ala | His | Thr | Arg |

565 570 575  
 Ile Asp Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu  
 580 585 590  
 Ala Ser Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu  
 595 600 605  
 Glu Leu Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr  
 610 615 620  
 Gly Lys Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp  
 625 630 635 640  
 Ala Glu Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp  
 645 650 655  
 Arg Ile Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys  
 660 665 670  
 Tyr Lys Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg  
 675 680 685  
 Gly Glu His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His  
 690 695 700  
 Asn Ala Asn Leu Lys Gly Glu His His Glu  
 705 710

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 77...445
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ATTTAGTTCA AGAGCTTTTA GAAGAATTTT TGCAAAGCGG GGCTAAAGAG ATTTTAGAAA 60  
 AGGCGCAGTT GTTTTA ATG CGT TTG TTT ATC GCG CTA GTT TTG TTT TGG TGG 112  
 Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp  
 1 5 10  
 TGG TTA AGC TTG AAC GCT AAA GAA GCG GAT TTT ATC TCT GAT TTA GAA 160  
 Trp Leu Ser Leu Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu  
 15 20 25  
 TAC GGG ATG GCT CTT TAT AAA AAC CCT AGG GGT GTT GCG TGC GCG AAA 208  
 Tyr Gly Met Ala Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys  
 30 35 40  
 TGC CAT GGC ATT AAA GGC GAA CAA CAA GAA ATC ACC TTT TAT TAT GAA 256  
 Cys His Gly Ile Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu  
 45 50 55 60  
 AAA GGC GAG AAA AAA ATC CTC TAC GCC CCT AAA ATC AAC CAT TTG GAT 304  
 Lys Gly Glu Lys Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp





(D) OTHER INFORMATION:

[illegible]

Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe Phe Leu Lys  
 1 5 10 15  
 Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu Leu Lys Lys  
 20 25 30  
 Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn Glu Gln Thr  
 35 40 45  
 Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys Gly Leu Val  
 50 55 60  
 Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile Leu Tyr Thr  
 65 70 75 80  
 Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu Glu Lys Phe  
 85 90 95  
 Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe Lys Glu Asp  
 100 105 110  
 Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val Phe Ser Pro  
 115 120 125  
 Lys Glu Pro  
 130

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...222
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCTCCCTCTA AAAGGGTTTT TAAACTATCT TGAGATTTAC CCAATTTATA GGTG ATG   | 57  |
| Met                                                               |     |
| 1                                                                 |     |
| CTT TCA AAA CTC CCA TTT ACT GGT GTT TTA GCC TTA GTT TTA AAG GCT   | 105 |
| Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys Ala   |     |
| 5 10 15                                                           |     |
| GTC CAT GTT AGC TTA GCC GAA GAT AAA TCC AAA TTC ACC GCT TGC AAA   | 153 |
| Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys Lys   |     |
| 20 25 30                                                          |     |
| AAC CCT GCT AGT AAA ACC GAT ACC AAA ACC ATT TTT TTC ATT CAT TAT   | 201 |
| Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His Tyr   |     |
| 35 40 45                                                          |     |
| CCT TTA ATG TGG TCT TAT CAA TAACGCTTAT TATTTTAGTG TAAATAAGCA CGCT | 256 |
| Pro Leu Met Trp Ser Tyr Gln                                       |     |
| 50 55                                                             |     |

## (2) INFORMATION FOR SEQ ID NO:328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

Met Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys
 1 5 10 15
Ala Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys
 20 25 30
Lys Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His
 35 40 45
Tyr Pro Leu Met Trp Ser Tyr Gln
 50 55

```

## (2) INFORMATION FOR SEQ ID NO:329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...611
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

AATGACTTTTA GGGGATATTC TTAAAGAAAA ACTCTAAAGA GTGATTTTAA AAGCATGAGA 60
ATGGC ATG AGA TTT AAG GGT GTT GTT GCT TTT ATT TCC CTA GCT GTC GCT 110
 Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala
 1 5 10 15

CTT GGC GTT TTA GCC TAT TTG TTT TTA AGC GTT AAA AAA GAA ATG CCC 158
Leu Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro
 20 25 30

GCT ACT TCT CAT GCG ATC TCT CAA ACA CAT GCG ATC TCT CAA ACC AAT 206
Ala Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn
 35 40 45

GAA GGC CTC TCT CAA ACA GAT GCA AAA AGC CAT GAC ATC GAT CTA GAA 254
Glu Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu

```

|                              |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |     |
|------------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|-----|
| 50                           |            |            |            |            | 55         |            |            |            |            | 60         |            |            |            |            |            |      |     |
| GAA<br>Glu                   | AAT<br>Asn | AGC<br>Ser | CCC<br>Pro | ACT<br>Thr | GAA<br>Glu | ACC<br>Thr | TCT<br>Ser | CAT<br>His | AAT<br>Asn | GAA<br>Glu | AAA<br>Lys | GCC<br>Ala | TCC<br>Ser | CAT<br>His | AAC<br>Asn | 302  |     |
| 65                           |            |            |            |            | 70         |            |            |            |            | 75         |            |            |            |            |            |      |     |
| GAA<br>Glu                   | GAA<br>Glu | GAT<br>Asp | CAC<br>His | AAT<br>Asn | AAC<br>Asn | GCC<br>Ala | CTT<br>Leu | TCT<br>Ser | CAA<br>Gln | AAT<br>Asn | CTT<br>Leu | GAT<br>Asp | GCG<br>Ala | CAA<br>Gln | GAA<br>Glu | 350  |     |
| 80                           |            |            |            |            | 85         |            |            |            |            | 90         |            |            |            |            |            |      |     |
| TCT<br>Ser                   | ATC<br>Ile | AAT<br>Asn | TAC<br>Tyr | CCC<br>Pro | GTT<br>Val | GTG<br>Val | GAA<br>Glu | CAT<br>His | TAT<br>Tyr | TCT<br>Ser | GAA<br>Glu | ATC<br>Ile | CCT<br>Pro | TTT<br>Phe | GAA<br>Glu | 398  |     |
| 100                          |            |            |            |            | 105        |            |            |            |            | 110        |            |            |            |            |            |      |     |
| GAA<br>Glu                   | AAA<br>Lys | AAA<br>Lys | AGG<br>Arg | GAA<br>Glu | TAT<br>Tyr | TCA<br>Ser | AAG<br>Lys | CTT<br>Leu | ATC<br>Ile | ATT<br>Ile | AAG<br>Lys | GAT<br>Asp | TTA<br>Leu | AAG<br>Lys | GAC<br>Asp | 446  |     |
| 115                          |            |            |            |            | 120        |            |            |            |            | 125        |            |            |            |            |            |      |     |
| TAT<br>Tyr                   | CAA<br>Gln | TGG<br>Trp | TGG<br>Trp | TGC<br>Cys | TTA<br>Leu | AAA<br>Lys | GAA<br>Glu | ATC<br>Ile | CTC<br>Leu | AAA<br>Lys | AAA<br>Lys | GAA<br>Glu | CAG<br>Gln | ATT<br>Ile | GAT<br>Asp | 494  |     |
| 130                          |            |            |            |            | 135        |            |            |            |            | 140        |            |            |            |            |            |      |     |
| TAC<br>Tyr                   | GCT<br>Ala | TAC<br>Tyr | GAT<br>Asp | AAC<br>Asn | ACC<br>Thr | AAA<br>Lys | AAC<br>Asn | CAA<br>Gln | CCT<br>Pro | AAC<br>Asn | CTC<br>Leu | ATC<br>Ile | ATC<br>Ile | TAT<br>Tyr | TTA<br>Leu | 542  |     |
| 145                          |            |            |            |            | 150        |            |            |            |            | 155        |            |            |            |            |            |      |     |
| GAT<br>Asp                   | GAA<br>Glu | AAT<br>Asn | AAA<br>Lys | AAA<br>Lys | GAA<br>Glu | CGC<br>Arg | TTG<br>Leu | CTG<br>Leu | GCT<br>Ala | GAT<br>Asp | TTA<br>Leu | GAC<br>Asp | TAT<br>Tyr | TAT<br>Tyr | AAA<br>Lys | 590  |     |
| 160                          |            |            |            |            | 165        |            |            |            |            | 170        |            |            |            |            |            |      |     |
| ATA<br>Ile                   | CGC<br>Arg | TAT<br>Tyr | CAT<br>His | GCT<br>Ala | GTT<br>Val | TTT<br>Phe | TAAATTCAAA |            |            | GGATAAAAAT |            |            | GTATCAAGTA |            |            | GCCA | 645 |
| 180                          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |     |
| TTTGCGACCC CATCCATGCT AAAGGC |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            | 671  |     |

(2) INFORMATION FOR SEO ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

```
(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

|          |           |           |           |          |     |           |           |           |           |     |           |           |           |           |     |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Met<br>1 | Arg       | Phe       | Lys       | Gly<br>5 | Val | Val       | Ala       | Phe       | Ile<br>10 | Ser | Leu       | Ala       | Val       | Ala<br>15 | Leu |
| Gly      | Val       | Leu       | Ala<br>20 | Tyr      | Leu | Phe       | Leu       | Ser<br>25 | Val       | Lys | Lys       | Glu       | Met<br>30 | Pro       | Ala |
| Thr      | Ser       | His<br>35 | Ala       | Ile      | Ser | Gln       | Thr<br>40 | His       | Ala       | Ile | Ser       | Gln<br>45 | Thr       | Asn       | Glu |
| Gly      | Leu<br>50 | Ser       | Gln       | Thr      | Asp | Ala<br>55 | Lys       | Ser       | His       | Asp | Ile<br>60 | Asp       | Leu       | Glu       | Glu |
| Asn      | Ser       | Pro       | Thr       | Glu      | Thr | Ser       | His       | Asn       | Glu       | Lys | Ala       | Ser       | His       | Asn       | Glu |

65 70 75 80  
 Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu Ser  
 85 90 95  
 Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu Glu  
 100 105 110  
 Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp Tyr  
 115 120 125  
 Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp Tyr  
 130 135 140  
 Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu Asp  
 145 150 155 160  
 Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys Ile  
 165 170 175  
 Arg Tyr His Ala Val Phe  
 180

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 86...295
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

ACCCACAAAA CTAAACCCCA CTAACACAAT TAACCCTAAC AACACATAAA GATTGCCCAA 60  
 AGACGCGCAC AACACGCTCG CAACA ATG GTT GCA AAA ACA AAC ACA ATC CCC 112  
 Met Val Ala Lys Thr Asn Thr Ile Pro  
 1 5  
 CCC ATC GTA GGG GTA TCT TTT TTA TTC TGG TGG CTT GGC ACG AAG CTA 160  
 Pro Ile Val Gly Val Ser Phe Leu Phe Trp Trp Leu Gly Thr Lys Leu  
 10 15 20 25  
 GAA ATG GGC TGG TTA GCC TTT TTA GCC TTG GCC CAT AGA ATG AAT TTA 208  
 Glu Met Gly Trp Leu Ala Phe Leu Ala Leu Ala His Arg Met Asn Leu  
 30 35 40  
 GGC ATT AAA AAA AGC GTG AGA AAA AAA GCT ATG AAA AAC CCT AAC CCT 256  
 Gly Ile Lys Lys Ser Val Arg Lys Lys Ala Met Lys Asn Pro Asn Pro  
 45 50 55  
 GCT CTA AAA GTC AAA TAC TGG AAA AGA TTG ATA TTG AAA TAGCCATATA GT 307  
 Ala Leu Lys Val Lys Tyr Trp Lys Arg Leu Ile Leu Lys  
 60 65 70  
 AAAGAATAGA GCATAAAATC CCCTAAAATC GCCA 341

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```
Met Val Ala Lys Thr Asn Thr Ile Pro Pro Ile Val Gly Val Ser Phe
 1 5 10 15
Leu Phe Trp Trp Leu Gly Thr Lys Leu Glu Met Gly Trp Leu Ala Phe
 20 25 30
Leu Ala Leu Ala His Arg Met Asn Leu Gly Ile Lys Lys Ser Val Arg
 35 40 45
Lys Lys Ala Met Lys Asn Pro Asn Pro Ala Leu Lys Val Lys Tyr Trp
 50 55 60
Lys Arg Leu Ile Leu Lys
65 70
```

(2) INFORMATION FOR SEQ ID NO:333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...2430
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

```
TTTTTTTTTT TTTTGTATT TTATTTTSTA AATTTTSTA TTAAGGAGAG TTGTTGG ATG 60
 Met
 1
TTT TTA AGA GTA TAC CCA AAG CTT AGA TAC GCT TTA TGT TTC CCC CTA 108
Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro Leu
 5 10 15
CTC GCT GAG ACT TGC TAT AGC GAA GAG CGG ACT TTA AAT AAG GTT ACC 156
Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val Thr
 20 25 30
ACC CAA GCT AAA AGG ATT TTC ACT TAC AAC AAT GAG TTT AAA GTA ACT 204
Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val Thr
```

\_\_\_\_\_



|                                                                 |      |
|-----------------------------------------------------------------|------|
| TTT AGT CCT GAT AGT TCT CAA GGG TGT CCT AAT GTG TTA GAT AGT TTC | 924  |
| Phe Ser Pro Asp Ser Ser Gln Gly Cys Pro Asn Val Leu Asp Ser Phe |      |
| 275 280 285                                                     |      |
| ACA AGA TAC ATG TAT CAC TCT ATT AAT AGT GCC AAC AAT CTT TCC TTA | 972  |
| Thr Arg Tyr Met Tyr His Ser Ile Asn Ser Ala Asn Asn Leu Ser Leu |      |
| 290 295 300 305                                                 |      |
| CAA TAC AAA AGG GAA GCG GGA AAT TCT TTT GGC GAC CCA CGA TTA GAT | 1020 |
| Gln Tyr Lys Arg Glu Ala Gly Asn Ser Phe Gly Asp Pro Arg Leu Asp |      |
| 310 315 320                                                     |      |
| TTT ACC CTT TAT ACA AGC ATC AGG AAC GCT CAG TTT GAT CCC CTA TTT | 1068 |
| Phe Thr Leu Tyr Thr Ser Ile Arg Asn Ala Gln Phe Asp Pro Leu Phe |      |
| 325 330 335                                                     |      |
| GAT CCT AAT GGC GTT TAT GCT AAA TTC CCC ACT TCT TTA GCG AGC GCA | 1116 |
| Asp Pro Asn Gly Val Tyr Ala Lys Phe Pro Thr Ser Leu Ala Ser Ala |      |
| 340 345 350                                                     |      |
| TGG GAA AAA GAA AAT TAC CCA TGC GTT GAA GGC GCT TAT TGC ACC CCA | 1164 |
| Trp Glu Lys Glu Asn Tyr Pro Cys Val Glu Gly Ala Tyr Cys Thr Pro |      |
| 355 360 365                                                     |      |
| AGC TTT TCA GAT GTG GAT AAA CCA AGC TCA CAG CCT AGG AAT TTG TTT | 1212 |
| Ser Phe Ser Asp Val Asp Lys Pro Ser Ser Gln Pro Arg Asn Leu Phe |      |
| 370 375 380 385                                                 |      |
| TTA AAC AAC ACC GGC TTA AAC CTT AAA GTC GCG CAT GTG ATT GAT GAA | 1260 |
| Leu Asn Asn Thr Gly Leu Asn Leu Lys Val Ala His Val Ile Asp Glu |      |
| 390 395 400                                                     |      |
| GCC ACA GAC AGC CTT TTT GAA TAC GGA TTC AAC TAC CAA AAT TTG AGC | 1308 |
| Ala Thr Asp Ser Leu Phe Glu Tyr Gly Phe Asn Tyr Gln Asn Leu Ser |      |
| 405 410 415                                                     |      |
| GTT TTT GAC GCT CGC ATC CCT AAA TCA GAA TTA TAC AGG CCT AAT CAA | 1356 |
| Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn Gln |      |
| 420 425 430                                                     |      |
| GTT TAT ACT GAT GAT AAA GGA CAA AAA CAA ATC GCT TGC TCT CTT GTG | 1404 |
| Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu Val |      |
| 435 440 445                                                     |      |
| AAT AAT AAC CCC AAT GAC CCC ACT CTG TGC CAA AGA GGG AAA GCG AAC | 1452 |
| Asn Asn Asn Pro Asn Asp Pro Thr Leu Cys Gln Arg Gly Lys Ala Asn |      |
| 450 455 460 465                                                 |      |
| GGG AAT ATT TAT GGA GGC TAC GTG CAA GCG AAT TAC TCG CCT CAT AAA | 1500 |
| Gly Asn Ile Tyr Gly Gly Tyr Val Gln Ala Asn Tyr Ser Pro His Lys |      |
| 470 475 480                                                     |      |
| ATC ATC ACT TTT GGA GCC GGG GTA AGG TGG GAC GCT TAC ACG CTT TAT | 1548 |
| Ile Ile Thr Phe Gly Ala Gly Val Arg Trp Asp Ala Tyr Thr Leu Tyr |      |
| 485 490 495                                                     |      |
| GAT AAA GAC TGG AAC CAC CGC TAC ACT CAA GGC TTT AGC CCT AGC GCG | 1596 |
| Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser Ala |      |

| 500                                                                                                                                                   | 505 | 510 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| GCT CTT GTG CTA AGC CCC ATT GAG CCT TTA TCT TTA AAA ATC ACT TAT<br>Ala Leu Val Leu Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr Tyr<br>515 520 525     |     |     | 1644 |
| TCT CAA GTT ACA AGA GGG GTG ATG CCA GGA GAT GGC GTG TAC ATG CGT<br>Ser Gln Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met Arg<br>530 535 540 545 |     |     | 1692 |
| CAA AAC GAT TTA CGA TAC GCC AAA AAC ATC AAG CCT GAA GTG GGC TCT<br>Gln Asn Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly Ser<br>550 555 560     |     |     | 1740 |
| AAC GCT GAA TTT AAT ATT GAT TAT TCA AGC CAG TAT TTT AGC GGG AGG<br>Asn Ala Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly Arg<br>565 570 575     |     |     | 1788 |
| GCT GCG GCG TTT TAT CAG GCT TTG GAT AAT TTC ATC TCA CAA TAC GCA<br>Ala Ala Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr Ala<br>580 585 590     |     |     | 1836 |
| CAA AAT TTG ATT GTA ACC AAT TTG AGT CAA GCG ATT CGT ATT TAT GGC<br>Gln Asn Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr Gly<br>595 600 605     |     |     | 1884 |
| TAT GAA GTG GGT GGG ACT TTC AGA TAC AAG GGC GTG AGT TTG AAT GTA<br>Tyr Glu Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn Val<br>610 615 620 625 |     |     | 1932 |
| GGG GTC TCG CGC ACC TGG CCC ACC ACT AGG GGG TAT TTA ATG GCG GAT<br>Gly Val Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala Asp<br>630 635 640     |     |     | 1980 |
| AGC TAT GAG CTT GCC GCA AGC ACC GGT AAT GTT TTT ATC ATC AAA TTG<br>Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys Leu<br>645 650 655     |     |     | 2028 |
| GAT TAC ACC ATC CCC AAA ACA GGG ATC AAT CTT GCA TGG CTT AGC CGC<br>Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser Arg<br>660 665 670     |     |     | 2076 |
| TTT GTT ACC GGT TTA GAT TAT TGC GGG TTT GAT ATT TAC TTG CCT GAT<br>Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro Asp<br>675 680 685     |     |     | 2124 |
| TAT GGG ACG GCT GAG AAA CCC AAA ACC CCT ACC GAT TTA GCC AAA TGC<br>Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys Cys<br>690 695 700 705 |     |     | 2172 |
| GGA TCT CAA TTA GGG TTA GTG CAT ATG CAT AAA CCG GGC TAT GGC GTG<br>Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly Val<br>710 715 720     |     |     | 2220 |
| AGT AAT TTT TAT ATC AAT TGG AGT CCT AAA ACC AAA AGC CGC TGG AAG<br>Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp Lys<br>725 730 735     |     |     | 2268 |

GGT TTG TTG CTT TCA GCC GTG TTT AAT AAT GTT TTC AAC AAA TTC TAT 2316  
 Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe Tyr  
           740                              745                              750

GTG GAT CAA ACA AGC CCT TAT GTC ATG AGC CCG GAT ATG CCA GGC ACT 2364  
 Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly Thr  
           755                              760                              765

GAC GCT GTT AAA AGA GCG ATC GCT GAG CCT GGG TTT AAC GCG CGT TTT 2412  
 Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg Phe  
           770                              775                              780                              785

GAA GTG GCT TAC AAA TGG TAGTTAATGG AGCTTTAAGC GTTGCGCATG CGTGATAG 2468  
 Glu Val Ala Tyr Lys Trp  
                               790

CAACGGCTAT CGC 2481

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Arg | Val | Tyr | Pro | Lys | Leu | Arg | Tyr | Ala | Leu | Cys | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Glu | Thr | Cys | Tyr | Ser | Glu | Glu | Arg | Thr | Leu | Asn | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Thr | Gln | Ala | Lys | Arg | Ile | Phe | Thr | Tyr | Asn | Asn | Glu | Phe | Lys | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ser | Lys | Glu | Leu | Asp | Gln | Arg | Gln | Ser | Asn | Glu | Val | Lys | Asp | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Phe | Arg | Thr | Asn | Pro | Asp | Val | Asn | Val | Gly | Gly | Gly | Ser | Val | Met | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Lys | Ile | Tyr | Val | Arg | Gly | Val | Glu | Asp | Arg | Leu | Leu | Arg | Val | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Asp | Gly | Ala | Ala | Gln | Asn | Gly | Asn | Ile | Tyr | His | His | Gln | Gly | Asn |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Val | Ile | Asp | Pro | Gly | Met | Leu | Lys | Ser | Val | Glu | Val | Thr | Lys | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Asn | Ala | Ser | Ala | Gly | Pro | Gly | Ala | Ile | Ala | Gly | Val | Ile | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Glu | Thr | Lys | Gly | Ala | Ala | Asp | Phe | Ile | Pro | Arg | Gly | Lys | Asn | Tyr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Ala | Ser | Gly | Ala | Val | Ser | Phe | Tyr | Thr | Asn | Phe | Gly | Asp | Arg | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr | Phe | Arg | Ser | Ala | Tyr | Gln | Asn | Ala | His | Phe | Asp | Ile | Ile | Ala | Tyr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Tyr | Thr | His | Gln | Asn | Ile | Phe | Tyr | Tyr | Arg | Ser | Gly | Ala | Thr | Ala | Met |
|     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Lys | Asn | Leu | Phe | Asn | Pro | Thr | Gln | Ala | Asp | Lys | Glu | Pro | Gly | Thr | Pro |



675                      680                      685  
 Asp Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys  
 690                      695                      700  
 Cys Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly  
 705                      710                      715                      720  
 Val Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp  
 725                      730                      735  
 Lys Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe  
 740                      745                      750  
 Tyr Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly  
 755                      760                      765  
 Thr Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg  
 770                      775                      780  
 Phe Glu Val Ala Tyr Lys Trp  
 785                      790

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 120...428
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

|                                                                            |     |
|----------------------------------------------------------------------------|-----|
| GTCGGTCGGG TAATGTTCAA ATTCACAAAT GAGTCTGAAG ACAAAGAAGT CTTGATCTAG          | 60  |
| AAGCCGAAAT TCTCATACCG CACTTAGAAT TGCCTCAAAA ACAAATTGAT GCGCTGTTG           | 119 |
|                                                                            |     |
| GTG CAC GAT ATT ACC AAG CTA TGT TAC ACC AAA CCA CTA GGG TGT GTT            | 167 |
| Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val            |     |
| 1                      5                      10                      15   |     |
|                                                                            |     |
| GTG CTG TTC AGC AAG GAT ACT GAT CTT GTG CCT GTG TTA GAA TCC GCT            | 215 |
| Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala            |     |
| 20                      25                      30                         |     |
|                                                                            |     |
| TGG GAG AAA GGC TTT GAA GTC TTC ATT GCT AAC ATT CAA GAA TGC CCC            | 263 |
| Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro            |     |
| 35                      40                      45                         |     |
|                                                                            |     |
| AAT TCT GTC CCT TCA GAC TTG AAG AAG TCT TGC AAT GTG AGG GAA CGC            | 311 |
| Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg            |     |
| 50                      55                      60                         |     |
|                                                                            |     |
| AGT GTC GCT GAA ATT GTA GAT AAC TTG CCC AAA AAT CAG CAC ACT CCC            | 359 |
| Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro            |     |
| 65                      70                      75                      80 |     |

AAG AAA AAG AAC TTT TCC ACC AAC GAG CCT TTT AAC AAC CCA TTT AAA 407  
 Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys  
 85 90 95

GAC CAA CTC TTT AAG AAG AAC TAACACGATC CCCACACCAA GGGGACAAAA AAGCA 463  
 Asp Gln Leu Phe Lys Lys Asn  
 100

CCCATTTTTAA AAGG 477

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Asp | Ile | Thr | Lys | Leu | Cys | Tyr | Thr | Lys | Pro | Leu | Gly | Cys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Phe | Ser | Lys | Asp | Thr | Asp | Leu | Val | Pro | Val | Leu | Glu | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Glu | Lys | Gly | Phe | Glu | Val | Phe | Ile | Ala | Asn | Ile | Gln | Glu | Cys | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asn | Ser | Val | Pro | Ser | Asp | Leu | Lys | Lys | Ser | Cys | Asn | Val | Arg | Glu | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Ala | Glu | Ile | Val | Asp | Asn | Leu | Pro | Lys | Asn | Gln | His | Thr | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Lys | Lys | Asn | Phe | Ser | Thr | Asn | Glu | Pro | Phe | Asn | Asn | Pro | Phe | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Gln | Leu | Phe | Lys | Lys | Asn |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 220...624
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

TCTTTTGAAA TTGCCTGATG TGGAAAAAGA AATGCCCAAA GAGACGACTC AAAAAAGCTT 60

GTTTTCGCAC AAACACTTTG TTTTGGGGC TTGGGGATCT TTTTTTATGT GGGGGGAGAA 120  
 NTGGCGATTG GCTCATTCTT GGTGCTAAGC TTTGAAAAGC TTTTGAATTT AGACTCTCAA 180  
 TCAAGCGCGC ATTACTTGGT GTATTATTGG GGAGGCGCG ATG GTG GGC CGT TTC 234  
 Met Val Gly Arg Phe  
 1 5

TTA GGC AGT GTG TTG ATG AAT AAA ATT GCC CCT AAT AAA TAC TTG GCT 282  
 Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro Asn Lys Tyr Leu Ala  
 10 15 20

TTC AAC GCC TTA AGC TCT ATT GTT CTC ATC GCT TTA GCC ATT ATC ATT 330  
 Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala Leu Ala Ile Ile Ile  
 25 30 35

GGA GGC AAG ATC GCT TTA TTC GCT CTG ACT TTT GTG GGC TTT TTC AAC 378  
 Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe Val Gly Phe Phe Asn  
 40 45 50

TCT ATC ATG TTC CCT ACC ATC TTT TCT TTG GCT ACG CTC AAT TTA GGG 426  
 Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala Thr Leu Asn Leu Gly  
 55 60 65

CAT CTC ACT TCT AAA GCT TCT GGG GTG ATT AGC ATG GCG ATT GTG GGA 474  
 His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser Met Ala Ile Val Gly  
 70 75 80 85

GGG GCG TTA ATC CCC CCC ATT CAA GGT GCG GTT ACA GAC ATG CTA ACA 522  
 Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val Thr Asp Met Leu Thr  
 90 95 100

GCA ACC GAA TCA AAT TTG CTC TAC GCT TAT GGT GTG CCG TTG TTG TGC 570  
 Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly Val Pro Leu Leu Cys  
 105 110 115

TAT TTT TAT ATT CTC TTC TTT GCG CTT AAA GGG TAT AAG CAA GAA GAA 618  
 Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly Tyr Lys Gln Glu Glu  
 120 125 130

AAC TCC TAAAAAAGG GGGGGTTTCT TTCTTCTTTC CTTTCTTTTA TCTTGTTTAA AA 676  
 Asn Ser  
 135

AATCAGTAA 685

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Met Val Gly Arg Phe Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro

[illegible]

45

[REDACTED]

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 58...765  
(D) OTHER INFORMATION:

## 442







GTG GTG TTG TGC CGT ATT TCT GGA AAG ATG CGC ATG CAC TAT ATT AGG 207  
 Val Val Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg  
                   35                  40                  45

ATT GCT TTA GGC GAT AGG GTT AAG CTA GAG CTT ACG CCC TAT AGC TTA 255  
 Ile Ala Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu  
                   50                  55                  60

GAC AAA GGT CGG ATA ACT TTT AGA TAT AAA TGAATTTAAG GGTTATTTCA ATG 308  
 Asp Lys Gly Arg Ile Thr Phe Arg Tyr Lys  
                   65                  70

AAAATATGTT AATATAA 325

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile Glu Ala  
 1                  5                  10                  15  
 Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His Val Val  
                   20                  25                  30  
 Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg Ile Ala  
                   35                  40                  45  
 Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu Asp Lys  
                   50                  55                  60  
 Gly Arg Ile Thr Phe Arg Tyr Lys  
 65                  70

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...309
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

ATCGCTCAAA TTTCAACGAC CATGCTTGTT AAAAAAACT AAAGGAATGT T ATG CAA 57



(A) LENGTH: 841 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 46...795  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGACTAAAA AGATATAATT CATTCAAAAT TAAACAAGGA TTACA ATG AAA CTG ATT | 57  |
| Met Lys Leu Ile                                                   |     |
| 1                                                                 |     |
| TCA TGG AAT GTG AAC GGG TTA AGG GCT TGC ATG ACT AAG GGC TTT ATG   | 105 |
| Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr Lys Gly Phe Met   |     |
| 5 10 15 20                                                        |     |
| GAT TTT TTC AAT AGC GTT GAT GCG GAT GTT TTT TGC ATT CAA GAA TCT   | 153 |
| Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys Ile Gln Glu Ser   |     |
| 25 30 35                                                          |     |
| AAA ATG CAG CAA GAA CAA AAC ACC TTT GAA TTT AAA GGG TAT TTT GAT   | 201 |
| Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys Gly Tyr Phe Asp   |     |
| 40 45 50                                                          |     |
| TTT TGG AAT TGC GCG ATT AAA AAG GGC TAT TCT GGG GTG GTA ACT TTC   | 249 |
| Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly Val Val Thr Phe   |     |
| 55 60 65                                                          |     |
| ACT AAA AAA GAG CCT TTA AGC GTG AGC TAT GGT ATT AAT ATG GAA GAG   | 297 |
| Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile Asn Met Glu Glu   |     |
| 70 75 80                                                          |     |
| CAT GAC AAA GAA GGG CGC GTA ATA ACT TGC GAA TTT GAG TCG TTT TAT   | 345 |
| His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe Glu Ser Phe Tyr   |     |
| 85 90 95 100                                                      |     |
| TTG GTG AAT GTT TAT ACC CCT AAT TCC CAA CAA GCC CTA TCC AGG CTT   | 393 |
| Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala Leu Ser Arg Leu   |     |
| 105 110 115                                                       |     |
| AGT TAT CGC ATG AGT TGG GAA GTG GAG TTT AAG AAA TTT TTA AAA GCT   | 441 |
| Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys Phe Leu Lys Ala   |     |
| 120 125 130                                                       |     |
| TTA GAG TTG AAA AAA CCG GTC ATT GTG TGT GGG GAT TTG AAT GTG GCT   | 489 |
| Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp Leu Asn Val Ala   |     |
| 135 140 145                                                       |     |
| CAC AAT GAA ATT GAT TTA GAA AAC CCC AAA ACC AAC CGA AAA AAT GCC   | 537 |
| His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn Arg Lys Asn Ala   |     |

150 155 160

GGC TTT AGC GAT GAA GAG AGA GAA AAA TTC AGC GAG CTT TTG AAC GCC 585  
 Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu Leu Leu Asn Ala  
 165 170 175 180

GGT TTT ATT GAC ACT TTC CGT TAT TTT TAC CCT AAC AAA GAA AAG GCT 633  
 Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn Lys Glu Lys Ala  
 185 190 195

TAC ACC TGG TGG AGT TAC ATG CAA CAA GCA AGG GAT AAA AAC ATT GGT 681  
 Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp Lys Asn Ile Gly  
 200 205 210

TGG CGC ATT GAT TAT TTT TTA TGC TCT AAC CCT TTA AAA ACG CGC TTA 729  
 Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu Lys Thr Arg Leu  
 215 220 225

AAA GAC GCT TTA ATC TAT AAA GAT ATT TTA GGG AGC GAT CAT TGC CCG 777  
 Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser Asp His Cys Pro  
 230 235 240

GTA GGG TTG GAA TTA GTT TAAAGGTAGA AAGTGTGCGA AATAAAGACA GAAAAAAG 833  
 Val Gly Leu Glu Leu Val  
 245 250

CCTTACAA 841

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met Lys Leu Ile Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr  
 1 5 10 15  
 Lys Gly Phe Met Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys  
 20 25 30  
 Ile Gln Glu Ser Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys  
 35 40 45  
 Gly Tyr Phe Asp Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly  
 50 55 60  
 Val Val Thr Phe Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile  
 65 70 75 80  
 Asn Met Glu Glu His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe  
 85 90 95  
 Glu Ser Phe Tyr Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala  
 100 105 110  
 Leu Ser Arg Leu Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys  
 115 120 125  
 Phe Leu Lys Ala Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Leu Asn Val Ala His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn |     |     |
| 145                                                             | 150 | 155 |
| Arg Lys Asn Ala Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu |     |     |
|                                                                 | 165 | 170 |
| Leu Leu Asn Ala Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn |     |     |
|                                                                 | 180 | 185 |
| Lys Glu Lys Ala Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp |     |     |
|                                                                 | 195 | 200 |
| Lys Asn Ile Gly Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu |     |     |
|                                                                 | 210 | 215 |
| Lys Thr Arg Leu Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser |     |     |
|                                                                 | 225 | 230 |
| Asp His Cys Pro Val Gly Leu Glu Leu Val                         |     | 235 |
|                                                                 | 245 | 250 |

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...571
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGAATGCGAG CGTTAAAAAA GAAATTTATG TGCCTAATAA GCTTGTTAAT TTTGTTATCG | 60  |
| C ATG AGG GCT TTA CTT TTT TTT ATT TTG TTA CTT TGG TTC AAG GGT TGT | 109 |
| Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Leu Trp Phe Lys Gly Cys   |     |
| 1 5 10 15                                                         |     |
| GGG TAT AAG CCT ATT GCA GCT TAC GCT CAA AAC GCT TTA GGC GAT AGC   | 157 |
| Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser   |     |
| 20 25 30                                                          |     |
| GTA TAC GTG AAA CTC ATT GTG AAT TTG CCT AAC CCT GAA AAC TCT GTA   | 205 |
| Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val   |     |
| 35 40 45                                                          |     |
| GAG TTT AAG GAT TTG ATG AAT CGT TTA GTC GTG CAA CGC TTC CAA AGC   | 253 |
| Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser   |     |
| 50 55 60                                                          |     |
| CGC TTA GCG AGT GAA AAG GAT GCG GAT TCT ATC ATT ATT ATA GAA ATC   | 301 |
| Arg Leu Ala Ser Glu Lys Asp Ala Asp Ser Ile Ile Ile Ile Glu Ile   |     |
| 65 70 75 80                                                       |     |
| ACG AAT GTA ACC GAT ACG AGT ATC ACG CAA AAT AAA GAA GGC TTC ACG   | 349 |
| Thr Asn Val Thr Asp Thr Ser Ile Thr Gln Asn Lys Glu Gly Phe Thr   |     |

| 85                                                                | 90  | 95  |     |
|-------------------------------------------------------------------|-----|-----|-----|
| ACT TTC TAT CGC GCA ACC GTG TCT GTG AAT TAC ACC TAC GAT AAT AAA   |     |     | 397 |
| Thr Phe Tyr Arg Ala Thr Val Ser Val Asn Tyr Thr Tyr Asp Asn Lys   |     |     |     |
| 100                                                               | 105 | 110 |     |
| AGA GGC ACA CAA AAG ACT TTT CAA GAT AGC GGG TAT TAC AAT TAC GCT   |     |     | 445 |
| Arg Gly Thr Gln Lys Thr Phe Gln Asp Ser Gly Tyr Tyr Asn Tyr Ala   |     |     |     |
| 115                                                               | 120 | 125 |     |
| GTG AAT TTG CAA GAC CCC CTT AAT ACC TAC CAG AAC CGC TAT TAT GCT   |     |     | 493 |
| Val Asn Leu Gln Asp Pro Leu Asn Thr Tyr Gln Asn Arg Tyr Tyr Ala   |     |     |     |
| 130                                                               | 135 | 140 |     |
| ATC AAT CAG GCT GTG GAA CAG ACT TTG ACT AAA TTT GTG GCT CAA ATC   |     |     | 541 |
| Ile Asn Gln Ala Val Glu Gln Thr Leu Thr Lys Phe Val Ala Gln Ile   |     |     |     |
| 145                                                               | 150 | 155 | 160 |
| GCT TAT GAG GGG AAA TTC AAT AAT GAA AAA TAGCCCTTTG AATGGATTGA ATG |     |     | 594 |
| Ala Tyr Glu Gly Lys Phe Asn Asn Glu Lys                           |     |     |     |
| 165                                                               | 170 |     |     |

GACTAAAGGC GTTTTTAGAA ACAA 618

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ala | Leu | Leu | Phe | Phe | Ile | Leu | Leu | Leu | Trp | Phe | Lys | Gly | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Tyr | Lys | Pro | Ile | Ala | Ala | Tyr | Ala | Gln | Asn | Ala | Leu | Gly | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Tyr | Val | Lys | Leu | Ile | Val | Asn | Leu | Pro | Asn | Pro | Glu | Asn | Ser | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Phe | Lys | Asp | Leu | Met | Asn | Arg | Leu | Val | Val | Gln | Arg | Phe | Gln | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Ala | Ser | Glu | Lys | Asp | Ala | Asp | Ser | Ile | Ile | Ile | Ile | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Asn | Val | Thr | Asp | Thr | Ser | Ile | Thr | Gln | Asn | Lys | Glu | Gly | Phe | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Tyr | Arg | Ala | Thr | Val | Ser | Val | Asn | Tyr | Thr | Tyr | Asp | Asn | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gly | Thr | Gln | Lys | Thr | Phe | Gln | Asp | Ser | Gly | Tyr | Tyr | Asn | Tyr | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Asn | Leu | Gln | Asp | Pro | Leu | Asn | Thr | Tyr | Gln | Asn | Arg | Tyr | Tyr | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ile | Asn | Gln | Ala | Val | Glu | Gln | Thr | Leu | Thr | Lys | Phe | Val | Ala | Gln | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Tyr | Glu | Gly | Lys | Phe | Asn | Asn | Glu | Lys |     |     |     |     |     |     |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CTC | ATC | ACT | TTT | GTG | CCT | TAT | TCA | GTG | GTG | TTT | GTA | GCC | TTA | GCG | ATT | 540  |
| Leu | Ile | Thr | Phe | Val | Pro | Tyr | Ser | Val | Val | Phe | Val | Ala | Leu | Ala | Ile |      |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |      |
| GGG | GTG | GGG | GTT | TTG | CAA | AAC | GAT | TTG | GGG | CAG | ATT | GTT | CTT | TTG | GGG | 588  |
| Gly | Val | Gly | Val | Leu | Gln | Asn | Asp | Leu | Gly | Gln | Ile | Val | Leu | Leu | Gly |      |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |      |
| GCG | GTT | TTA | GCG | GTG | TTG | TTG | GTT | TTT | TCT | GGG | GGG | AGC | GTG | CAT | TTG | 636  |
| Ala | Val | Leu | Ala | Val | Leu | Leu | Val | Phe | Ser | Gly | Gly | Ser | Val | His | Leu |      |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |
| TTT | GGC | TTG | ATT | ATT | TCA | GGG | GCG | TTT | GCG | ATC | AGC | GTT | TTA | GCG | ATT | 684  |
| Phe | Gly | Leu | Ile | Ile | Ser | Gly | Ala | Phe | Ala | Ile | Ser | Val | Leu | Ala | Ile |      |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| GTT | ACA | AGC | GAG | CAT | AGG | ATT | TTG | CGC | CTG | AAA | TTG | TGG | TGG | TCT | AAT | 732  |
| Val | Thr | Ser | Glu | His | Arg | Ile | Leu | Arg | Leu | Lys | Leu | Trp | Trp | Ser | Asn |      |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| TTG | CAA | AAT | TCG | CTT | TTC | ACG | CTC | TTG | CCG | GAT | AGA | TTA | GCG | AAC | GCT | 780  |
| Leu | Gln | Asn | Ser | Leu | Phe | Thr | Leu | Leu | Pro | Asp | Arg | Leu | Ala | Asn | Ala |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| CTT | AGA | ATA | AGC | GAC | TTG | CCC | GAA | TCC | TAT | CAG | GTC | TTT | CAT | GCA | GGC | 828  |
| Leu | Arg | Ile | Ser | Asp | Leu | Pro | Glu | Ser | Tyr | Gln | Val | Phe | His | Ala | Gly |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| AAT | GCC | ATG | CAT | AAT | GGG | GGG | TTG | TTT | GGG | CAA | GGG | CTT | GGG | CTT | GGG | 876  |
| Asn | Ala | Met | His | Asn | Gly | Gly | Leu | Phe | Gly | Gln | Gly | Leu | Gly | Leu | Gly |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| CAA | ATC | AAG | CTT | GGG | TTT | TTG | AGC | GAA | GTG | CAT | ACG | GAC | ATG | GTC | TTA | 924  |
| Gln | Ile | Lys | Leu | Gly | Phe | Leu | Ser | Glu | Val | His | Thr | Asp | Met | Val | Leu |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| GCT | GGG | ATC | GCC | GAA | GAA | TGG | GGG | TTT | TTG | GGG | CTA | TGC | GTT | TGT | TTT | 972  |
| Ala | Gly | Ile | Ala | Glu | Glu | Trp | Gly | Phe | Leu | Gly | Leu | Cys | Val | Cys | Phe |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| ATT | TTG | TTT | TCT | GTT | TTG | ATT | GTT | TTG | ATT | TTT | AGG | ATC | GCT | AAC | CGC | 1020 |
| Ile | Leu | Phe | Ser | Val | Leu | Ile | Val | Leu | Ile | Phe | Arg | Ile | Ala | Asn | Arg |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| TTG | AAA | GAG | CCA | AAA | TAT | TCG | CTA | TTT | TGC | GTG | GGC | GTG | GTG | CTG | CTT | 1068 |
| Leu | Lys | Glu | Pro | Lys | Tyr | Ser | Leu | Phe | Cys | Val | Gly | Val | Val | Leu | Leu |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| ATT | AGT | TTT | TCT | TTG | GTG | ATC | AAC | GCC | TTT | GGG | GTG | GGC | GGG | ATT | CTT | 1116 |
| Ile | Ser | Phe | Ser | Leu | Val | Ile | Asn | Ala | Phe | Gly | Val | Gly | Gly | Ile | Leu |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| CCG | GTT | AAA | GGT | CTA | GCG | GTG | CCG | TTT | TTG | AGC | TAT | GGA | GGG | AGT | TCG | 1164 |
| Pro | Val | Lys | Gly | Leu | Ala | Val | Pro | Phe | Leu | Ser | Tyr | Gly | Gly | Ser | Ser |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| CTT | CTA | GCG | AAT | TGT | ATC | GCT | ATA | GGG | CTT | GTT | CTA | AGC | CTA | GCG | CGA | 1212 |
| Leu | Leu | Ala | Asn | Cys | Ile | Ala | Ile | Gly | Leu | Val | Leu | Ser | Leu | Ala | Arg |      |

370

375

380

TAC ACG AAA GGC TAAAAACATC AACCCCTTTT TAAAAATTAA TGCCATAAAA AGGGC 1269  
 Tyr Thr Lys Gly  
 385

TCAACCTC

1277

## (2) INFORMATION FOR SEQ ID NO:350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Asp | Arg | Asn | Leu | Phe | Phe | Cys | Ala | Ser | Leu | Leu | Ile | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gly | Val | Leu | Met | Ser | Tyr | Ser | Leu | Ser | Thr | Tyr | Thr | Thr | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Tyr | His | Tyr | Gly | Glu | Phe | His | Phe | Phe | Ile | Arg | Gln | Leu | Val | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Ile | Ile | Gly | Ile | Val | Ile | Met | Trp | Gly | Leu | Ser | Arg | Val | Asp | Pro |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Lys | Trp | Phe | Ser | Arg | Leu | Gly | Phe | Phe | Leu | Leu | Phe | Val | Pro | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Leu | Ile | Ile | Gly | Met | Phe | Phe | Leu | Pro | Glu | Ser | Leu | Ser | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gly | Gly | Ala | Lys | Arg | Trp | Ile | Arg | Leu | Gly | Phe | Phe | Ser | Leu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Leu | Glu | Phe | Leu | Lys | Ile | Gly | Phe | Thr | Phe | Phe | Leu | Ala | Trp | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Arg | Thr | Phe | Val | Ala | Lys | Glu | Lys | Ala | Asn | Val | Lys | Glu | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ile | Thr | Phe | Val | Pro | Tyr | Ser | Val | Val | Phe | Val | Ala | Leu | Ala | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Val | Gly | Val | Leu | Gln | Asn | Asp | Leu | Gly | Gln | Ile | Val | Leu | Leu | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Val | Leu | Ala | Val | Leu | Leu | Val | Phe | Ser | Gly | Gly | Ser | Val | His | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Gly | Leu | Ile | Ile | Ser | Gly | Ala | Phe | Ala | Ile | Ser | Val | Leu | Ala | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Thr | Ser | Glu | His | Arg | Ile | Leu | Arg | Leu | Lys | Leu | Trp | Trp | Ser | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Gln | Asn | Ser | Leu | Phe | Thr | Leu | Leu | Pro | Asp | Arg | Leu | Ala | Asn | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Arg | Ile | Ser | Asp | Leu | Pro | Glu | Ser | Tyr | Gln | Val | Phe | His | Ala | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Ala | Met | His | Asn | Gly | Gly | Leu | Phe | Gly | Gln | Gly | Leu | Gly | Leu | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Ile | Lys | Leu | Gly | Phe | Leu | Ser | Glu | Val | His | Thr | Asp | Met | Val | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Gly | Ile | Ala | Glu | Glu | Trp | Gly | Phe | Leu | Gly | Leu | Cys | Val | Cys | Phe |

290 295 300  
 Ile Leu Phe Ser Val Leu Ile Val Leu Ile Phe Arg Ile Ala Asn Arg  
 305 310 315 320  
 Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu  
 325 330 335  
 Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu  
 340 345 350  
 Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser  
 355 360 365  
 Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg  
 370 375 380  
 Tyr Thr Lys Gly  
 385

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGAACAGTAT CTATTTTGTG TGCGGTTGTA TATTTAATTA GGAGTTTGGT GTG AAA  | 56  |
| Val Lys                                                         |     |
| 1                                                               |     |
| CGG ATT TTA TTT TTT TTA GTA GCT ACG ACT TTT TTG TTG AGA GCA GAA | 104 |
| Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg Ala Glu |     |
| 5 10 15                                                         |     |
| ACG GAT TCT GCC ACT ATT AAC ACT ACA GTT GAT CCC AAT GTT ATG TTT | 152 |
| Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val Met Phe |     |
| 20 25 30                                                        |     |
| TCT GAA AGC TCC ACA GGG AAT GTG AAA AAA GAC CGC AAG AGG GTT TTA | 200 |
| Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg Val Leu |     |
| 35 40 45 50                                                     |     |
| AAG AGC ATG GTT AAT TTG GAA AAA GAG CGC GTG AAG AAT TTT AAC CGG | 248 |
| Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe Asn Arg |     |
| 55 60 65                                                        |     |
| TAT TCT GAA ACC AAG ATG AGT AAG GGC GAC TTA TCC GCT TTT GGA GCT | 296 |
| Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe Gly Ala |     |
| 70 75 80                                                        |     |
| TTC TTT AAG GGG AGT TTG GAA AGT TGT GTG GAT CAA AAG ATT TGT TAT | 344 |



(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Arg | Ile | Leu | Phe | Phe | Leu | Val | Ala | Thr | Thr | Phe | Leu | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Thr | Asp | Ser | Ala | Thr | Ile | Asn | Thr | Thr | Val | Asp | Pro | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Phe | Ser | Glu | Ser | Ser | Thr | Gly | Asn | Val | Lys | Lys | Asp | Arg | Lys | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Lys | Ser | Met | Val | Asn | Leu | Glu | Lys | Glu | Arg | Val | Lys | Asn | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Arg | Tyr | Ser | Glu | Thr | Lys | Met | Ser | Lys | Gly | Asp | Leu | Ser | Ala | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Ala | Phe | Phe | Lys | Gly | Ser | Leu | Glu | Ser | Cys | Val | Asp | Gln | Lys | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Tyr | Tyr | Glu | His | Lys | Asp | Gly | Lys | Val | Ser | Phe | Val | Val | Asn | Asp |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Arg | Glu | Lys | Phe | Tyr | Lys | His | Val | Leu | Lys | Asp | Leu | Gly | Thr | Glu | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Leu | Pro | Leu | Phe | Asn | Trp | Leu | Tyr | Lys | Gly | Ser | Asp | Phe | Gly | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | His | Glu | Gln | Phe | Gly | Asp | Met | Tyr | Asp | Gly | Tyr | Ile | Lys | Tyr | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Ser | Met | Val | Arg | Ile | Ser | Gln | Lys | Glu | Lys | Ala | Arg | Lys | Val | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Ile | Val | Leu | Lys | Lys | Met | Glu | Glu | Gln | Ala | Glu | Lys | Asp | Thr | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ala | Phe | Gln | Lys | Arg | Ser | Ser | Gly | Glu | Leu | Glu | Ser | His | Thr | Asp |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Pro | Glu | Phe | Ile | Ser | Ser | Ser | Lys | Arg | Thr | Gln | Asn | Ala | Ser | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Asp | Leu | Asn | Ser | Met | Thr | Asn | Ala | Asn | Ala | Leu | Lys | Glu | Thr | Ala |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Ser | Lys | Glu | Pro | Glu | Ala | Ser | Ser | Lys | Lys | Glu | Lys | Lys | Ser | Lys | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Arg | Arg | Leu | Ser | Lys | Lys | Glu | Lys | Gln | Gln | Gln | Ala | Leu | Gln | Gln |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Glu | Phe | Glu | Lys | Gln | Ile | Ser | Asp | Ser | Ser | Lys | Ser | Glu | Lys |     |     |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...1499

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

|       |       |            |            |            |            |     |     |     |
|-------|-------|------------|------------|------------|------------|-----|-----|-----|
| CTTTT | TAGCC | TCAAGACTTG | GGCTTTAACA | TTAAAGAATT | ATTTTAAGGA | ATG | ATC | 56  |
|       |       |            |            |            |            | Met | Ile |     |
|       |       |            |            |            |            | 1   |     |     |
| ATG   | GAA   | AAA        | TAC        | CAT        | AGC        | GAC | CAA | 5   |
| Met   | Glu   | Lys        | Tyr        | His        | Ser        | Asp | Gln | 10  |
|       |       |            |            |            |            |     |     | 15  |
|       |       |            |            |            |            |     |     | 15  |
| 104   |       |            |            |            |            |     |     |     |
| CAA   | TTA   | GGC        | GAT        | ATG        | CAA        | TTA | AGG | 20  |
| Gln   | Leu   | Gly        | Asp        | Met        | Gln        | Leu | Arg | 25  |
|       |       |            |            |            |            |     |     | 30  |
|       |       |            |            |            |            |     |     | 30  |
| 152   |       |            |            |            |            |     |     |     |
| ACC   | TTA   | AGG        | GCT        | AAT        | CGT        | AAG | AAT | 35  |
| Thr   | Leu   | Arg        | Ala        | Asn        | Arg        | Lys | Asn | 40  |
|       |       |            |            |            |            |     |     | 45  |
|       |       |            |            |            |            |     |     | 50  |
| 200   |       |            |            |            |            |     |     |     |
| TGG   | GAA   | AAT        | TTA        | AGG        | GAA        | TTA | GGC | 55  |
| Trp   | Glu   | Asn        | Leu        | Arg        | Glu        | Leu | Gly | 60  |
|       |       |            |            |            |            |     |     | 65  |
|       |       |            |            |            |            |     |     | 65  |
| 248   |       |            |            |            |            |     |     |     |
| TCC   | AGG   | CTT        | GAT        | GAA        | TAT        | TTG | GAA | 70  |
| Ser   | Arg   | Leu        | Asp        | Glu        | Tyr        | Leu | Glu | 75  |
|       |       |            |            |            |            |     |     | 80  |
|       |       |            |            |            |            |     |     | 80  |
| 296   |       |            |            |            |            |     |     |     |
| AAC   | GGC   | TTT        | AAA        | ATC        | CAT        | TAC | GCT | 85  |
| Asn   | Gly   | Phe        | Lys        | Ile        | His        | Tyr | Ala | 90  |
|       |       |            |            |            |            |     |     | 95  |
|       |       |            |            |            |            |     |     | 95  |
| 344   |       |            |            |            |            |     |     |     |
| ATC   | ATT   | TAC        | AAC        | CTC        | GCT        | AAA | GAA | 100 |
| Ile   | Ile   | Tyr        | Asn        | Leu        | Ala        | Lys | Glu | 105 |
|       |       |            |            |            |            |     |     | 110 |
|       |       |            |            |            |            |     |     | 110 |
| 392   |       |            |            |            |            |     |     |     |
| CAA   | AAA   | TCC        | ATG        | GCG        | AGC        | GAA | GAA | 115 |
| Gln   | Lys   | Ser        | Met        | Ala        | Ser        | Glu | Glu | 120 |
|       |       |            |            |            |            |     |     | 125 |
|       |       |            |            |            |            |     |     | 130 |
| 440   |       |            |            |            |            |     |     |     |
| GAA   | AAG   | GGC        | ATT        | CAA        | GCA        | CAA | GAA | 135 |
| Glu   | Lys   | Gly        | Ile        | Gln        | Ala        | Gln | Glu | 140 |
|       |       |            |            |            |            |     |     | 145 |
|       |       |            |            |            |            |     |     | 145 |
| 488   |       |            |            |            |            |     |     |     |
| CAA   | CTC   | ATC        | AAT        | GAA        | CAC        | CCT | GTG | 150 |
| Gln   | Leu   | Ile        | Asn        | Glu        | His        | Pro | Val | 155 |
|       |       |            |            |            |            |     |     | 160 |
|       |       |            |            |            |            |     |     | 160 |
| 536   |       |            |            |            |            |     |     |     |
| AAA   | AAC   | CGC        | AAG        | CAA        | ATC        | GGT | AAG | 165 |
| Lys   | Asn   | Arg        | Lys        | Gln        | Ile        | Gly | Lys | 170 |
|       |       |            |            |            |            |     |     | 175 |
|       |       |            |            |            |            |     |     | 175 |
| 584   |       |            |            |            |            |     |     |     |
| GCT   | TAT   | GAA        | GAA        | GAG        | CCT        | GAA | AAG | 180 |
| Ala   | Tyr   | Glu        | Glu        | Glu        | Pro        | Glu | Lys | 185 |
|       |       |            |            |            |            |     |     | 190 |
|       |       |            |            |            |            |     |     | 190 |
| 632   |       |            |            |            |            |     |     |     |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| ATG CGC AAA GAA TTT GAA AGC TTT AAA ATG GGG ATT AGT GGG GTT AAT | 680  |
| Met Arg Lys Glu Phe Glu Ser Phe Lys Met Gly Ile Ser Gly Val Asn |      |
| 195 200 205 210                                                 |      |
| TTT GCT ATC GCT AAC GAA GGA GCG ATC TGG TTA GTG GAA AAT GAA GGC | 728  |
| Phe Ala Ile Ala Asn Glu Gly Ala Ile Trp Leu Val Glu Asn Glu Gly |      |
| 215 220 225                                                     |      |
| AAT GGC AGA ATG AGC ACC ACT GCA TGC GAT GTG CAT GTC GCA ATT TGT | 776  |
| Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala Ile Cys |      |
| 230 235 240                                                     |      |
| GGG ATT GAA AAA TTA GTA GAA AGC TTT GAT GAT GCG GCG ATT TTA AAC | 824  |
| Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile Leu Asn |      |
| 245 250 255                                                     |      |
| AAT TTG CTC GCC CCA AGC GCT GTG GGT GTG CCT ATC ACT TGC TAT CAA | 872  |
| Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys Tyr Gln |      |
| 260 265 270                                                     |      |
| AAC ATT ATC ACA GGC CCT AGA AAA GAG GGC GAT TTA GAC GGC CCT AAA | 920  |
| Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly Pro Lys |      |
| 275 280 285 290                                                 |      |
| GAA GCC CAC ATC ATT TTA TTA GAC AAC AAC CGC TCT AAT ATT TTG GCT | 968  |
| Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile Leu Ala |      |
| 295 300 305                                                     |      |
| GAT GAA AAG TAT TAT CGC GCT CTT TCA TGC ATC CGT TGC GGG ACT TGT | 1016 |
| Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly Thr Cys |      |
| 310 315 320                                                     |      |
| TTG AAC CAC TGC CCT GTG TAT GAT AAA ATC GGT GGG CAT GCC TAT CTT | 1064 |
| Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala Tyr Leu |      |
| 325 330 335                                                     |      |
| TCT ACT TAT CCT GGC CCT ATA GGC GTG GTG GTA TCC CCC CAA CTC TTT | 1112 |
| Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln Leu Phe |      |
| 340 345 350                                                     |      |
| GGC TTG AAT AAT TAC GGC CAT ATC CCT AAT TTG TGC AGT CTT TGC GGG | 1160 |
| Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu Cys Gly |      |
| 355 360 365 370                                                 |      |
| CGT TGC ACT GAA GTA TGC CCC GTA GAA ATC CCT TTA GCC GAA CTC ATT | 1208 |
| Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu Leu Ile |      |
| 375 380 385                                                     |      |
| AGG GAT TTA CGA TCC GAT AAA GTG GGC GAG GGC AGG GGT GTA ATT AAG | 1256 |
| Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val Ile Lys |      |
| 390 395 400                                                     |      |
| GGG GCT AAA AGC ACC CAA CAC AGC GGG ATG GAA AAA TTC TCT ATG AAA | 1304 |
| Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser Met Lys |      |
| 405 410 415                                                     |      |
| ATG TTT GCC AAA ATG GCA AGC GAT GGG GCT AAG TGG CGT TTC CAA TTG | 1352 |
| Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe Gln Leu |      |





|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 210                                                             |     | 215 |     | 220 |
| Glu Gly Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala |     |     |     |     |
| 225                                                             |     | 230 |     | 235 |
| Ile Cys Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile |     |     |     |     |
|                                                                 | 245 |     | 250 | 255 |
| Leu Asn Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys |     |     |     |     |
|                                                                 | 260 |     | 265 | 270 |
| Tyr Gln Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly |     |     |     |     |
|                                                                 | 275 |     | 280 | 285 |
| Pro Lys Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile |     |     |     |     |
|                                                                 | 290 |     | 295 | 300 |
| Leu Ala Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly |     |     |     |     |
| 305                                                             |     | 310 |     | 315 |
| Thr Cys Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala |     |     |     |     |
|                                                                 | 325 |     | 330 | 335 |
| Tyr Leu Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln |     |     |     |     |
|                                                                 | 340 |     | 345 | 350 |
| Leu Phe Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu |     |     |     |     |
|                                                                 | 355 |     | 360 | 365 |
| Cys Gly Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu |     |     |     |     |
|                                                                 | 370 |     | 375 | 380 |
| Leu Ile Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val |     |     |     |     |
| 385                                                             |     | 390 |     | 395 |
| Ile Lys Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser |     |     |     |     |
|                                                                 | 405 |     | 410 | 415 |
| Met Lys Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe |     |     |     |     |
|                                                                 | 420 |     | 425 | 430 |
| Gln Leu Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala |     |     |     |     |
|                                                                 | 435 |     | 440 | 445 |
| Pro Ile Leu Pro Leu Val Lys Glu Trp Ala Ser Val Arg Thr Leu Pro |     |     |     |     |
|                                                                 | 450 |     | 455 | 460 |
| Asn Met Asp Thr Ser Leu His Ala Lys Val Gln His Leu Glu Gly Val |     |     |     |     |
| 465                                                             |     | 470 |     | 475 |
| Ile Tyr Glu                                                     |     |     |     | 480 |

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 294...1577
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GTATCGCCAC | TTTGCGTAAC | AGGATGTTGA | AAGTGGGTAA | AAGCCGCTAA | TTTCTTTTAA | 60  |
| GTGGGTCGTT | TTTGAAAATC | TTTTTAGTCT | TTTAAAGCGT | CTTTTTTTTT | AATGGGTGTT | 120 |
| TTGGGTTAGT | CTATAAGACT | CCCATTTCAA | GCTCTCCTAT | CTCTTATGAT | CCCTACACTA | 180 |



|       |       |      |      |     |     |     |     |     |     |     |     |     |      |     |     |      |      |
|-------|-------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|------|------|
| Asn   | Ala   | Ile  | Phe  | Leu | Ala | Asp | Ser | Pro | Lys | Lys | Ile | Asp | Thr  | Pro | Leu |      |      |
| 210   |       |      |      |     | 215 |     |     |     |     | 220 |     |     |      |     | 225 |      |      |
| TAT   | TCG   | CCT  | ATC  | AAA | ATC | GCT | TTT | GAG | AAA | GCC | CTT | AAA | AAC  | GCT | AAG | 1016 |      |
| Tyr   | Ser   | Pro  | Ile  | Lys | Ile | Ala | Phe | Glu | Lys | Ala | Leu | Lys | Asn  | Ala | Lys |      |      |
|       |       |      |      | 230 |     |     |     |     | 235 |     |     |     |      | 240 |     |      |      |
| GAC   | TCC   | GTT  | TTT  | ATC | GCT | TCA | TCG | TAT | TTT | ATT | CCA | GGC | AAA  | AAG | ATG | 1064 |      |
| Asp   | Ser   | Val  | Phe  | Ile | Ala | Ser | Ser | Tyr | Phe | Ile | Pro | Gly | Lys  | Lys | Met |      |      |
|       |       |      | 245  |     |     |     |     | 250 |     |     |     |     | 255  |     |     |      |      |
| ATG   | AAA   | ATC  | TTT  | AAA | AAT | CAA | ATT | TCT | AAG | GGG | ATT | GAA | TTG  | AAC | ATC | 1112 |      |
| Met   | Lys   | Ile  | Phe  | Lys | Asn | Gln | Ile | Ser | Lys | Gly | Ile | Glu | Leu  | Asn | Ile |      |      |
|       |       | 260  |      |     |     |     | 265 |     |     |     |     | 270 |      |     |     |      |      |
| CTT   | ACC   | AAT  | TCC  | CTT | TCA | TCT | ACT | GAT | GCG | ATA | GTG | GTC | TAT  | GGG | GCA | 1160 |      |
| Leu   | Thr   | Asn  | Ser  | Leu | Ser | Ser | Thr | Asp | Ala | Ile | Val | Val | Tyr  | Gly | Ala |      |      |
|       | 275   |      |      |     |     | 280 |     |     |     |     | 285 |     |      |     |     |      |      |
| TGG   | GAA   | AGG  | TAT  | CGC | AAC | CAA | TTA | GTG | CGA | ATG | GGC | GCG | AAT  | GTC | TAT | 1208 |      |
| Trp   | Glu   | Arg  | Tyr  | Arg | Asn | Gln | Leu | Val | Arg | Met | Gly | Ala | Asn  | Val | Tyr |      |      |
| 290   |       |      |      |     | 295 |     |     |     | 300 |     |     |     |      | 305 |     |      |      |
| GAA   | ATA   | CGA  | AAC  | GAT | TTT | TTC | AAC | CGC | CAG | ATT | AAA | GGG | CGC  | TTT | AGC | 1256 |      |
| Glu   | Ile   | Arg  | Asn  | Asp | Phe | Phe | Asn | Arg | Gln | Ile | Lys | Gly | Arg  | Phe | Ser |      |      |
|       |       |      | 310  |     |     |     |     |     | 315 |     |     |     |      | 320 |     |      |      |
| ACC   | AAA   | CAT  | TCC  | TTG | CAT | GGC | AAG | ACG | ATT | GTT | TTT | GAT | GAC  | AAT | TTA | 1304 |      |
| Thr   | Lys   | His  | Ser  | Leu | His | Gly | Lys | Thr | Ile | Val | Phe | Asp | Asp  | Asn | Leu |      |      |
|       |       |      | 325  |     |     |     |     | 330 |     |     |     |     | 335  |     |     |      |      |
| ACG   | CTT   | CTA  | GGG  | AGT | TTC | AAT | ATT | GAT | CCG | CGC | TCT | GCA | TAC  | ATC | AAC | 1352 |      |
| Thr   | Leu   | Leu  | Gly  | Ser | Phe | Asn | Ile | Asp | Pro | Arg | Ser | Ala | Tyr  | Ile | Asn |      |      |
|       |       | 340  |      |     |     |     | 345 |     |     |     |     | 350 |      |     |     |      |      |
| ACT   | GAA   | AGC  | GCG  | GTT | TTG | TTT | GAC | AAC | CCG | TCT | TTT | GCT | AAA  | AGG | GTG | 1400 |      |
| Thr   | Glu   | Ser  | Ala  | Val | Leu | Phe | Asp | Asn | Pro | Ser | Phe | Ala | Lys  | Arg | Val |      |      |
|       | 355   |      |      |     |     | 360 |     |     |     |     | 365 |     |      |     |     |      |      |
| CGT   | TTG   | TCG  | CTT  | AAA | GAT | CAT | GCC | CAA | CAA | TCA | TGG | CAT | TTG  | GTG | GTG | 1448 |      |
| Arg   | Leu   | Ser  | Leu  | Lys | Asp | His | Ala | Gln | Gln | Ser | Trp | His | Leu  | Val | Val |      |      |
| 370   |       |      |      |     | 375 |     |     |     |     | 380 |     |     |      | 385 |     |      |      |
| TAT   | CGG   | CAT  | AGA  | GTG | ATT | TGG | GAA | GCG | GTG | GAA | GAA | GGC | ATT  | TTA | ATC | 1496 |      |
| Tyr   | Arg   | His  | Arg  | Val | Ile | Trp | Glu | Ala | Val | Glu | Glu | Gly | Ile  | Leu | Ile |      |      |
|       |       |      |      | 390 |     |     |     |     | 395 |     |     |     |      | 400 |     |      |      |
| CAT   | GAA   | AAA  | ACT  | TCG | CCT | GAC | ACT | TCC | TTC | TTT | TTG | CGC | TTG  | ATT | AAA | 1544 |      |
| His   | Glu   | Lys  | Thr  | Ser | Pro | Asp | Thr | Ser | Phe | Phe | Leu | Arg | Leu  | Ile | Lys |      |      |
|       |       |      | 405  |     |     |     |     | 410 |     |     |     |     | 415  |     |     |      |      |
| GAA   | TGG   | TCT  | AAA  | GTC | CTT | CCT | GAA | AGA | GAG | CTT | TAA | AAC | TTTT | AAT | GCG | CTTT | 1597 |
| Glu   | Trp   | Ser  | Lys  | Val | Leu | Pro | Glu | Arg | Glu | Leu |     |     |      |     |     |      |      |
|       |       | 420  |      |     |     |     | 425 |     |     |     |     |     |      |     |     |      |      |
| ATTTT | GCGAA | AAAG | CGAT | GT  | TAT | TG  | GTA | AC  | GGC |     |     |     |      |     |     |      | 1630 |

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Lys | Ser | Ile | Asp | Met | Gln | Thr | Tyr | Ile | Tyr | Lys | Asn | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Ser | Gln | Val | Ile | Ala | Lys | Glu | Leu | Leu | Asn | Ala | Ala | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Val | Lys | Val | Arg | Ile | Leu | Leu | Asp | Asp | Asn | Gly | Leu | Asp | Ser | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ser | Asp | Ile | Met | Leu | Leu | Asn | Phe | His | Lys | Asn | Ile | Glu | Val | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Phe | Asn | Pro | Tyr | Tyr | Ile | Arg | Asn | Lys | Gly | Leu | Arg | Tyr | Phe | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Leu | Ala | Asp | Tyr | Glu | Arg | Ile | Lys | Lys | Arg | Met | His | Asn | Lys | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ile | Val | Asp | Asn | Phe | Ala | Val | Ile | Ile | Gly | Gly | Arg | Asn | Ile | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Asn | Tyr | Phe | Asp | Asn | Asp | Leu | Asp | Thr | Asn | Phe | Leu | Asp | Leu | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Leu | Phe | Phe | Gly | Gly | Val | Ala | Ser | Lys | Ala | Lys | Glu | Ser | Phe | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Tyr | Trp | Arg | Phe | His | Arg | Ser | Ile | Pro | Val | Ser | Leu | Leu | Arg | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Lys | Arg | Leu | Lys | Asn | Asn | Ala | Lys | Glu | Ile | Ala | Lys | Leu | His | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Ile | Pro | Ile | Ser | Ala | Glu | Asp | Lys | Asn | Gln | Phe | Glu | Lys | Lys | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Asp | Phe | Ile | Asp | Arg | Phe | Gln | Lys | Tyr | Gln | Tyr | Pro | Ile | Tyr | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Asn | Ala | Ile | Phe | Leu | Ala | Asp | Ser | Pro | Lys | Lys | Ile | Asp | Thr | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Tyr | Ser | Pro | Ile | Lys | Ile | Ala | Phe | Glu | Lys | Ala | Leu | Lys | Asn | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Asp | Ser | Val | Phe | Ile | Ala | Ser | Ser | Tyr | Phe | Ile | Pro | Gly | Lys | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Met | Lys | Ile | Phe | Lys | Asn | Gln | Ile | Ser | Lys | Gly | Ile | Glu | Leu | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Leu | Thr | Asn | Ser | Leu | Ser | Ser | Thr | Asp | Ala | Ile | Val | Val | Tyr | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Trp | Glu | Arg | Tyr | Arg | Asn | Gln | Leu | Val | Arg | Met | Gly | Ala | Asn | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Glu | Ile | Arg | Asn | Asp | Phe | Phe | Asn | Arg | Gln | Ile | Lys | Gly | Arg | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Thr | Lys | His | Ser | Leu | His | Gly | Lys | Thr | Ile | Val | Phe | Asp | Asp | Asn |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Thr | Leu | Leu | Gly | Ser | Phe | Asn | Ile | Asp | Pro | Arg | Ser | Ala | Tyr | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Thr | Glu | Ser | Ala | Val | Leu | Phe | Asp | Asn | Pro | Ser | Phe | Ala | Lys | Arg |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Val | Arg | Leu | Ser | Leu | Lys | Asp | His | Ala | Gln | Gln | Ser | Trp | His | Leu | Val |

370 375 380  
 Val Tyr Arg His Arg Val Ile Trp Glu Ala Val Glu Glu Gly Ile Leu  
 385 390 395 400  
 Ile His Glu Lys Thr Ser Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile  
 405 410 415  
 Lys Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu  
 420 425

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...510
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AACTCTTTTG GTGTAGGATA GCGATCAAGG TTTTATGAA AATAAAAGCC TAAAACAATT | 60  |
| TTAAAAAAG GACTTTTG ATG AAA ACA TTT GAA ATT CTA AAA CAT TTG CAA   | 111 |
| Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln                      |     |
| 1 5 10                                                           |     |
| GCG GAT GCG ATC GTG TTA TTT ATG AAA GTG CAT AAC TTC CAT TGG AAT  | 159 |
| Ala Asp Ala Ile Val Leu Phe Met Lys Val His Asn Phe His Trp Asn  |     |
| 15 20 25                                                         |     |
| GTG AAA GGC ACC GAT TTT TTC AAT GTG CAT AAA GCC ACT GAA GAA ATT  | 207 |
| Val Lys Gly Thr Asp Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile  |     |
| 30 35 40                                                         |     |
| TAT GAA GAG TTT GCG GAC ATG TTT GAC GAT CTC GCT GAA AGG ATC GTT  | 255 |
| Tyr Glu Glu Phe Ala Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val  |     |
| 45 50 55                                                         |     |
| CAA TTA GGG CAT CAC CCC TTA GTC ACT TTA TCC GAA GCG ATC AAA CTC  | 303 |
| Gln Leu Gly His His Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu  |     |
| 60 65 70 75                                                      |     |
| ACT CGT GTT AAA GAA GAA ACT AAA ACG AGC TTC CAC TCT AAA GAC ATC  | 351 |
| Thr Arg Val Lys Glu Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile  |     |
| 80 85 90                                                         |     |
| TTT AAA GAA ATT CTA GAG GAC TAC AAA TAT CTA GAA AAA GAA TTT AAA  | 399 |
| Phe Lys Glu Ile Leu Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys  |     |
| 95 100 105                                                       |     |
| GAG CTC TCT AAC ACC GCT GAA AAA GAA GGC GAT AAA GTT ACC GTA ACT  | 447 |
| Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr  |     |

110 115 120

TAT GCG GAT GAT CAA TTA GCC AAG TTG CAA AAA TCC ATT TGG ATG CTG 495  
 Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu  
 125 130 135

CAA GCC CAT TTG GCT TAAGCGACCA AAAAGAAGCC AGCATGAGAG ATTACAGCGA 550  
 Gln Ala His Leu Ala  
 140

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln Ala Asp Ala Ile Val  
 1 5 10 15  
 Leu Phe Met Lys Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp  
 20 25 30  
 Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile Tyr Glu Glu Phe Ala  
 35 40 45  
 Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His  
 50 55 60  
 Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu  
 65 70 75 80  
 Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu  
 85 90 95  
 Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr  
 100 105 110  
 Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln  
 115 120 125  
 Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu Gln Ala His Leu Ala  
 130 135 140

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...323
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

|                                                                    |         |     |
|--------------------------------------------------------------------|---------|-----|
| CTTTTTTCTC TTCCACTTTT TCCACTTTTT TAAGAGCCTT GTGTTTATGA             | TTG GGC | 56  |
|                                                                    | Leu Gly |     |
|                                                                    | 1       |     |
| TTT TTG GGT TCA GGT TTG GGT TTT GGT TTA GGC TCA GGC TTA GGC TTT    |         | 104 |
| Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu Gly Phe    |         |     |
| 5 10 15                                                            |         |     |
| TCT ATA GGT TTT GGC GGG GTT GGC GGG GTT GGC GGA GTT GGG GGT GTG    |         | 152 |
| Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly Gly Val    |         |     |
| 20 25 30                                                           |         |     |
| GGA GGC GTT GGA GGT TTT TGG GGG CCA GCC AGC GTG GGT TTA GGA GCG    |         | 200 |
| Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu Gly Ala    |         |     |
| 35 40 45 50                                                        |         |     |
| CCC TGG GTG TTT TTA CTG GGA TCT TGC GAA TGG CCT CTT TTT AAA ACC    |         | 248 |
| Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe Lys Thr    |         |     |
| 55 60 65                                                           |         |     |
| AAT AAA TTT TCA GGA TTT AAT TTA ACA AGC TTG GGT TTT GAA GGA AAA    |         | 296 |
| Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu Gly Lys    |         |     |
| 70 75 80                                                           |         |     |
| AAA TCT TCT CTG TGT TCA AAT AAA AAA TAAATCAACC AGTGTAAACAA TACAGAC |         | 350 |
| Lys Ser Ser Leu Cys Ser Asn Lys Lys                                |         |     |
| 85 90                                                              |         |     |
| AGAATGAGAG AAAAGAAAAA ATTCCT                                       |         | 376 |

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Leu Gly Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu |  |
| 1 5 10 15                                                       |  |
| Gly Phe Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly |  |
| 20 25 30                                                        |  |
| Gly Val Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu |  |
| 35 40 45                                                        |  |
| Gly Ala Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe |  |
| 50 55 60                                                        |  |
| Lys Thr Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu |  |
| 65 70 75 80                                                     |  |
| Gly Lys Lys Ser Ser Leu Cys Ser Asn Lys Lys                     |  |
| 85 90                                                           |  |



(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 458...2836
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TCAAAATTTA | AGTTAATTTT | AATAATTATT | TTTATAGTAT | GCATCGGTTT | GAATTAAATG | 60  |
| AGAAAGGTTA | TCACAATGAA | TGGTTATTTG | AGAGTAAAAA | CCTCTTATTT | TTTAGCGTTG | 120 |
| AACGCTTTGA | CTTTTTTGTC | TTTAACTCT  | TTGGTGGGCG | CGAAAGAACA | GCATCACACT | 180 |
| TTGCAAAAAG | TGACAACCAC | TGAGCAAAAA | TTCAATCCAA | GCGCGCCGCT | TTCATGGCAA | 240 |
| AGCGAAGAGA | TGCGTAATTC | CACAAGCTCT | CGCACGGTGA | TTTCCAACAA | GGAACTCAAA | 300 |
| AAAACGGGGA | ATTTGAATAT | TGAAAACGCC | TTGCAAAACG | TGCCAGGGAT | TCAAATCAGA | 360 |
| GACGCTACAG | GCACAGGCGT | GCTGCCCTAA | ATTTCGGTGC | TCAAATTTA  | AGTTAATTTT | 420 |
| AATAATTATT | TTTATAGTAT | GCATCGGTTT | GAATTAA    | ATG        | AGA        | AAG |
|            |            |            |            | Met        | Arg        | Lys |
|            |            |            |            | 1          |            | 5   |
|            |            |            |            |            |            |     |
| ATG        | AAT        | GGT        | TAT        | TTG        | AGA        | GTA |
| Met        | Asn        | Gly        | Tyr        | Leu        | Arg        | Val |
|            | 10         |            |            |            |            | 15  |
|            |            |            |            |            |            |     |
| GCT        | TTG        | ACT        | TTT        | TTG        | TCT        | TTT |
| Ala        | Leu        | Thr        | Phe        | Leu        | Ser        | Phe |
|            | 25         |            |            |            |            | 30  |
|            |            |            |            |            |            |     |
| CAT        | CAC        | ACT        | TTG        | CAA        | AAA        | GTG |
| His        | His        | Thr        | Leu        | Gln        | Lys        | Val |
|            | 40         |            |            |            |            | 45  |
|            |            |            |            |            |            |     |
| AGC        | GCG        | CCG        | CTT        | TCA        | TGG        | CAA |
| Ser        | Ala        | Pro        | Leu        | Ser        | Trp        | Gln |
| 55         |            |            |            |            |            | 60  |
|            |            |            |            |            |            |     |
| TCT        | CGC        | ACG        | GTG        | ATT        | TCC        | AAC |
| Ser        | Arg        | Thr        | Val        | Ile        | Ser        | Asn |
|            |            |            |            |            |            | 75  |
|            |            |            |            |            |            |     |
| AAT        | ATT        | GAA        | AAC        | GCC        | TTG        | CAA |
| Asn        | Ile        | Glu        | Asn        | Ala        | Leu        | Gln |
|            |            |            |            |            |            | 90  |
|            |            |            |            |            |            |     |
| GCT        | ACA        | GGC        | ACA        | GGC        | GTG        | CTG |
| Ala        | Thr        | Gly        | Thr        | Gly        | Val        | Leu |
|            |            |            |            |            |            | 105 |
|            |            |            |            |            |            |     |
| GGG        | GGC        | GGT        | AAC        | GGG        | CAT        | AGC |
|            |            |            |            |            |            |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Gly | Gly | Gly | Asn | Gly | His | Ser | Asn | Thr | Asn | Met | Ile | Leu | Val | Asn | Gly |      |
| 120 |     |     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     |      |
| ATC | CCC | ATT | TAT | GGC | GCG | CCG | TAT | TCC | AAT | ATT | GAA | CTG | GCG | ATT | TTC | 907  |
| Ile | Pro | Ile | Tyr | Gly | Ala | Pro | Tyr | Ser | Asn | Ile | Glu | Leu | Ala | Ile | Phe |      |
| 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |      |
| CCT | GTA | ACT | TTC | CAG | TCA | GTG | GAT | AGG | ATT | GAT | GTG | ATT | AAA | GGG | GGC | 955  |
| Pro | Val | Thr | Phe | Gln | Ser | Val | Asp | Arg | Ile | Asp | Val | Ile | Lys | Gly | Gly |      |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |      |
| ACG | AGC | GTG | CAA | TAC | GGC | CCT | AAT | ACT | TTT | GGA | GGC | GTG | GTG | AAT | ATC | 1003 |
| Thr | Ser | Val | Gln | Tyr | Gly | Pro | Asn | Thr | Phe | Gly | Gly | Val | Val | Asn | Ile |      |
|     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |     |     |      |
| ATC | ACT | AAA | GAA | ATC | CCT | AAA | GAG | TGG | GAA | AAT | CAA | GCG | GCT | GAA | AGG | 1051 |
| Ile | Thr | Lys | Glu | Ile | Pro | Lys | Glu | Trp | Glu | Asn | Gln | Ala | Ala | Glu | Arg |      |
|     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |      |
| ATC | ACT | TTT | TGG | GGG | CGA | TCC | TCT | AAT | GGG | AAT | TTT | GTA | GAT | CCC | AAA | 1099 |
| Ile | Thr | Phe | Trp | Gly | Arg | Ser | Ser | Asn | Gly | Asn | Phe | Val | Asp | Pro | Lys |      |
|     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     |      |
| GAA | AAA | GGC | AAG | CCT | TTA | GCC | CAA | ACT | TTA | GGA | AAC | CAA | ATG | CTG | TTT | 1147 |
| Glu | Lys | Gly | Lys | Pro | Leu | Ala | Gln | Thr | Leu | Gly | Asn | Gln | Met | Leu | Phe |      |
| 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |      |
| AAC | ACT | TAC | GGG | CGA | ACG | GCT | GGA | ATG | TTG | GGT | AAG | CAT | GTA | GGA | ATT | 1195 |
| Asn | Thr | Tyr | Gly | Arg | Thr | Ala | Gly | Met | Leu | Gly | Lys | His | Val | Gly | Ile |      |
|     |     |     |     | 235 |     |     |     | 240 |     |     |     |     | 245 |     |     |      |
| AGC | GCT | CAA | GGC | AAT | TGG | ATT | AAC | GGG | CAA | GGT | TTC | AGG | CAA | AAC | AGC | 1243 |
| Ser | Ala | Gln | Gly | Asn | Trp | Ile | Asn | Gly | Gln | Gly | Phe | Arg | Gln | Asn | Ser |      |
|     |     |     | 250 |     |     |     |     | 255 |     |     |     |     | 260 |     |     |      |
| CCC | ACA | AAG | GTG | CAA | AAC | TAC | TTG | CTT | GAT | GCG | GTT | TAT | AAG | ATT | AAT | 1291 |
| Pro | Thr | Lys | Val | Gln | Asn | Tyr | Leu | Leu | Asp | Ala | Val | Tyr | Lys | Ile | Asn |      |
|     |     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     |      |
| GCG | ACC | AAT | ACT | TTT | AAA | GCT | TAT | TAC | CAA | TAT | TAT | CAA | TAC | AAC | TCT | 1339 |
| Ala | Thr | Asn | Thr | Phe | Lys | Ala | Tyr | Tyr | Gln | Tyr | Tyr | Gln | Tyr | Asn | Ser |      |
|     | 280 |     |     |     |     | 285 |     |     |     |     |     | 290 |     |     |     |      |
| TAC | CAT | CCA | GGC | ACT | TTG | AGT | GCA | CAA | GAT | TAT | GCT | TAT | AAC | CGC | TTC | 1387 |
| Tyr | His | Pro | Gly | Thr | Leu | Ser | Ala | Gln | Asp | Tyr | Ala | Tyr | Asn | Arg | Phe |      |
| 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |      |
| ATT | AAT | GAG | CGC | CCT | GAC | AAT | CAA | GAT | GGA | GGG | CGA | GCC | AAG | CGC | TTT | 1435 |
| Ile | Asn | Glu | Arg | Pro | Asp | Asn | Gln | Asp | Gly | Gly | Arg | Ala | Lys | Arg | Phe |      |
|     |     |     |     | 315 |     |     |     |     | 320 |     |     |     |     | 325 |     |      |
| GGG | ATC | GTG | TAT | CAA | AAT | TAT | TTT | GGC | GAT | CCG | GAT | AGG | AAA | GTG | GGG | 1483 |
| Gly | Ile | Val | Tyr | Gln | Asn | Tyr | Phe | Gly | Asp | Pro | Asp | Arg | Lys | Val | Gly |      |
|     |     |     | 330 |     |     |     |     | 335 |     |     |     |     | 340 |     |     |      |
| GGA | GAT | TTT | AAA | TTC | ACT | TAT | TTC | ACG | CAT | GAC | ATG | AGT | AGG | GAT | TTT | 1531 |
| Gly | Asp | Phe | Lys | Phe | Thr | Tyr | Phe | Thr | His | Asp | Met | Ser | Arg | Asp | Phe |      |
|     |     | 345 |     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |      |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GGG TTT TCC AAC CAA TAC CAA AGC GTG TAT ATG AGC AGT CAA AAC AAG | 1579 |
| Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr Met Ser Ser Gln Asn Lys |      |
| 360 365 370                                                     |      |
| ATT TTA CCT TTT AAA GGC AAG GGA AAA ATT AGC GCG ACT AAC CCT AAT | 1627 |
| Ile Leu Pro Phe Lys Gly Lys Gly Lys Ile Ser Ala Thr Asn Pro Asn |      |
| 375 380 385 390                                                 |      |
| TGC GGT TTG TAT TCT TAT AGC GAC ACG AAC AGC CCT TGT TGG CAA TTT | 1675 |
| Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn Ser Pro Cys Trp Gln Phe |      |
| 395 400 405                                                     |      |
| TTT GAC AAT ATC CGC CGA TCC GTG GTG AAT GCC TTT GAG CCA AAA CTC | 1723 |
| Phe Asp Asn Ile Arg Arg Ser Val Val Asn Ala Phe Glu Pro Lys Leu |      |
| 410 415 420                                                     |      |
| AAT CTT ATC GTC AAT ACC GGT AAA GTC AAA CAA ACT TTT AAT ATG GGA | 1771 |
| Asn Leu Ile Val Asn Thr Gly Lys Val Lys Gln Thr Phe Asn Met Gly |      |
| 425 430 435                                                     |      |
| ATG CGC TTT TTA ACT GAA GAT TTA TAC CGC CGA TCC ACC ACC AGG AAA | 1819 |
| Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg Arg Ser Thr Thr Arg Lys |      |
| 440 445 450                                                     |      |
| AAC CCT AGC ATG CCT AAT AAT GGG AGT GGT TTT GAT GCA GGA ACT TCA | 1867 |
| Asn Pro Ser Met Pro Asn Asn Gly Ser Gly Phe Asp Ala Gly Thr Ser |      |
| 455 460 465 470                                                 |      |
| CTC AAT AAT TTC AAC AAT TAT ACC GCT GTG TAT GCC AGC GAT GAG ATC | 1915 |
| Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val Tyr Ala Ser Asp Glu Ile |      |
| 475 480 485                                                     |      |
| AAT TTC AAT AAC GGC ATG CTA ACG ATC ACG CCG GGC TTG AGA TAC ACT | 1963 |
| Asn Phe Asn Asn Gly Met Leu Thr Ile Thr Pro Gly Leu Arg Tyr Thr |      |
| 490 495 500                                                     |      |
| TTT TTA AAT TAC GAA AAA AAA GAC GCT CCT CCT TTT AAA GCA GGC CAA | 2011 |
| Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro Pro Phe Lys Ala Gly Gln |      |
| 505 510 515                                                     |      |
| ACA GGA AAA ACC ATT AAA GAT CGT TAT AAC CAA TGG AAT CCA GCA GTG | 2059 |
| Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn Gln Trp Asn Pro Ala Val |      |
| 520 525 530                                                     |      |
| AAT GTC GGC TAT AAA CCC ATT AAA GAA TTG TTG TTT TAT TTC AAT TAC | 2107 |
| Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu Leu Phe Tyr Phe Asn Tyr |      |
| 535 540 545 550                                                 |      |
| CAA AGA AGC TAC ATT CCG CCT CAA TTC AGC AAT ATC GGT AGT TTT GTA | 2155 |
| Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser Asn Ile Gly Ser Phe Val |      |
| 555 560 565                                                     |      |
| GGC ACA AGC ACG GAT TAT TTT CAA ATC TTT AAT GTC ATG GAA GGC GGC | 2203 |
| Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe Asn Val Met Glu Gly Gly |      |
| 570 575 580                                                     |      |
| TCA AGA TAT TAT TTT AAC AAC CAA GTG AGT TTT AAC GCG AAT TAT TTT | 2251 |
| Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser Phe Asn Ala Asn Tyr Phe |      |

| 585                                                                                                                                                   | 590 | 595 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| GTG ATT TTT GCG AAT AAC TAT TTT ACC GGG CGC TAT GGG GAT AAT AAA<br>Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly Arg Tyr Gly Asp Asn Lys<br>600 605 610     |     |     | 2299 |
| GAG CCG GTC AAT GCG AGA TCG CAA GGC GTG GAG CTA GAG TTG TAT TAC<br>Glu Pro Val Asn Ala Arg Ser Gln Gly Val Glu Leu Glu Leu Tyr Tyr<br>615 620 625 630 |     |     | 2347 |
| ACG CCG ATT AGA GGG CTT AAT TTC CAT GCG GCT TAC ACT TTC ATA GAT<br>Thr Pro Ile Arg Gly Leu Asn Phe His Ala Ala Tyr Thr Phe Ile Asp<br>635 640 645     |     |     | 2395 |
| GCC AAT ATC ACA AGC CAC ACG ATG GTT ACT AAC CCC GCT AAT CCT AAA<br>Ala Asn Ile Thr Ser His Thr Met Val Thr Asn Pro Ala Asn Pro Lys<br>650 655 660     |     |     | 2443 |
| GGG CCT AAA AAA GAT ATT TTT GGC AAA AAG CTC CCT TTT GTA AGC CCG<br>Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys Leu Pro Phe Val Ser Pro<br>665 670 675     |     |     | 2491 |
| CAC CAA TTC ATT TTA GAC GCG AGC TAC ACT TAC GCT AAA ACC ACG ATT<br>His Gln Phe Ile Leu Asp Ala Ser Tyr Thr Tyr Ala Lys Thr Thr Ile<br>680 685 690     |     |     | 2539 |
| GGG TTG AGT TCT TTC TTT TAT AGC CGA ACT TAT AGC GAT GTG TTA AAC<br>Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr Tyr Ser Asp Val Leu Asn<br>695 700 705 710 |     |     | 2587 |
| ACC GTG CCT TTT ATT CAA TAC GCG CCC ACG ATC AAA AAT GGT GCT ATC<br>Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr Ile Lys Asn Gly Ala Ile<br>715 720 725     |     |     | 2635 |
| ACT ACC AAA ACA GCG GGC ATG ACG CCA TGG TAT TGG GTG TGG AAT TTG<br>Thr Thr Lys Thr Ala Gly Met Thr Pro Trp Tyr Trp Val Trp Asn Leu<br>730 735 740     |     |     | 2683 |
| CAA ATT TCT ACC ACT TTT TGG GAA CGC AAA AAG CAA AGC GTT AAT GCG<br>Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys Lys Gln Ser Val Asn Ala<br>745 750 755     |     |     | 2731 |
| AGC TTG CAA ATC AAT AAC ATT TTT AAC ATG AAA TAT TGG TTT AGC GGG<br>Ser Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Trp Phe Ser Gly<br>760 765 770     |     |     | 2779 |
| ATA GGC ACT AGC CTA ACG GGA AAG AAG CCG CGC CTC CTA GGA GCA TCA<br>Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro Arg Leu Leu Gly Ala Ser<br>775 780 785 790 |     |     | 2827 |
| CAG CGT ATG TGAGCTATCA TTTTAAATTT TAGGGTTGTA ATGTTTGTGAG AAGTTGGGC<br>Gln Arg Met                                                                     |     |     | 2885 |

GTAAA 2890

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 793 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Val | Ile | Thr | Met | Asn | Gly | Tyr | Leu | Arg | Val | Lys | Thr | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Phe | Leu | Ala | Leu | Asn | Ala | Leu | Thr | Phe | Leu | Ser | Phe | Asn | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gly | Ala | Lys | Glu | Gln | His | His | Thr | Leu | Gln | Lys | Val | Thr | Thr | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Gln | Lys | Phe | Asn | Pro | Ser | Ala | Pro | Leu | Ser | Trp | Gln | Ser | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Arg | Asn | Ser | Thr | Ser | Ser | Arg | Thr | Val | Ile | Ser | Asn | Lys | Glu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Lys | Thr | Gly | Asn | Leu | Asn | Ile | Glu | Asn | Ala | Leu | Gln | Asn | Val | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ile | Gln | Ile | Arg | Asp | Ala | Thr | Gly | Thr | Gly | Val | Leu | Pro | Lys | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Val | Arg | Gly | Phe | Gly | Gly | Gly | Gly | Asn | Gly | His | Ser | Asn | Thr | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Met | Ile | Leu | Val | Asn | Gly | Ile | Pro | Ile | Tyr | Gly | Ala | Pro | Tyr | Ser | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Glu | Leu | Ala | Ile | Phe | Pro | Val | Thr | Phe | Gln | Ser | Val | Asp | Arg | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Val | Ile | Lys | Gly | Gly | Thr | Ser | Val | Gln | Tyr | Gly | Pro | Asn | Thr | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Gly | Val | Val | Asn | Ile | Ile | Thr | Lys | Glu | Ile | Pro | Lys | Glu | Trp | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Gln | Ala | Ala | Glu | Arg | Ile | Thr | Phe | Trp | Gly | Arg | Ser | Ser | Asn | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Phe | Val | Asp | Pro | Lys | Glu | Lys | Gly | Lys | Pro | Leu | Ala | Gln | Thr | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Asn | Gln | Met | Leu | Phe | Asn | Thr | Tyr | Gly | Arg | Thr | Ala | Gly | Met | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Lys | His | Val | Gly | Ile | Ser | Ala | Gln | Gly | Asn | Trp | Ile | Asn | Gly | Gln |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Phe | Arg | Gln | Asn | Ser | Pro | Thr | Lys | Val | Gln | Asn | Tyr | Leu | Leu | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Val | Tyr | Lys | Ile | Asn | Ala | Thr | Asn | Thr | Phe | Lys | Ala | Tyr | Tyr | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Tyr | Tyr | Gln | Tyr | Asn | Ser | Tyr | His | Pro | Gly | Thr | Leu | Ser | Ala | Gln | Asp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Ala | Tyr | Asn | Arg | Phe | Ile | Asn | Glu | Arg | Pro | Asp | Asn | Gln | Asp | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Arg | Ala | Lys | Arg | Phe | Gly | Ile | Val | Tyr | Gln | Asn | Tyr | Phe | Gly | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Asp | Arg | Lys | Val | Gly | Gly | Asp | Phe | Lys | Phe | Thr | Tyr | Phe | Thr | His |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asp | Met | Ser | Arg | Asp | Phe | Gly | Phe | Ser | Asn | Gln | Tyr | Gln | Ser | Val | Tyr |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Met | Ser | Ser | Gln | Asn | Lys | Ile | Leu | Pro | Phe | Lys | Gly | Lys | Gly | Lys | Ile |

|                                                                 |                     |                         |     |     |
|-----------------------------------------------------------------|---------------------|-------------------------|-----|-----|
| 370                                                             |                     | 375                     |     | 380 |
| Ser Ala Thr Asn Pro                                             | Asn Cys Gly Leu Tyr | Ser Tyr Ser Asp Thr Asn |     |     |
| 385                                                             | 390                 | 395                     | 400 |     |
| Ser Pro Cys Trp Gln Phe Phe Asp Asn Ile Arg Arg Ser Val Val Asn |                     |                         |     |     |
| 405                                                             | 410                 | 415                     |     |     |
| Ala Phe Glu Pro Lys Leu Asn Leu Ile Val Asn Thr Gly Lys Val Lys |                     |                         |     |     |
| 420                                                             | 425                 | 430                     |     |     |
| Gln Thr Phe Asn Met Gly Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg |                     |                         |     |     |
| 435                                                             | 440                 | 445                     |     |     |
| Arg Ser Thr Thr Arg Lys Asn Pro Ser Met Pro Asn Asn Gly Ser Gly |                     |                         |     |     |
| 450                                                             | 455                 | 460                     |     |     |
| Phe Asp Ala Gly Thr Ser Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val |                     |                         |     |     |
| 465                                                             | 470                 | 475                     | 480 |     |
| Tyr Ala Ser Asp Glu Ile Asn Phe Asn Asn Gly Met Leu Thr Ile Thr |                     |                         |     |     |
| 485                                                             | 490                 | 495                     |     |     |
| Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro |                     |                         |     |     |
| 500                                                             | 505                 | 510                     |     |     |
| Pro Phe Lys Ala Gly Gln Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn |                     |                         |     |     |
| 515                                                             | 520                 | 525                     |     |     |
| Gln Trp Asn Pro Ala Val Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu |                     |                         |     |     |
| 530                                                             | 535                 | 540                     |     |     |
| Leu Phe Tyr Phe Asn Tyr Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser |                     |                         |     |     |
| 545                                                             | 550                 | 555                     | 560 |     |
| Asn Ile Gly Ser Phe Val Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe |                     |                         |     |     |
| 565                                                             | 570                 | 575                     |     |     |
| Asn Val Met Glu Gly Gly Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser |                     |                         |     |     |
| 580                                                             | 585                 | 590                     |     |     |
| Phe Asn Ala Asn Tyr Phe Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly |                     |                         |     |     |
| 595                                                             | 600                 | 605                     |     |     |
| Arg Tyr Gly Asp Asn Lys Glu Pro Val Asn Ala Arg Ser Gln Gly Val |                     |                         |     |     |
| 610                                                             | 615                 | 620                     |     |     |
| Glu Leu Glu Leu Tyr Tyr Thr Pro Ile Arg Gly Leu Asn Phe His Ala |                     |                         |     |     |
| 625                                                             | 630                 | 635                     | 640 |     |
| Ala Tyr Thr Phe Ile Asp Ala Asn Ile Thr Ser His Thr Met Val Thr |                     |                         |     |     |
| 645                                                             | 650                 | 655                     |     |     |
| Asn Pro Ala Asn Pro Lys Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys |                     |                         |     |     |
| 660                                                             | 665                 | 670                     |     |     |
| Leu Pro Phe Val Ser Pro His Gln Phe Ile Leu Asp Ala Ser Tyr Thr |                     |                         |     |     |
| 675                                                             | 680                 | 685                     |     |     |
| Tyr Ala Lys Thr Thr Ile Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr |                     |                         |     |     |
| 690                                                             | 695                 | 700                     |     |     |
| Tyr Ser Asp Val Leu Asn Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr |                     |                         |     |     |
| 705                                                             | 710                 | 715                     | 720 |     |
| Ile Lys Asn Gly Ala Ile Thr Thr Lys Thr Ala Gly Met Thr Pro Trp |                     |                         |     |     |
| 725                                                             | 730                 | 735                     |     |     |
| Tyr Trp Val Trp Asn Leu Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys |                     |                         |     |     |
| 740                                                             | 745                 | 750                     |     |     |
| Lys Gln Ser Val Asn Ala Ser Leu Gln Ile Asn Asn Ile Phe Asn Met |                     |                         |     |     |
| 755                                                             | 760                 | 765                     |     |     |
| Lys Tyr Trp Phe Ser Gly Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro |                     |                         |     |     |
| 770                                                             | 775                 | 780                     |     |     |
| Arg Leu Leu Gly Ala Ser Gln Arg Met                             |                     |                         |     |     |
| 785                                                             | 790                 |                         |     |     |

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...353  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

|                                                                   |         |     |
|-------------------------------------------------------------------|---------|-----|
| TCGTCTTTTG TCGGTTCAAA AAAATCTCTC GACTTAAAAA AACCTATTAA            | ATC AAG | 56  |
|                                                                   | Ile Lys |     |
|                                                                   | 1       |     |
| ATA ATC TAT CAA ATC ATC AAG TTT TTT CGT TCT AAG AAT TTT ATT TTG   |         | 104 |
| Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe Ile Leu   |         |     |
| 5 10 15                                                           |         |     |
| TTT TTT AGA ATA GCA ACG ATA AAG TTC TTC TTT TAT CTC ATT TGG GAA   |         | 152 |
| Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile Trp Glu   |         |     |
| 20 25 30                                                          |         |     |
| TTT TTG AAT GTT ATA GAC AAT TTC ACT ATC TCT TTG ATT TTG TTT ATA   |         | 200 |
| Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu Phe Ile   |         |     |
| 35 40 45 50                                                       |         |     |
| TTT TTT AGC CCC ATA CCA AAG AAA TAT TTG ATA AAA AAT AAG AAA AAT   |         | 248 |
| Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys Lys Asn   |         |     |
| 55 60 65                                                          |         |     |
| AGC GTA AAA GAA AAA GAA AAT AAA GAA AAA AGA AAG AGA AAA AGA AAG   |         | 296 |
| Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys Arg Lys   |         |     |
| 70 75 80                                                          |         |     |
| GAT TTT GTT TTG GGT GTA TTG GAA AAT AGA CTC AAA AAT CAA TTG AAA   |         | 344 |
| Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln Leu Lys   |         |     |
| 85 90 95                                                          |         |     |
| AAC CCC TTT TAGATTAAAA ATAAAAACAA TAAGCGAAAC GACAAAAGCA AGCAGAAAA |         | 402 |
| Asn Pro Phe                                                       |         |     |
| 100                                                               |         |     |
| GAAG                                                              |         | 406 |

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Ile Lys Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe  
1 5 10 15  
Ile Leu Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile  
20 25 30  
Trp Glu Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu  
35 40 45  
Phe Ile Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys  
50 55 60  
Lys Asn Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys  
65 70 75 80  
Arg Lys Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln  
85 90 95  
Leu Lys Asn Pro Phe  
100

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 89...1087
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GATTTTGTGA AAAATAGTTT CATTTTACT GCTTGATTTT CCTTAATGGT GTTATAATCG 60  
CTCCATAAAT CATACAAAAA GGATCGTT ATG TTA GTT ACT CGC TTT AAA AAA 112  
Met Leu Val Thr Arg Phe Lys Lys  
1 5  
GCT TTA ATC TCT TAT TCT TTA GGC GCG CTT CTT GTT TCA TCG TTA TTG 160  
Ala Leu Ile Ser Tyr Ser Leu Gly Ala Leu Leu Val Ser Ser Leu Leu  
10 15 20  
GGC GTG GCT AGT GCT TCC AAT CAA GAA ATC CAA GTC AAA GAT TAT TTT 208  
Gly Val Ala Ser Ala Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe  
25 30 35 40  
GGG GAT CAA GCC ATC AAG CTT CCT GTT TCT AAA ATA ATC TAC TTG GGT 256  
Gly Asp Gln Ala Ile Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly  
45 50 55  
AGC TTT GCA GAA GTG CCT GCT ATG TTC CAT ACT TGG GAT AGG GTC GTG 304  
Ser Phe Ala Glu Val Pro Ala Met Phe His Thr Trp Asp Arg Val Val  
60 65 70  
GGA ATT TCG GAT TAC GCT TTT AAA TCT GAT ATT GTT AAA GCT ACT CTC 352  
Gly Ile Ser Asp Tyr Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu



| 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| AAA | GAT | CCT | AAA | CGC | ATT | AAA | TCC | ATG | AGC | AGT | GAT | CAT | GTG | GCG | GCG | 400  |
| Lys | Asp | Pro | Lys | Arg | Ile | Lys | Ser | Met | Ser | Ser | Asp | His | Val | Ala | Ala |      |
| 90  |     |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     |      |
| TTG | AAT | GTG | GAG | CTT | TTA | AAA | AAG | CTT | GGC | CCC | GAT | CTT | GTG | GTA | ACC | 448  |
| Leu | Asn | Val | Glu | Leu | Leu | Lys | Lys | Leu | Gly | Pro | Asp | Leu | Val | Val | Thr |      |
| 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |      |
| TTT | GTG | GGC | AAC | CCT | AAA | GCG | GTA | GAG | CAT | GCG | AAA | AAA | TTT | GGT | ATA | 496  |
| Phe | Val | Gly | Asn | Pro | Lys | Ala | Val | Glu | His | Ala | Lys | Lys | Phe | Gly | Ile |      |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |      |
| TTA | TTT | CTT | TCT | TTC | CAA | GAA | AAA | ACC | ATT | GCA | GAA | GTC | ATG | GAA | GAT | 544  |
| Leu | Phe | Leu | Ser | Phe | Gln | Glu | Lys | Thr | Ile | Ala | Glu | Val | Met | Glu | Asp |      |
|     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |      |
| ATT | GAC | GCT | CAA | GCT | AAA | GCC | TTA | GAA | ATT | GAT | GCT | TCT | AAA | AAA | CTG | 592  |
| Ile | Asp | Ala | Gln | Ala | Lys | Ala | Leu | Glu | Ile | Asp | Ala | Ser | Lys | Lys | Leu |      |
|     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |      |
| GCC | AAA | ATG | CAA | GAA | ACT | TTG | GAT | TTT | ATT | GCT | GAG | CGT | TTG | AAA | GGT | 640  |
| Ala | Lys | Met | Gln | Glu | Thr | Leu | Asp | Phe | Ile | Ala | Glu | Arg | Leu | Lys | Gly |      |
| 170 |     |     |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     |      |
| GTC | AAA | AAG | AAA | AAA | GGG | GTG | GAG | CTT | TTC | CAT | AAG | GCC | AAT | AAG | ATC | 688  |
| Val | Lys | Lys | Lys | Lys | Gly | Val | Glu | Leu | Phe | His | Lys | Ala | Asn | Lys | Ile |      |
| 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |      |
| AGC | GGC | CAT | CAA | GCC | CTT | GAT | TCA | GAC | ATT | TTA | GAA | AAA | GGA | GGC | ATA | 736  |
| Ser | Gly | His | Gln | Ala | Leu | Asp | Ser | Asp | Ile | Leu | Glu | Lys | Gly | Gly | Ile |      |
|     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |      |
| GAC | AAT | TTT | GGC | TTG | AAA | TAT | GTC | AAA | TTT | GGG | CGT | GCT | GAC | ATT | AGC | 784  |
| Asp | Asn | Phe | Gly | Leu | Lys | Tyr | Val | Lys | Phe | Gly | Arg | Ala | Asp | Ile | Ser |      |
|     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |      |
| GTG | GAA | AAA | ATC | GTT | AAA | GAA | AAC | CCT | GAG | ATT | ATC | TTT | ATT | TGG | TGG | 832  |
| Val | Glu | Lys | Ile | Val | Lys | Glu | Asn | Pro | Glu | Ile | Ile | Phe | Ile | Trp | Trp |      |
|     |     | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |      |
| ATA | AGC | CCA | CTC | ACG | CCT | GAA | GAT | GTG | TTA | AAC | AAC | CCC | AAA | TTT | GCT | 880  |
| Ile | Ser | Pro | Leu | Thr | Pro | Glu | Asp | Val | Leu | Asn | Asn | Pro | Lys | Phe | Ala |      |
|     | 250 |     |     |     |     | 255 |     |     |     |     | 260 |     |     |     |     |      |
| ACC | ATC | AAA | GCC | ATT | AAA | AAC | AAG | CAG | GTT | TAT | AAA | CTC | CCC | ACA | ATG | 928  |
| Thr | Ile | Lys | Ala | Ile | Lys | Asn | Lys | Gln | Val | Tyr | Lys | Leu | Pro | Thr | Met |      |
| 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     |     | 280 |      |
| GAT | ATT | GGC | GGG | CCT | AGA | GCC | CCA | CTC | ATA | AGT | CTT | TTT | ATC | GCT | CTA | 976  |
| Asp | Ile | Gly | Gly | Pro | Arg | Ala | Pro | Leu | Ile | Ser | Leu | Phe | Ile | Ala | Leu |      |
|     |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |      |
| AAA | GCC | CAC | CCT | GAA | GCC | TTT | AAG | GGC | GTG | GAT | ATT | AAT | GCG | ATT | GTT | 1024 |
| Lys | Ala | His | Pro | Glu | Ala | Phe | Lys | Gly | Val | Asp | Ile | Asn | Ala | Ile | Val |      |
|     |     |     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |     |     |      |



275                      280                      285  
 Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys  
 290                      295                      300  
 Gly Val Asp Ile Asn Ala Ile Val Lys Asp Tyr Tyr Lys Val Val Phe  
 305                      310                      315                      320  
 Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His  
 325                      330

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...845
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

|                                                                            |         |     |
|----------------------------------------------------------------------------|---------|-----|
| GGGGGGTTAT AGTAAAAACA TGCAAGTAAT TTAAAGTTAA TTTAAGATAA                     | TTA GGC | 56  |
|                                                                            | Leu Gly |     |
|                                                                            | 1       |     |
| ACA ATA GCC ACA AAA AGT TTA AGG CTG TAT TTG AAA ACT CTA TTT AGT            |         | 104 |
| Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu Phe Ser            |         |     |
| 5                      10                      15                          |         |     |
| ATT TAT CTC TTT TTA TCG TTG AAC CCA CTC TTT TTA GAA GCT AAT GAA            |         | 152 |
| Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala Asn Glu            |         |     |
| 20                      25                      30                         |         |     |
| ATC ACT TGG TCT AAA TTC TTG GAA AAT TTT AAA AAC AAG AAT GAT GAT            |         | 200 |
| Ile Thr Trp Ser Lys Phe Leu Glu Asn Phe Lys Asn Lys Asn Asp Asp            |         |     |
| 35                      40                      45                      50 |         |     |
| GAC AAA CCT AAA CCC CTA ACT ATT GAT AAA AAC AAT GAA AAA CAG CAA            |         | 248 |
| Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys Gln Gln            |         |     |
| 55                      60                      65                         |         |     |
| ATC TTA GAC AAA AAC CAG CAA ATC TTA AAA AGG GCT TTG GAA AAA AGC            |         | 296 |
| Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu Lys Ser            |         |     |
| 70                      75                      80                         |         |     |
| CTT AAA TTC TTT TTC ATT TTT GGA TAC AAC TAT TCG CAA GCC ACT TTT            |         | 344 |
| Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala Thr Phe            |         |     |
| 85                      90                      95                         |         |     |
| TCA ACT TCT AAC CAA ACC TTG ACT TTT GTA GCC AAT AGC ATA GGG TTT            |         | 392 |
| Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile Gly Phe            |         |     |
| 100                      105                      110                      |         |     |

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAC ACC GCT ACC GGT TTA GAG CAT TTT TTA AGA AAC CAC CCT AAA GTC  | 440 |
| Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro Lys Val  |     |
| 115 120 125 130                                                  |     |
| GGT TTT AGA ATC TTT AGC GTC TAT AAC TAT TTC CAT TCT GTT TCC CTC  | 488 |
| Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val Ser Leu  |     |
| 135 140 145                                                      |     |
| TCC CAG CCT CAA ACC TTA ATG GTG CAA AAT TAT GGG GGC GCG TTA GAT  | 536 |
| Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala Leu Asp  |     |
| 150 155 160                                                      |     |
| TTT TCT TGG ATT TTT GTA GAT AAA AAT ATT TAT CGC TTT AGG AGT TAT  | 584 |
| Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg Ser Tyr  |     |
| 165 170 175                                                      |     |
| TTA GGG ATC GCT TTA GAA CAA GGG GTG TTG TTA GTG GAT ACG ATT AAA  | 632 |
| Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr Ile Lys  |     |
| 180 185 190                                                      |     |
| CCA GGT GCT ATC ACA ACG ATT ATC CCA AGA ACC AAA AAA ACC TTT TTT  | 680 |
| Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr Phe Phe  |     |
| 195 200 205 210                                                  |     |
| CAA GCC CCT TTG CGT TTT GGT TTT ATC GTG GAT TTT ATC GGC TAT TTG  | 728 |
| Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly Tyr Leu  |     |
| 215 220 225                                                      |     |
| TCT TTG CAA TTA GGG ATT GAA ATG CCT TTA GTG AGG AAT GTT TTT TAC  | 776 |
| Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val Phe Tyr  |     |
| 230 235 240                                                      |     |
| ACC TAC AAC AAC CAT CAA GAA AGA TTC AAA CCA CGA TTT AAC GCT AAT  | 824 |
| Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn Ala Asn  |     |
| 245 250 255                                                      |     |
| CTT TCT TTA ATC GTT TCG TTT TAGCCCCCT TTTCCCCTTT TAAATAAGCC CATG | 879 |
| Leu Ser Leu Ile Val Ser Phe                                      |     |
| 260 265                                                          |     |
| ATTTTCCTAG GGTATTTTA                                             | 898 |

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

|                                                                 |
|-----------------------------------------------------------------|
| Leu Gly Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu |
| 1 5 10 15                                                       |
| Phe Ser Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Glu | Ile | Thr | Trp | Ser | Lys | Phe | Leu | Glu | Asn | Phe | Lys | Asn | Lys | Asn |
| 35  |     |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Asp | Asp | Lys | Pro | Lys | Pro | Leu | Thr | Ile | Asp | Lys | Asn | Asn | Glu | Lys |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gln | Ile | Leu | Asp | Lys | Asn | Gln | Gln | Ile | Leu | Lys | Arg | Ala | Leu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ser | Leu | Lys | Phe | Phe | Phe | Ile | Phe | Gly | Tyr | Asn | Tyr | Ser | Gln | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Ser | Thr | Ser | Asn | Gln | Thr | Leu | Thr | Phe | Val | Ala | Asn | Ser | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Phe | Asn | Thr | Ala | Thr | Gly | Leu | Glu | His | Phe | Leu | Arg | Asn | His | Pro |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Val | Gly | Phe | Arg | Ile | Phe | Ser | Val | Tyr | Asn | Tyr | Phe | His | Ser | Val |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Leu | Ser | Gln | Pro | Gln | Thr | Leu | Met | Val | Gln | Asn | Tyr | Gly | Gly | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Asp | Phe | Ser | Trp | Ile | Phe | Val | Asp | Lys | Asn | Ile | Tyr | Arg | Phe | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Tyr | Leu | Gly | Ile | Ala | Leu | Glu | Gln | Gly | Val | Leu | Leu | Val | Asp | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Lys | Pro | Gly | Ala | Ile | Thr | Thr | Ile | Ile | Pro | Arg | Thr | Lys | Lys | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Phe | Gln | Ala | Pro | Leu | Arg | Phe | Gly | Phe | Ile | Val | Asp | Phe | Ile | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Leu | Ser | Leu | Gln | Leu | Gly | Ile | Glu | Met | Pro | Leu | Val | Arg | Asn | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Tyr | Thr | Tyr | Asn | Asn | His | Gln | Glu | Arg | Phe | Lys | Pro | Arg | Phe | Asn |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Asn | Leu | Ser | Leu | Ile | Val | Ser | Phe |     |     |     |     |     |     |     |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...689
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

|                                                                 |            |            |            |            |         |     |
|-----------------------------------------------------------------|------------|------------|------------|------------|---------|-----|
| GCACTTCACG                                                      | CATTCCATAA | ACGATATTGA | TTATTTGCTA | GACAGCTTGA | AAA AAG | 56  |
|                                                                 |            |            |            |            | Lys Lys |     |
|                                                                 |            |            |            |            | 1       |     |
| CAG TTA AAA AAT TGC GTT AAG CTA AAA CTA TTT TTA AGG AAA AAT TTG |            |            |            |            |         | 104 |
| Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys Asn Leu |            |            |            |            |         |     |
| 5                                                               |            | 10         |            | 15         |         |     |

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GAT ATT TTA GAT TTG AAC AAA GCG CAA GCG GTG CAA CAA AAT GAA CAA<br>Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn Glu Gln<br>20 25 30        | 152 |
| GAG GTA GAG GAT AAA GAG CGA GAG TCT AAA GAG CCG GTG GTT TTA GAA<br>Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val Leu Glu<br>35 40 45 50     | 200 |
| GAT TTG AGC GCT TTA GCG TGG CTT GAA TTA GAA GAG TTT AGC CGC CTT<br>Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser Arg Leu<br>55 60 65        | 248 |
| TCA GGG CTT CCT AAA GAA AGG ATT TTG GAA TTA GTG AAT CTT GGT AAA<br>Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu Gly Lys<br>70 75 80        | 296 |
| ATC AAG AGC AAA ATA AGC AGC AAC AAG CTT TTA ATT GAT GCG AGC AGC<br>Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala Ser Ser<br>85 90 95        | 344 |
| GGG ACA AAC GCT TTA ATC AAA AAG GTA GAA AAT AGT TTG ATT TCT ATG<br>Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile Ser Met<br>100 105 110     | 392 |
| GAT ATG AAC GGG CGT TCT TTA GAA CCT GTG TTT GTG GAA AAG ACC ATT<br>Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys Thr Ile<br>115 120 125 130 | 440 |
| AAC ACG ATT TTA AAC TTG CAT GAT AAG GTC ATT GGC GCT AAA GAT GAA<br>Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys Asp Glu<br>135 140 145     | 488 |
| ACG ATT TCA GCC TTT AAA AAT GAA AAC ATG TTT TTA AAA GAC GCT TTA<br>Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp Ala Leu<br>150 155 160     | 536 |
| ATC TCT ATG CAA GAA GTC TAT GAA GAA GAT AAA AAA ACC ATT GAT CTT<br>Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile Asp Leu<br>165 170 175     | 584 |
| TTG CGC GAT GAA CTC AAT CAA GCG AGA GAA GAA ATT GAA TTT ATG AAG<br>Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe Met Lys<br>180 185 190     | 632 |
| AGG AAA TAC CGC TTG ATG TGG GGG AAA GTC GCT GAC ATG AGC AGC GTG<br>Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser Ser Val<br>195 200 205 210 | 680 |
| AAT AAA AAG TAGTTTAA TTAACGCCCA TGCTGAGGGC TTATTAGCGG TAATTTTAG<br>Asn Lys Lys                                                                        | 738 |
| GTGA                                                                                                                                                  | 742 |

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Gln | Leu | Lys | Asn | Cys | Val | Lys | Leu | Lys | Leu | Phe | Leu | Arg | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Leu | Asp | Ile | Leu | Asp | Leu | Asn | Lys | Ala | Gln | Ala | Val | Gln | Gln | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gln | Glu | Val | Glu | Asp | Lys | Glu | Arg | Glu | Ser | Lys | Glu | Pro | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | Asp | Leu | Ser | Ala | Leu | Ala | Trp | Leu | Glu | Leu | Glu | Glu | Phe | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Leu | Ser | Gly | Leu | Pro | Lys | Glu | Arg | Ile | Leu | Glu | Leu | Val | Asn | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Lys | Ile | Lys | Ser | Lys | Ile | Ser | Ser | Asn | Lys | Leu | Leu | Ile | Asp | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Gly | Thr | Asn | Ala | Leu | Ile | Lys | Lys | Val | Glu | Asn | Ser | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Met | Asp | Met | Asn | Gly | Arg | Ser | Leu | Glu | Pro | Val | Phe | Val | Glu | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ile | Asn | Thr | Ile | Leu | Asn | Leu | His | Asp | Lys | Val | Ile | Gly | Ala | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Glu | Thr | Ile | Ser | Ala | Phe | Lys | Asn | Glu | Asn | Met | Phe | Leu | Lys | Asp |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Leu | Ile | Ser | Met | Gln | Glu | Val | Tyr | Glu | Glu | Asp | Lys | Lys | Thr | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Leu | Leu | Arg | Asp | Glu | Leu | Asn | Gln | Ala | Arg | Glu | Glu | Ile | Glu | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Lys | Arg | Lys | Tyr | Arg | Leu | Met | Trp | Gly | Lys | Val | Ala | Asp | Met | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Val | Asn | Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 210 |